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(54) Title: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of lung cancer and similar pathologies. Also described herein are methods that can be used to identify modulators of lung cancer and similar pathologies.



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METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

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CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to USSN 60/284,770, filed April 18, 2001; USSN 60/290,492, filed May 10, 2001; USSN 60/334,370, filed November 29, 2001; USSN 60/339,245, filed November 9, 2001; USSN 60/350,666, filed November 13, 2001; and
10 USSN 60/xxx,xxx, filed April 12, 2002 (Docket OMNI-002P); each of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression
15 profiles and nucleic acids, products, and antibodies thereto that are involved in lung cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of lung cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit lung cancer or related conditions.

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BACKGROUND OF THE INVENTION

Lung cancer is the second most commonly occurring cancer in the United States and is the leading cause of cancer-related death. It is estimated that there are over 160,000 new cases of lung cancer in the United States every year. Of those who are diagnosed with lung cancer, 86 percent will die within five years. Lung cancer is the most common visceral
25 cancer in men and accounts for nearly one third of all cancer deaths in both men and women. In fact, lung cancer accounts for 7% of all deaths, due to any cause, in both men and women.

Smoking is the primary cause of lung cancer, with more than 80% of lung cancers resulting from smoking. About 400 to 500 separate gaseous substances are present in the smoke of a non-filter cigarette. The most noteworthy substances include nitrogen oxides,
30 hydrogen cyanide, formaldehyde, benzene, and toluene. The particles present in cigarette smoke contain at least 3,500 individual compounds such as nicotine, tobacco alkaloids (nornicotine, anatabine, anabasine), polycyclic aromatic hydrocarbons (e.g., benzo(a)pyrene, B(a)P), naphthalenes, aromatic amines, phenols, and tobacco-specific nitrosamines.

Tobacco-specific nitrosamines are formed during tobacco curing and processing, and are suspected of causing lung cancer in humans. In rodent studies, regardless of the where or how it is applied, the tobacco-specific nitrosamine known as NNK produces lung adenomas and lung adenocarcinomas. The tobacco-specific nitrosamine known as NNAL also produces lung adenocarcinomas in rodents.

Many of the chemicals found in cigarette smoke also affect the nonsmoker inhaling "secondhand" or sidestream smoke. Indeed, the smoke inhaled by non-smokers has a chemical composition similar to the smoke inhaled by smokers, but, importantly, the concentrations of the carcinogenic tobacco-specific nitrosamines are present in higher concentrations in second hand smoke. For this and other reasons, "passive smoking" is an important cause of lung cancer, causing as many as 3,000 lung cancer deaths in nonsmokers each year.

In addition to smoking, other factors thought to be causes of lung cancer include on-the-job exposure to carcinogens such as asbestos and uranium, exposure to chemical hazards such as radon, polycyclic aromatic hydrocarbons, chromium, nickel, and inorganic arsenic, genetic factors, and diet.

Histological classification of various lung cancers define the types of cancer that begin in the lung. See, e.g., Travis, et al. (1999) Histological Typing of Lung and Pleural Tumours (International Histological Classification of Tumours, No 1. Four major cell types make up more than 88% of all primary lung neoplasms. These are: squamous or epidermoid carcinoma, small cell (also called oat cell) carcinoma, adenocarcinoma, and large cell (also called large cell anaplastic) carcinoma. The remainder include undifferentiated carcinomas, carcinoids, bronchial gland tumors, and other rarer types. The various cell types have different natural histories and responses to therapy, and, thus, a correct histologic diagnosis is the first step of effective treatment.

Small cell lung cancer (SCLC) accounts for 18-25% of all lung cancers, and occurs less frequently than non-small cell lung cancers, and generally spread to distant organs more rapidly than non-small cell lung cancer. In general, at the time of presentation small cell lung cancers have already spread beyond the bounds where surgery and curative intent can be undertaken. However, if identified early enough, these cancers are often responsive to chemotherapy and thoracic radiation treatment.

Non-small cell lung cancers (NSCLC) are the more frequently occurring form of lung cancer. They comprise squamous cell carcinoma, adenocarcinoma, and large cell carcinoma

5 The screening of asymptomatic persons at high risk for lung cancer has often proven ineffective. In general, only 5 to 15 percent of lung cancer patients have their disease detected while they are asymptomatic. Of course, early detection and treatment are critical factors in the fight against lung cancer. The average survival rate is 49% for those whose cancer is detected early, before the cancer has spread from the lung. Lung cancer often
10 spreads outside of the lung, and it may have spread to the bones or brain by the time it is diagnosed. While the prognosis may be better for lung cancers that are detected early, because of the lack of effective curative treatments, early detection does not necessarily alter the total death rate from lung cancer.

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bronchiectasis. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. Alternatively, the sample may be contacted with a specific binding reagent, e.g., antibody.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1A-16.

In one embodiment, the biological sample is a tissue sample, or a body fluid. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label. In one embodiment, the polynucleotide is immobilized on a solid surface. In one embodiment, the patient is undergoing a therapeutic regimen to treat lung cancer. In another embodiment, the patient is suspected of having lung cancer. In one embodiment, the patient is a primate, e.g., a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. Or the sample may be evaluated for protein, e.g., contacting the sample with an antibody.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. Or the sample may be evaluated for comparison of protein.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a

biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16. In one embodiment, an expression vector or cell comprises the isolated nucleic acid. In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical. In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting lung cancer in a patient, the method comprising contacting a biological sample from the patient with an antibody or protein as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to a lung cancer gene in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

5 In another aspect, the present invention provides a method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and (ii) determining the functional effect of the
10 compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect. In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant. In one
15 embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation or another critical process of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein. In one embodiment, the compound is an
20 antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables
25 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

In one embodiment, the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal
30 cell or mammal, or a non-malignant lung disease.

In another aspect, the present invention provides a method for treating a mammal having lung cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of lung disease or cancer, as well as methods for screening for compositions which modulate lung cancer. "Treatment, monitoring, detection or modulation of lung disease or cancer" includes treatment, monitoring, detection, or modulation of lung disease in those patients who have lung disease (whether malignant or non-malignant, e.g., emphysema, bronchitis, or fibrosis) as well as patients with lung cancers in which gene expression from a gene in Tables 1A-16 is increased or decreased, indicating that the subject is more likely to have disease. In particular, while these targets are identified primarily from lung cancer samples, these same targets are likely to be similarly found in analyses of other medical conditions. These other conditions may result from similar pathological processes which affect similar tissues, e.g., lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), interstitial pneumonitis, nonspecific idiopathic pneumonitis (NSIP)), chronic obstructive pulmonary disease (COPD, e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, and esophageal cancer. See, e.g., the NCI webpage and USSN 60/347,349 and USSN 60/xxx,xxx (docket LFBR-001-1P, filed March 29, 2002), each of which is incorporated herein by reference. The treatment may be of lung cancer or related condition itself, or treatment of metastasis.

In particular, identification of markers selectively expressed on these cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of lung diseases, which subsets may actually require

very different treatments. Moreover, the markers may also be important in related diseases to the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 1A-16 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in lung cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster. In Table 1A, genes marked as "target 1" or "target 2" are particularly useful as therapeutic targets. Genes marked as "target 3" are particularly useful as diagnostic markers. Genes marked as "chron" are upregulated in chronically diseased lung (e.g., emphysema, bronchitis, fibrosis) relative to lung tumors and normal tissue. In certain analyses, the ratio for the "chron" category was determined using the 70th percentile of chronically diseased lung samples divided by the 90th percentile of normal lung samples. The ratio for the targets was determined using the 70th percentile of lung tumor samples divided by the 90th percentile of normal lung samples.

Definitions

The term "lung cancer protein" or "lung cancer polynucleotide" or "lung cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-16 and conservatively modified variants thereof; or (4)

have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence

5 encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "lung cancer polypeptide" and a "lung cancer polynucleotide," include both naturally occurring or recombinant forms.

10 A "full length" lung cancer protein or nucleic acid refers to a lung cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains the elements normally contained in one or more naturally occurring, wild type lung cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

15 "Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a lung cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, 20 archival materials, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; 25 fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the 30 methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the

same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

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Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between

two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified.

In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of

conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3rd ed.) and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghui and Cook, eds. Carbohydrate Modifications in Antisense Research, ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary

strand; thus the sequences described herein also provide the complement of the sequence.

The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine

5 hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic
10 acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins
15 or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. Many methods known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry
20 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth., 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody.
25 The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either
30 covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method

using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered

recombinant for the purposes of the invention. Similarly, a “recombinant protein” is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term “heterologous” when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A “promoter” is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A “constitutive” promoter is a promoter that is active under most environmental and developmental conditions. An “inducible” promoter is a promoter that is active under environmental or developmental regulation. The term “operably linked” refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An “expression vector” is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase “selectively (or specifically) hybridizes to” refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32° C and 48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90° C - 95° C for 0.5 - 2 min., an annealing phase lasting 0.5 - 2 min., and an extension phase of about 72° C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al.(1990) PCR Protocols, A Guide to Methods and Applications.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This

occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., Ausubel, et al. (ed.) Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a lung cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the lung cancer protein or nucleic acid, e.g., a physiological, enzymatic, functional, physical, or chemical effect, such as the ability to decrease lung cancer. It includes ligand binding activity; cell viability, cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of lung cancer cells. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a lung cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the lung cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on lung cancer can also be performed using lung cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein

expression in cells undergoing metastasis, and other characteristics of lung cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for lung cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of lung cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of lung cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of lung cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein.

"Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate lung cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of lung cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the lung cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of lung cancer can also be identified by incubating lung cancer cells with the test compound and determining increases or decreases in the expression of 1 or more lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more lung cancer proteins, such as lung cancer proteins encoded by the sequences set out in Tables 1A-16.

Samples or assays comprising lung cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a lung cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more

preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney (1994) Culture of Animal Cells a Manual of Basic Technique pp. 231-241 (3rd ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells, or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, Fundamental Immunology.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible

for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H - C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.)). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985), pp. 77-96 in Monoclonal Antibodies and Cancer Therapy; Coligan (1991 and supplements) Current Protocols in Immunology; Harlow and Lane (1988) Antibodies, A Laboratory Manual; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783).

A "chimeric antibody" is an antibody molecule in which, e.g., (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the

variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of lung cancer-associated sequences

5 In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is
10 characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.
15 Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of lung cancer (chronic disease, adenocarcinoma, etc.)

The identification of sequences that are differentially expressed in lung cancer versus non-lung cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-
20 regulate lung cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine
25 the stage of lung cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the lung cancer expression profile. This may be done by making biochips comprising sets of the important lung cancer genes,
30 which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the lung cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the lung cancer

nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

5 Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in lung cancer relative to normal tissues and/or non-malignant lung disease, or in different types of lung disease, herein termed "lung cancer sequences." As outlined below, lung cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the lung cancer sequences are from humans; 10 however, as will be appreciated by those in the art, lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Lung cancer sequences from other organisms may be 15 obtained using the techniques outlined below.

Lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, 20 which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the lung cancer sequences can be generated.

A lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the lung cancer sequences outlined herein. Such 25 homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying lung cancer-associated sequences, the lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, 30 cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing lung cancer samples with metastatic cancer samples from other cancers, such as, breast, other gastrointestinal cancers, prostate, ovarian,

etc. Samples of, non metastatic disease tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal lung, but also including, and not limited to colon, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the lung cancer screen that are expressed in significant amounts in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensable at a later stage of life). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs.

In a preferred embodiment, lung cancer sequences are those that are up-regulated in lung cancer; that is, the expression of these genes is higher in cancerous tissue than in normal lung or other tissue. "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al (1998) *Nucleic Acids Research* 26:1-7 and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev (2000) *Genome Res.* 10:516-522). In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, lung cancer sequences are those that are down-regulated in the lung cancer; that is, the expression of these genes is lower in cancerous tissue

or normal lung or other tissue. "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

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Informatics

The ability to identify genes that are over or under expressed in lung cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with lung cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

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Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

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The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing lung cancer, i.e., the identification of lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with

pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S.

Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene

sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-

dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics; Durbin, et al. (eds., 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids (; Baxeavanis and Oeullette (eds., 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins); Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology; Misener and Krawetz (eds, 2000) Bioinformatics: Methods and Protocols; Higgins and Taylor (eds., 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical

Approach; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet; Han and Kamber (2000) Data Mining: Concepts and Techniques (2000); and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes.

5 The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

10 In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample
15 source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU
20 data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern
25 encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in
30 or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may

be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux,
5 SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices
10 linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

15 The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

20 In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results.

25 Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary
30 memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC,

WO 02/086443 PCT/US02/12476
MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain
molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a
data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM,
SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can
5 be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal
adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O
device.

The invention also preferably provides the use of a computer system, such as that
described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a
10 collection of peptide sequence specificity records obtained by the methods of the invention,
which may be stored in the computer; (3) a comparison target, such as a query target; and (4)
a program for alignment and comparison, typically with rank-ordering of comparison results
on the basis of computed similarity values.

15 **Characteristics of lung cancer-associated proteins**

Lung cancer proteins of the present invention may be classified as secreted proteins,
transmembrane proteins or intracellular proteins. In one embodiment, the lung cancer protein
is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the
nucleus. Intracellular proteins are involved in all aspects of cellular function and replication
20 (including, e.g., signaling pathways); aberrant expression of such proteins often results in
unregulated or dysregulated cellular processes (see, e.g., Alberts (ed. 1994) Molecular
Biology of the Cell (3d ed.)). For example, many intracellular proteins have enzymatic
activity such as protein kinase activity, protein phosphatase activity, protease activity,
nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve
25 as docking proteins that are involved in organizing complexes of proteins, or targeting
proteins to various subcellular localizations, and are involved in maintaining the structural
integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the
proteins of one or more structural motifs for which defined functions have been attributed. In
30 addition to the highly conserved sequences found in the enzymatic domain of proteins, highly
conserved sequences have been identified in proteins that are involved in protein-protein
interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated
targets in a sequence dependent manner. PTB domains, which are distinct from SH2

domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (see, e.g., Bateman, et al (2000) *Nuc. Acids Res.* 28:263-266; Sonnhammer, et al. (1997) *Proteins* 28:405-420; Bateman, et al. (1999) *Nuc. Acids Res.* 27:260-262; and Sonnhammer, et al. (1998) *Nuc. Acids Res.* 26:320-322).

In another embodiment, the lung cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the

localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ* or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeabilized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit

signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of lung cancer nucleic acids

As described above, lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the lung cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant lung cancer nucleic acid can be further-used as a probe to identify and isolate

other lung cancer nucleic acids, e.g., extended coding regions. It can also be used as a “precursor” nucleic acid to make modified or variant lung cancer nucleic acids and proteins.

The lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, RNAi, vaccine, and/or antisense applications. Alternatively, the lung cancer nucleic acids that include coding regions of lung cancer proteins can be put into expression vectors for the expression of lung cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to lung cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the lung cancer nucleic acids, i.e., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by “substantially complementary” herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often the substrate may contain discrete individual sites appropriate for individual partitioning and identification. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in US application entitled Reusable Low Fluorescent Plastic Biochip, U.S.

Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of lung cancer-associated sequences. These assays are typically performed in conjunction with

reverse transcription. In such assays, a lung cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of lung cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560, Landegren, et al. (1988) Science 241:1077, and Barringer, et al. (1990) Gene 89:117), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874), dot PCR, and linker adapter PCR, etc.

Expression of lung cancer proteins from nucleic acids

In a preferred embodiment, lung cancer nucleic acids, e.g., encoding lung cancer proteins, are used to make a variety of expression vectors to express lung cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, *supra*, and Fernandez and Hoeffler (eds 1999) Gene Expression Systems) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the lung cancer protein. The term "control sequences" refers to DNA

sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

5 Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding
10 sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction
15 sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

 In general, transcriptional and translational regulatory sequences may include, but are
20 not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

 Promoter sequences may be either constitutive or inducible promoters. The promoters
25 may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

 In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two
30 organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating

vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez and Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable
5 marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The lung cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a lung cancer protein, under the appropriate conditions to induce or cause expression of the lung
10 cancer protein. Conditions appropriate for lung cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate
15 growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae*
20 and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the lung cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and
25 adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and
30 polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, lung cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the lung cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, lung cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, lung cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*,

Kluyveromyces fragilis and *K. lactis*, *Pichia guilliermondii*, and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The lung cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the lung cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the lung cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the lung cancer protein is a lung cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the lung cancer protein is purified or isolated after expression. Lung cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the lung cancer protein may be purified using a standard anti-lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification. The degree of purification necessary will vary depending on the use of the lung cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of lung cancer proteins

In one embodiment, the lung cancer proteins are derivative or variant lung cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative lung cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the lung cancer peptide.

Also included within one embodiment of lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three

classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the lung cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above.

5 However, variant lung cancer protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the lung cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as the naturally occurring analogue,
10 although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be
15 conducted at the target codon or region and the expressed lung cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of lung cancer protein activities.

20 Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions generally range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive
25 at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

30 Variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of lung cancer proteins as needed. Alternatively, the

variant may be designed or reorganized such that a biological activity of the lung cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Covalent modifications of lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid
5 residues of a lung cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking lung cancer polypeptides to a water-insoluble support matrix or surface for use in a method for purifying anti-lung cancer polypeptide antibodies or screening assays, as is more fully
10 described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

15 Other modifications include deamidation of glutamyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl or tyrosyl residues, methylation of the γ -amino groups of lysine, arginine, and histidine side chains (Creighton (1983) Proteins: Structure and Molecular Properties, pp. 79-86), acetylation of the N-terminal
20 amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence lung cancer polypeptide. Glycosylation patterns
25 can be altered in many ways. For example the use of different cell types to express lung cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence
30 lung cancer polypeptide (for O-linked glycosylation sites). The lung cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the lung cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the lung cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin and Wriston (1981) CRC Crit. Rev. Biochem., pp. 259-306.

5 Removal of carbohydrate moieties present on the lung cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al. (1987) Arch. Biochem. Biophys., 259:52 and by Edge, et al. (1981) Anal. Biochem., 118:131.

10 Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, et al. (1987) Meth. Enzymol., 138:350.

Another type of covalent modification of lung cancer comprises linking the lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent
15 Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

Lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a lung cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric
20 molecule comprises a fusion of a lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the lung cancer polypeptide. The presence of such epitope-tagged forms of a lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the lung
25 cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a lung cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

30 Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies

thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other lung cancer proteins of the lung cancer family, and lung cancer proteins from other organisms, which are cloned and expressed as outlined below.

Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, *supra*).

Antibodies to lung cancer proteins

In a preferred embodiment, when a lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller lung cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, *supra*; and Harlow and Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1A-16 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding (1986) Monoclonal Antibodies: Principles and Practice, pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovin, or primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to lung cancer protein are capable of reducing or eliminating a biological function of a lung cancer protein, in a naked form or conjugated to an effector moiety. That is, the addition of anti-lung cancer protein antibodies (either polyclonal or preferably monoclonal) to lung cancer tissue (or cells containing lung cancer) may reduce or eliminate the lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the lung cancer proteins are humanized antibodies (e.g., Xenex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. A humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeven, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381; Marks, et al. (1991) J. Mol. Biol. 222:581). The techniques of Cole, et al. and Boerner, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985) Monoclonal Antibodies and Cancer Therapy, p. 77 and Boerner, et al. (1991) J. Immunol. 147(1):86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-51; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of lung cancer with an antibody raised against a lung cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the lung cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted lung cancer protein.

In another preferred embodiment, the lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The

antibody may cause down-regulation of the transmembrane lung cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the lung cancer protein. The antibody may be an antagonist of the lung cancer protein or may prevent activation of a transmembrane lung cancer protein, or
5 may induce or suppress a particular cellular pathway. In some embodiments, when the antibody prevents the binding of other molecules to the lung cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or
10 chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, lung cancer may be treated by administering to a patient antibodies directed against the transmembrane lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide
15 means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a lung cancer protein. In another
20 aspect the therapeutic moiety may modulate an activity of molecules associated with or in close proximity to a lung cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase activity associated with lung cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to lung cancer tissue or cells results in a reduction
25 in the number of afflicted cells, thereby reducing symptoms associated with lung cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include
30 radiochemicals made by conjugating radioisotopes to antibodies raised against lung cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane lung cancer proteins not only serves to increase the local concentration of therapeutic moiety in the lung cancer

afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the lung cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the lung cancer protein can be targeted within a cell, i.e., the nucleus, an antibody theretomay contain a signal for that target localization, i.e., a nuclear localization signal.

The lung cancer antibodies of the invention specifically bind to lung cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related other sequences is also important.

Detection of lung cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the lung cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing lung cancer), in lung cancer tissue (and in some cases, for varying severities of lung cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g.,

normal versus lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart (1996) Nature Biotechnology 14:1675-1680, hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the lung cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to lung cancer genes, e.g., those identified as being important in a lung cancer or disease phenotype, can be evaluated in a lung cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The lung cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the lung cancer protein are detected. Although DNA or RNA encoding the lung cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a lung cancer protein is detected.

Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a lung cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, lung cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of lung cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative lung cancer tissue allows for detection, prognosis, or diagnosis of lung cancer or similar disease, and perhaps for selection of therapeutic strategy. In one embodiment, antibodies are used to detect lung cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the lung cancer protein is detected, e.g., by immunoblotting with antibodies raised against the lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the lung cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) Methods in Cell Biology:

Antibodies in Cell Biology, volume 37. In this method cells are contacted with from one to many antibodies to the lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of lung cancer proteins. Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing lung cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of lung cancer proteins. Antibodies can be used to detect a lung cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous lung cancer protein or vaccine.

In a preferred embodiment, *in situ* hybridization of labeled lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including lung cancer tissue and/or normal tissue, are made. *In situ* hybridization (see, e.g., Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to lung cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple

genes may be useful in various combinations. As above, lung cancer probes may be attached to biochips for the detection and quantification of lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

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Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in drug screening
10 assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-8; Heid (1996) Genome Res. 6:986-94.

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In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the lung cancer phenotype or an identified physiological function of a lung cancer protein. As above, this can be done on an individual gene level or
20 by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

Having identified differentially expressed genes herein, a variety of assays may be
25 performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in lung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the lung cancer protein. "Modulation" thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the
30 gene expression in normal versus tissue undergoing lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in lung

cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more lung cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate lung cancer, modulate lung cancer proteins, bind to a lung cancer protein, or interfere with the binding of a lung cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the lung cancer phenotype or the expression of a lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a lung cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induces a lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a lung cancer protein. By “neutralize” is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a lung cancer polypeptide or to modulate activity.

Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a “lead compound”) with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such “combinatorial chemical libraries” are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional “lead compounds” or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical “building blocks” such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37(9):1233-1251).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature, 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et

al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661), oligocarbamates (Cho, et al. (1993) Science 261:1303), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum (1993) C&EN, Jan 18, page 33; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of lung cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins,

U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g.,
5 Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman
Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems
typically automate procedures, including sample and reagent pipetting, liquid dispensing,
timed incubations, and final readings of the microplate in detector(s) appropriate for the
assay. These configurable systems provide high throughput and rapid start up as well as a
10 high degree of flexibility and customization. The manufacturers of such systems provide
detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides
technical bulletins describing screening systems for detecting the modulation of gene
transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or
15 fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or
random or directed digests of proteinaceous cellular extracts, may be used. In this way
libraries of proteins may be made for screening in the methods of the invention. Particularly
preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins,
with the latter being preferred, and human proteins being especially preferred. Particularly
20 useful test compound will be directed to the class of proteins to which the target belongs, e.g.,
substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30
amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to
about 15 being particularly preferred. The peptides may be digests of naturally occurring
25 proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical
equivalents herein is meant that the nucleic acid or peptide consists of essentially random
sequences of nucleotides and amino acids, respectively. Since these random peptides (or
nucleic acids, discussed below) are often chemically synthesized, they may incorporate a
nucleotide or amino acid at any position. The synthetic process can be designed to generate
30 randomized proteins or nucleic acids, to allow the formation of all or most of the possible
combinations over the length of the sequence, thus forming a library of randomized candidate
bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, 5 sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of lung cancer can also be nucleic acids, as defined above.

10 As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

15 After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription 20 with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, 25 alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin 30 is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos.

5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of
5 nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step
10 parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at
15 higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc.
20 which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in
25 expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the lung cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes
30 important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state,

screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a lung cancer expression pattern leading to a normal expression pattern, or to modulate a single lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated lung cancer tissue reveals genes that are not expressed in normal tissue or lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for lung cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated lung cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of lung cancer cells, that have an associated lung cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., lung cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on lung cancer activity. By defining such a signature for the lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of lung cancer polypeptide activity, or of lung cancer or the lung cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian lung cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a lung cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the lung cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a lung cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed

genes are sometimes referred to herein as "lung cancer proteins." The lung cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another
5 embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated
10 gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the lung cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a lung cancer
15 protein and a candidate compound, and determining the binding of the compound to the lung cancer protein. Preferred embodiments utilize the human lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative lung cancer proteins may be used.

20 Generally, in a preferred embodiment of the methods herein, the lung cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of
25 screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents
30 and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation

sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the lung cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (i.e., a lung cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically

between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the lung cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the lung cancer proteins. In one embodiment, the methods comprise combining a lung cancer protein and a competitor in a first sample. A second sample comprises a test compound, a lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the lung cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native lung cancer protein, but cannot bind to modified lung cancer proteins. The structure of the lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a lung cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results.

Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting lung cancer cell division is provided. The method comprises administration of a lung cancer inhibitor. In another embodiment, a method of inhibiting lung cancer is provided. The method may comprise administration of a lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with lung cancer are provided, e.g., comprising administration of a lung cancer inhibitor.

In one embodiment, a lung cancer inhibitor is an antibody as discussed above. In another embodiment, the lung cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

5 Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and
10 grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

15 Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.), herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

20 *Contact inhibition and density limitation of growth*

 Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a
25 higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a
30 normal phenotype and become contact inhibited and would grow to a lower density.

 In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a lung cancer-associated sequence and are grown for 24 hours at saturation density in

non-limiting medium conditions. The percentage of cells labeling with (^3H)-thymidine is determined autoradiographically. See, Freshney (1994), *supra*.

Growth factor or serum dependence

5 Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

10

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g.,
15 Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) "Angiogenesis and Cancer" in Sem Cancer Biol.

Various techniques which measure the release of these factors are described in
20 Freshney (1994), *supra*. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184; Freshney Anticancer Res. 5:111-130 (1985).

25

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate lung cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and
30 invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

Effects of lung cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the lung cancer gene is disrupted or in which a lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous lung cancer gene with a mutated version of the lung cancer gene, or by mutating the endogenous lung cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263; Selby, et al. (1980) Br. J. Cancer 41:52) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a lung cancer-associated sequences are injected subcutaneously. After a suitable length of time,

preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

5 Polynucleotide modulators of lung cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense or an inhibitory polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a
10 coding mRNA nucleic acid sequence, e.g., a lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their
15 close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the lung cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

20 Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides.
25 Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for lung cancer molecules. A preferred antisense molecule is for a lung cancer sequence in the tables, or for a ligand or activator thereof. Antisense or sense
30 oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein

is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659 and van der Krol, et al. (1988) BioTechniques 6:958).

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (19994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126).

Polynucleotide modulators of lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by

formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating lung cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-lung cancer antibody that reduces or eliminates the biological activity of an endogenous lung cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a lung cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the lung cancer sequence is down-regulated in lung cancer, such state may be reversed by increasing the amount of lung cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous lung cancer gene or administering a gene encoding the lung cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the lung cancer sequence is up-regulated in lung cancer, the activity of the endogenous lung cancer gene is decreased, e.g., by the administration of a lung cancer antisense or RNAi nucleic acid.

In one embodiment, the lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to lung cancer proteins. Similarly, the lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify lung cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the lung cancer protein.

Methods of identifying variant lung cancer-associated sequences

Without being bound by theory, expression of various lung cancer sequences is correlated with lung cancer. Accordingly, disorders based on mutant or variant lung cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant lung cancer genes, e.g., determining all or part of the sequence of at least one endogenous lung cancer genes in a cell. In a preferred embodiment, the invention provides methods of identifying the lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one lung cancer gene of the individual.

5 This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced lung cancer gene to a known lung cancer gene, i.e., a wild-type gene.

10 The sequence of all or part of the lung cancer gene can then be compared to the sequence of a known lung cancer gene to determine if any differences exist. This can be done using known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the lung cancer gene of the patient and the known lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

15 In a preferred embodiment, the lung cancer genes are used as probes to determine the number of copies of the lung cancer gene in the genome.

In another preferred embodiment, the lung cancer genes are used as probes to determine the chromosomal localization of the lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when
20 chromosomal abnormalities such as translocations, and the like are identified in the lung cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a lung cancer protein or
25 modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel, et al. (1992) Pharmaceutical Dosage Forms and Drug Delivery; Lieberman, Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846,
30 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding; and Pickar (1999) Dosage Calculations). Adjustments for lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration,

drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and
5 veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly,
10 intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the lung cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a lung cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the
15 pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid,
20 sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases
25 such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic
30 ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose,

lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms
5 suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that lung cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the
10 molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a lung cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions
15 are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like,
20 e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman, et al. (eds. 1996) Goodman and Gilman: The Pharmacological Basis of Therapeutics).

25 Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally
30 administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman, The Pharmacological Basis of Therapeutics, *supra*.

The compositions containing modulators of lung cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present lung cancer protein-modulating compounds can be administered alone or in combination with additional lung cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the tables, such as antisense or RNAi polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of lung cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo*, or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g.,

Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 (Berger), Ausubel, et al. (eds. 1999) Current Protocols (supplemented through 1999), and Sambrook, et al. (1989) Molecular Cloning - A Laboratory Manual (2nd ed., Vol. 1-3).

5 In a preferred embodiment, lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the lung cancer coding regions) can be administered in a gene therapy application. These lung cancer genes can include antisense or inhibitory applications, e.g., as inhibitory RNA or gene
10 therapy (e.g., for incorporation into the genome) or as antisense compositions.

Lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres
15 (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. U.S.A. 85:5409-5413; Tam
20 (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379 In: Kaufmann (ed. 1996) Concepts in vaccine development; Chakrabarti, et al. (1986) Nature 320:535; Hu, et al. (1986) Nature 320:537; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148; Chanda, et al.
25 (1990) Virology 175:535), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25; Eldridge, et al. (1993) Sem. Hematol. 30:16; Falo, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369; Gupta, et al. (1993) Vaccine 11:293), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585; Rock (1996) Immunol. Today 17:131), or, naked or particle absorbed cDNA (Ulmer, et al. (1993)
30 Science 259:1745; Robinson, et al. (1993) Vaccine 11:957; Shiver, et al., p. 423 In: Kaufmann (ed. 1996) Concepts in vaccine development; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923 and Eldridge, et al. (1993) Sem. Hematol. 30:16). Toxin-targeted

delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et. al. (1990) Science 247:1465 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the

like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85).

5 Methods for the use of genes as DNA vaccines are well known, and include placing a lung cancer gene or portion of a lung cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a lung cancer patient. The lung cancer gene used for DNA vaccines can encode full-length lung cancer proteins, but more preferably encodes portions of the lung cancer proteins including peptides derived from the lung cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a
10 plurality of nucleotide sequences derived from a lung cancer gene. For example, lung cancer-associated genes or sequence encoding subfragments of a lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular
15 epitopes.

 In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the lung cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

20 In another preferred embodiment lung cancer genes find use in generating animal models of lung cancer. When the lung cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense or inhibitory RNA directed to the lung cancer gene will also diminish or repress expression of the gene. Animal models of lung cancer find use in screening for modulators of a lung cancer-associated sequence or
25 modulators of lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the lung cancer protein. When desired, tissue-specific expression or knockout of the lung cancer protein may be necessary.

 It is also possible that the lung cancer protein is overexpressed in lung cancer. As
30 such, transgenic animals can be generated that overexpress the lung cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.

Animals generated by such methods will find use as animal models of lung cancer and are additionally useful in screening for modulators to treat lung cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

5 For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications such kits may include at least one of the following: assay reagents, buffers, lung cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, RNAi, dominant negative lung cancer polypeptides or polynucleotides, small molecule inhibitors of
10 lung cancer-associated sequences, etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

 In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium
15 capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

 The present invention also provides for kits for screening for modulators of lung
20 cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a lung cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing lung cancer-associated activity. Optionally, the kit contains biologically active lung cancer protein. A wide variety of kits and components can be prepared according to the present
25 invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes typically will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

5 Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Tables 1A and 1B were previously filed on April 18, 2001 in USSN 60/284,770 (18501-001500US) and on November 29, 2001 in USSN 60/334,370 (18501-001520US)

5	Table 1A					
	Pkey	ExAccn	UnigeneID	Unigene Title	70% chron/90% NL	70% SQAD/90% NL
	100134	D13264	Hs.49	macrophage scavenger receptor 1	1.61	0.74
	100780	HG3731-HT4001		***immunoglobulin Heavy Chain, Vdrc Reg	2.68	3.28
10	100971	J02874	Hs.83213	fatty acid binding protein 4; adipocyte	1.96	0.14
	101088	L05568	Hs.553	solute carrier family 6 (neurotransmitter)	0.79	0.07
	101102	L07594	Hs.79059	transforming growth factor; beta receptor	2.55	1
	101168	L15388	Hs.211569	G protein-coupled receptor kinase 5	0.88	0.27
	101277	L38486	Hs.118223	microfibrillar-associated protein 4	0.89	0.26
15	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.59	0.29
	101336	L49169	Hs.75678	FBJ murine osteosarcoma viral oncogene h	1.15	0.41
	101345	L76380	Hs.152175	calcitonin receptor-like	0.81	0.31
	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	1.31	0.77
	101764	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	1.44	0.82
20	101771	M81750	Hs.153837	myeloid cell nuclear differentiation ant	0.96	0.45
	101842	M93221	Hs.75182	mannose receptor; C type 1	1.27	0.37
	102283	U31384	Hs.83381	guanine nucleotide binding protein 11	1.04	0.3
	102363	U39447	Hs.198241	amine oxidase; copper containing 3 (vasc	0.96	0.26
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel; s	2.81	3.45
25	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	0.95	0.23
	103025	X54131	Hs.123641	protein tyrosine phosphatase; receptor t	1.62	0.21
	103280	X79981	Hs.76206	cadherin 5; VE-cadherin (vascular epithe	0.9	0.41
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2	1.27	0.49
	103541	Z11697	Hs.79197	CD83 antigen (activated B lymphocytes; I	1.86	1
30	103554	Z18951	Hs.74034	caveolin 1; caveolae protein; 22kD	1.27	0.47
	104212	AB002298	Hs.173035	KIAA0300 protein	1.17	0.16
	104691	AA011176	Hs.37744	ESTs	1.08	0.35
	104825	AA035613	Hs.141883	ESTs	0.75	0.27
	104857	AA043219	Hs.19058	ESTs	2.6	3.3
35	104865	AA045136	Hs.22575	ESTs	1.23	0.49
	104989	AA102098	Hs.118615	ESTs	0.63	0.32
	105729	AA292694	Hs.3807	ESTs; Weakly similar to PHOSPHOLEMMAN PR	0.86	0.34
	105847	AA398606	Hs.32241	ESTs	1.32	0.4
	105894	AA400979	Hs.25691	calcitonin receptor-like receptor activi	0.78	0.28
40	106490	AA451861	Hs.115537	ESTs; Weakly similar to dipeptidase prec	1.2	0.47
	106536	AA453997	Hs.23804	ESTs	0.82	0.15
	106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	0.99	0.07
	106667	AA481086	Hs.16578	ESTs	1.17	0.4
	106773	AA478109	Hs.188833	ESTs	1.46	0.43
45	106797	AA478962	Hs.169943	ESTs	1.18	0.32
	106844	AA485055	Hs.158213	sperm associated antigen 6	0.98	0.51
	106870	AA487576	Hs.26530	serum deprivation response (phosphatidy)	1.05	0.14
	106954	AA496980	Hs.204038	ESTs	1.25	0.33
	107054	AA600150	Hs.14366	ESTs	1.11	0.4
50	107292	T30407	Hs.4789	ESTs; Weakly similar to oxidative-stress	1.07	2.58
	107994	AA036811	Hs.165030	ESTs	0.7	0.21
	107997	AA037388	Hs.82223	Human DNA sequence from clone 141H5 on c	1.02	0.48
	108041	AA041552	Hs.61957	ESTs	1.44	0.51
	108087	AA045709	Hs.40545	ESTs	1.98	1
55	108382	AA074885	Hs.67726	macrophage receptor with collagenous str	1.52	0.72
	108435	AA078787	Hs.194101	ESTs	2.53	1.53
	108480	AA081093	Hs.68055	ESTs	1.66	0.48
	109252	AA194830	Hs.85944	ESTs	2.69	3.18
	109550	F01534	Hs.26981	ESTs	1.19	0.65
60	109613	F03031	Hs.27519	ESTs	1.01	0.29
	109837	H00656	Hs.29792	ESTs	0.81	0.15
	109893	H04768	Hs.30484	ESTs	1.44	0.32
	109984	H09594	Hs.10299	ESTs	0.62	0.14
	110099	H16568	Hs.23748	ESTs	1.01	0.28
65	110837	N30796	Hs.17424	ESTs; Weakly similar to semaphorin F [H.	1.1	0.22
	111247	N59825	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.26	0.26
	111341	N80935	Hs.22483	ESTs	1.57	0.52
	111510	R07856	Hs.16355	ESTs	3.96	1
	111737	R25410	Hs.9218	ESTs	0.97	0.24
70	113195	T57112		***yc20g11.s1 Stratagene lung (#937210)	1.22	0.35
	113238	T62979	Hs.189813	ESTs	2.27	0.45
	113540	T90496	Hs.16757	ESTs	1.06	0.22
	113552	T90889	Hs.16026	ESTs	1.16	0.42
	113606	T93093	Hs.17125	ESTs	1.48	0.7
75	113695	T96965	Hs.17948	ESTs	1.54	0.28
	113946	W84753	Hs.37896	ESTs	1.79	0.72
	114261	Z39898	Hs.21948	ESTs	1.95	0.25
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride	1.42	0.13
	115230	AA278300	Hs.182980	ESTs	2.62	0.42
80	115279	AA279760	Hs.63671	ESTs	1.79	0.91
	115566	AA398083	Hs.43977	ESTs	0.86	0.2
	115985	AA446661	Hs.173233	ESTs	0.79	0.04
	116166	AA461556	Hs.202949	KIAA1102 protein	2.29	0.68
	116279	AA486073	Hs.57362	ESTs	2.27	0.78
	117023	H88167	Hs.41105	ESTs	1.38	0.16

	117209	H99959	Hs.42768	ESTs	1.46	0.48
	118901	N90719	Hs.94445	ESTs	1.51	1
	118981	N93839	Hs.39288	ESTs	1.34	0.48
5	118073	R32894	Hs.45514	v-ets avian erythroblastosis virus E26 o	1.14	0.27
	119221	R98105		***yr30g11.s1 Soares fetal liver spleen	1.32	0.53
	119824	W74536	Hs.184	advanced glycosylation end product-speci	1	0.19
	119861	W80715		ESTs; Moderately similar to IIII ALU SUB	1.83	0.45
	120041	W92775	Hs.59368	ESTs	1.23	0.55
10	120132	Z38839	Hs.125019	ESTs; Highly similar to KIAA0886 protein	0.91	0.37
	120467	AA251579	Hs.187628	ESTs	1.87	1.91
	121314	AA402799	Hs.182538	ESTs	1.3	0.31
	121643	AA417078	Hs.193767	ESTs	2.31	0.68
	121690	AA418074	Hs.110286	ESTs	1.47	0.51
	122633	AA454080	Hs.34853	inhibitor of DNA binding 4; dominant neg	1.31	0.63
15	123978	C20553	Hs.170278	ESTs	1.52	0.32
	124214	H58608	Hs.151323	ESTs	0.93	0.35
	124357	N22401		***yw37g07.s1 Morton Fetal Cochlea Homo	1.29	1
	124438	N40188	Hs.102550	ESTs	1.36	0.7
	125167	W45560	Hs.102541	ESTs	1.46	0.69
20	125174	W51835	Hs.231082	EST	3.07	3.76
	125422	AA903229	Hs.153717	ESTs	1.34	0.3
	125561	AI417667	Hs.22978	ESTs	1.89	0.63
	125831	D60988		***HUM145B09B Clontech human fetal brain	0.94	0.36
25	127002	R35380	Hs.24979	ESTs	3.02	4.06
	127307	AA369367	Hs.126712	ESTs; Weakly similar to pL2 hypothetical	1.01	0.69
	127609	AA622559	Hs.150318	ESTs	1.21	0.32
	127959	AI302471	Hs.124292	ESTs	2.5	1
	128458	D52183	Hs.56340	ESTs	1.13	0.33
30	128624	AA479209	Hs.102647	ESTs	1.45	0.58
	128789	AA486567	Hs.105895	ESTs	1.1	0.34
	128798	AF014958	Hs.105938	chemokine (C-C motif) receptor-like 2	1.16	0.55
	128952	R51076	Hs.107361	ESTs; Highly similar to Rap2 interacting	2.04	2.4
	129057	X62466	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	1.77	0.73
35	129210	AA401654	Hs.202949	KIAA1102 protein	1.11	0.36
	129240	W24360	Hs.237868	interleukin 7 receptor	0.91	0.41
	129402	T63781		***yc21g01.s1 Stratagene lung (#937210)	1.36	0.43
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1	0.67	0.08
	129593	AA487015	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	1.3	0.42
40	129626	AA447410	Hs.11712	ESTs; Weakly similar to IIII ALU SUBFAM1	1.28	0.46
	129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ublqu	1.58	1
	129898	N48595	Hs.13256	ESTs	1.13	0.53
	129958	L20591	Hs.1378	annexin A3	0.81	0.31
45	130273	U59914	Hs.153863	MAD (mothers against decapentaplegic; Dr	0.59	0.22
	130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)	1.44	0.76
	130657	T94452	Hs.201591	ESTs	0.96	0.42
	131061	N64328	Hs.22567	ESTs; Moderately similar to HYPOTHETICAL	1.51	0.45
	131066	F09006	Hs.22588	ESTs	0.97	0.37
	131263	R38334	Hs.24950	regulator of G-protein signalling 5	2.34	2.82
50	131589	U52100	Hs.29191	epithelial membrane protein 2	1.2	0.62
	131686	AA157428	Hs.30687	Grb2-associated binder 2	0.95	0.38
	131751	H18335	Hs.31562	ESTs	1.47	0.52
	132430	T23830	Hs.258875	EST	1.86	2.09
	132476	N67192	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	1.73	0.58
55	132836	F09557	Hs.57929	silt (Drosophila) homolog 3	0.91	0.29
	133120	X64559	Hs.65424	tetranectin (plasminogen-binding protein	0.82	0.2
	133488	D45370	Hs.74120	adipose specific 2	1.29	0.48
	133565	H57058	Hs.204831	ESTs	2.25	0.57
	133651	U97105	Hs.173381	dihydropyrimidinase-like 2	1.65	0.62
60	133835	AA059489	Hs.76640	ESTs; Highly similar to RGC-32 [R.norveg	1.16	0.34
	133978	W73859	Hs.78061	transcription factor 21	0.79	0.27
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec	0.99	0.28
	134299	AA487558	Hs.8135	ESTs	1.02	0.46
	134300	U81984	Hs.166082	endothelial PAS domain protein 1	0.86	0.42
65	134323	AA028976	Hs.8175	Homo sapiens mRNA; cDNA DKFZp564M0763 (f	1.19	0.27
	134343	D50683	Hs.82028	transforming growth factor; beta recepto	1.21	0.67
	134417	D87969	Hs.82921	solute carrier family 35 (CMP-sialic aci	1.28	1
	134561	U76421	Hs.85302	adenosine deaminase; RNA-specific; B1 (h	2.12	0.55
	134624	W67147	Hs.8700	deleted in liver cancer 1	2.35	2.74
70	134696	H68354	Hs.8881	ESTs	1.35	0.33
	134749	L10956	Hs.89485	carbonic anhydrase IV	0.89	0.2
	134786	L06139	Hs.89640	TEK tyrosine kinase; endothelial (venous	0.48	0.21
	134869	T35288	Hs.90421	ESTs; Moderately similar to IIII ALU SUB	2.14	2.64
	135346	M21056	Hs.992	phospholipase A2; group IB (pancreas)	0.63	0.13
75	100113	D00591	Hs.84746	Chromosome condensation 1	1	2.15
	100147	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specifi	0.5	2
	100280	D42085	Hs.155314	KIAA0095 gene product	1.02	1.39
	100335	D63391	Hs.6793	platelet-activating factor acetylhydrola	1	5.58
	100360	D78335	Hs.75939	Uridine monophosphate kinase	0.91	2.04
80	100372	D79997	Hs.184339	KIAA0175 gene product	0.75	2.03
	100486	HG1112-HT1112		TIGR: ras-like protein TC4	1.09	1.93
	100559	HG2197-HT2267		*collagen, type VII, alpha 1*	0.97	3.6
	100576	HG2290-HT2386		*calcitonin/alpha-CGRP, all. transcript	1	1
	100668	HG2981-HT3938		*TIGR: CD44 (epican, all. transcript 12	0.85	1.9
85	100906	HG4716-HT5158		Guanosine 5'-Monophosphate Synthase	1.18	2.29
	100930	HG721-HT4827		*TIGR: placental protein 14, endometrial	1	1.45

5	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	0.84	2.6
	101031	J05070	Hs.151738	*Matrix metalloproteinase 9 (gelatinase	0.77	1.52
	101111	L08424	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
	101124	L10343	Hs.112341	*Protease Inhibitor 3, skn-derived (SKA	0.62	2.67
	101175	L18920	Hs.36980	*Melanoma antigen, family A, 2"	1	1
10	101204	L24203	Hs.82237	Ataxia-telangiectasia group D-associated	0.74	4.1
	101431	M19888	Hs.1076	Small proline-rich protein 1B (cornifin)	0.85	2.51
	101448	M21389	Hs.195850	keratin 5 (epidermolysis bullosa simplex	0.61	8.83
	101511	M27826	Hs.267319	Endogenous retroviral protease	1.03	1.13
	101526	M29540	Hs.220529	Carcinoembryonic antigen-related cell ad	1.07	4.61
15	101548	M31328	Hs.71642	*Guanine nucleotide binding protein (G p	0.97	1.13
	101625	M57293		*Human parathyroid hormone-related pepti	1	1
	101849	M60047	Hs.1690	Heparin-binding growth factor binding pr	1	2.7
	101724	M69225	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	1	8.98
	101748	M76482	Hs.1925	Desmoglein 3 (pemphigus vulgaris antigen	1	2.78
20	101759	M80244	Hs.184601	*Solute carrier family 7 (cationic amino	1.07	2.45
	101804	M86699	Hs.169840	TTK protein kinase	1	1
	101806	M86757	Hs.112408	S100 calcium-binding protein A7 (psorias	0.74	1.76
	101809	M86849		*Homo sapiens connexin 26 (GJB2) mRNA, c	1	7
	101845	M93426	Hs.78867	*Protein tyrosine phosphatase, receptor-	1	1
25	101851	M94250	Hs.82045	Midkine (neurite growth-promoting factor	1.13	2.6
	102083	U10323	Hs.75117	*Interleukin enhancer binding factor 2,	1.03	1.61
	102154	U17760	Hs.75517	*Laminin, beta 3 (nlcein (125kD), kalin	0.94	3.62
	102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	0.34	4.59
	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)	1.45	2.97
30	102348	U37519	Hs.87539	Aldehyde dehydrogenase 8	0.52	2.25
	102581	U61145	Hs.77258	Enhancer of zeste (Drosophila) homolog 2	0.91	2.46
	102610	U65011	Hs.30743	Preferentially expressed antigen in mela	1	3.88
	102623	U66083	Hs.37110	*Melanoma antigen, family A, 9 (MAGE-9)"	1	1
	102669	U71207	Hs.29279	Eyes absent (Drosophila) homolog 2	1	1
35	102696	U74612	Hs.239	Forkhead box M1	1.06	2.77
	102829	U91618	Hs.80962	Neurotensin	1	1
	102888	X04741	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.13	2.59
	102913	X07696	Hs.80342	keratin 15	0.7	4.72
	102915	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin	1.15	3.35
40	102963	X15943	Hs.37058	*Calcitonin/calcitonin-related polypepti	1	1
	103021	X53587	Hs.85266	*Integrin, beta 4"	1.38	2.34
	103036	X54925	Hs.83169	Matrix metalloprotease 1 (interstitial c	1	14.93
	103058	X57348	Hs.184510	Stratiferin	1.25	4.17
	103060	X57766	Hs.155324	matrix metalloproteinase 11 (stromelysin	1	1.72
45	103119	X63629	Hs.2877	*Cadherin 3, P-cadherin (placental)"	1.16	7.38
	103206	X72755	Hs.77367	monokine Induced by gamma Interferon	0.71	1.48
	103242	X76342	Hs.389	*Alcohol dehydrogenase 7 (class IV), mu	1	1
	103312	X82693	Hs.3185	*Lymphocyte antigen 6 complex, locus D;	0.92	1.28
	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.05	5.81
50	103558	Z19574	Hs.2785	keratin 17	0.65	6.68
	103576	Z26317	Hs.2631	Desmoglein 2	0.79	1.73
	103587	Z29083	Hs.82128	ST4 Oncofetal antigen	1	3.93
	103594	Z31560	Hs.816	*SRY (sex determining region Y)-box 2, p	0.71	7.23
	103768	AA089997		*ESTs, Highly similar to integral membra	0.99	1.8
55	104168	AA454908	Hs.8127	KIAA0144 gene product	0.95	1.29
	104558	R56678	Hs.88959	Human DNA sequence from clone 987N21 on	1.23	7.23
	104689	AA010665		ESTs	0.96	2.11
	104733	AA018498	Hs.23071	ESTs	1.18	1.88
	104905	AA065809	Hs.26802	Protein kinase domains containing protei	1.11	3.15
60	104978	AA088458	Hs.19322	ESTs; Weakly similar to !!!!! ALU SUBFAM1	1.64	2.89
	105012	AA116036	Hs.9329	*Homo sapiens mRNA for fls353, complete	1.19	3.91
	105175	AA186804	Hs.25740	ESTs; Weakly similar to unknown [S.cerev	0.9	4.63
	105263	AA227926	Hs.6682	ESTs	0.95	2.87
	105298	AA233459	Hs.26369	ESTs	1	1.13
65	105312	AA233854	Hs.23348	S-phase kinase-associated protein 2 (p45	1.32	3.01
	105719	AA291644	Hs.36793	Hypothetical protein FLJ23188	1.28	2.31
	105743	AA293300	Hs.9598	ESTs	1	1
	106012	AA411621	Hs.8895	ESTs; same as 8FH67	0.94	2.04
	106231	AA429571	Hs.38002	KIAA1355 protein	1.04	1.5
70	106540	AA454607	Hs.38114	Hypothetical protein FLJ11100	1.26	2.26
	106575	AA456039	Hs.105421	ESTs	1	2
	106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	0.87	1.32
	106727	AA465342	Hs.34045	Hypothetical protein FLJ20764	0.87	1.59
	106908	AA490237	Hs.222024	Transcription factor BMAL2 (cycle-like f	0.61	1.6
75	107059	AA608545	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	0.48	2.67
	107104	AA609788	Hs.15243	Nucleolar protein 1 (120kD)	1.01	1.44
	107151	AA621169	Hs.8687	ESTs; procollagen I-N proteinase	0.97	2.89
	107284	S74039	Hs.291904	Accessory proteins BAP31/BAP29	1.15	3.65
	107901	AA026418	Hs.91539	ESTs	0.72	3.44
80	107922	AA028028	Hs.61480	Ig superfamily receptor LNIR precursor	1	2.48
	107932	AA029317	Hs.18878	Hypothetical protein FLJ21620	1	1
	108695	AA121315	Hs.70823	KIAA1077 protein	0.91	3.53
	108857	AA133250	Hs.62180	ESTs	1	1
	108860	AA133334	Hs.129911	ESTs	0.73	7.3
85	108990	AA152296	Hs.72045	ESTs	1	1
	109166	AA179845	Hs.73625	*RAB6 Interacting, kinesin-like (rakline	1	4.55
	109424	AA227919	Hs.85962	Hyaluronan synthase 3	1	1.28
	109565	F05012	Hs.27027	Hypothetical protein DKFZp762H1311	1.42	2
	109970	H09281	Hs.13234	ESTs	1.13	2.16

	110015	H10998	Hs.7164	A disintegrin and metalloproteinase doma	0.84	1.95
	110156	H18957	Hs.4213	ESTs	0.94	1.41
	110561	H59617	Hs.5199	HSPC150 protein similar to ubiquitin-con	0.91	3.18
5	111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapi	0.91	3.13
	111345	N89820	Hs.14559	Hypothetical protein FLJ10540	1	1.25
	111876	R38239	Hs.293246	*ESTs, Weakly similar to putative p150 [0.83	1.27
	111902	R39191	Hs.109445	KIAA1020 protein	0.91	0.91
	112244	R51309	Hs.70823	KIAA1077 protein	0.77	3.01
10	112973	T17271		*cDNA FLJ13308 fis, clone OVARC1001436,	1	1
	112989	T23482	Hs.89981	*Diacylglycerol kinase, zeta (104kD)*	0.55	1.03
	113047	T25867	Hs.7549	ESTs	0.87	2
	113095	T40920	Hs.126733	ESTs	1	1
	113531	T90345	Hs.16740	Hypothetical protein FLJ11036	0.42	1.44
15	113970	W86748	Hs.8109	ESTs	1.17	1.73
	114346	Z41450	Hs.130489	*ATPase, aminophospholipid transporter-I	0.86	0.82
	114407	AA010188	Hs.103305	ESTs	0.8	1.88
	114471	AA028074	Hs.104613	RP42 homolog	1.06	1.34
	114509	AA043551	Hs.101799	KIAA1350 protein	1.82	2.32
20	115060	AA253214	Hs.198249	*Gap junction protein, beta 5 (connexin	0.79	1.49
	115091	AA255900	Hs.184523	KIAA0965 protein	0.72	1.92
	115123	AA256642	Hs.236894	*ESTs, High sim to LRP1_hu low density l	0.59	1.97
	115291	AA279943	Hs.122579	ESTs	1	1.25
	115506	AA292537	Hs.45207	Hypothetical protein KIAA1335	1.15	1.48
25	115522	AA331393	Hs.47378	ESTs	0.5	3.29
	115536	AA347193	Hs.62180	ESTs	1	1
	115697	AA411502	Hs.63325	Homo sapiens type II membrane serine pro	1	6.53
	115909	AA436666	Hs.59761	ESTs	1	6.98
	115978	AA447522	Hs.69517	Differentially expressed in Fanconi anem	1	2.31
30	116028	AA452112	Hs.42644	thioredoxin-like	0.99	1.68
	116107	AA456968	Hs.92030	ESTs	1.14	1.8
	116134	AA460246	Hs.50441	CGI-04 protein	1.11	1.86
	116157	AA461063	Hs.44298	Hypothetical protein	0.99	1.9
	116158	AA461187	Hs.61762	Hypoxia-Inducible protein 2	0.44	0.86
35	116335	AA495830	Hs.87013	*Homo sapiens cDNA FLJ10238 fis, clone H	0.62	3.89
	116483	C14092	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.04	2.36
	117320	N23239	Hs.211092	LUNX protein; PLUNC (palate lung & nasal	0.51	0.64
	117557	N33920	Hs.44532	Diubiquitin	1.11	2.63
	117693	N40939	Hs.112110	PTD007 protein	0.98	1.79
40	117881	N50073	Hs.260622	Butyrate-induced transcript 1	1	1.43
	118368	N64339	Hs.48956	ESTs	0.67	2.86
	118566	N68558	Hs.42824	Hypothetical protein FLJ10718	1.21	0.83
	118695	N71781	Hs.50081	KIAA1199 see CVA7.doc	0.88	1.63
	119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical pro	1	1
45	119845	W79920	Hs.58561	G protein-coupled receptor 87	1	1
	120102	W95428	Hs.132927	*ESTs, Moderately similar to p53 regulat	1	1
	120104	W95477	Hs.180479	ESTs	0.69	3.07
	120486	AA253400	Hs.137569	Tumor protein 63 kDa with strong homolog	1.08	12.05
	120859	AA350158	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
50	120880	AA360240	Hs.97019	EST	1	1
	120948	AA397822	Hs.104650	Hypothetical protein FLJ10292	1.04	2.15
	120983	AA398209	Hs.97687	EST	1	1
	121362	AA405500	Hs.97932	Chondromodulin I precursor	1	1
	121369	AA405657	Hs.128791	CGI-09 protein	1	1.8
55	121791	AA423978	Hs.293317	*ESTs, Weakly similar to JM27 [H.sapiens	1	1
	123005	AA479726	Hs.105577	ESTs	1	1
	123044	AA481549	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	0.95	1.88
	123160	AA488687	Hs.284235	ESTs	1.59	4.98
	123479	AA599469	Hs.135056	clone RP5-850E9 on chromosome 20	1.19	1.64
60	123571	AA608956	Hs.112619	*ESTs, Weakly similar to PQ0109 Purkinje	1.03	1.14
	123829	AA620697	Hs.112208	XAGE-1 protein	1.39	2.2
	124006	D60302	Hs.108977	ESTs	1	4.85
	124059	F13673	Hs.99769	ESTs	1.49	8.62
	124960	T15386	Hs.194766	Seizure related gene 6 (mouse)-like	0.76	0.77
65	125218	W73561	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33	1.77
	125453	R06041	Hs.18048	*Melanoma antigen, family A, 10*	0.8	1.42
	125759	AA425587	Hs.82226	Glycoprotein (transmembrane) nmb	1.52	2.26
	125972	AA434562	Hs.35406	*ESTs, Highly similar to unnamed protein	1.05	2.48
	125994	H55782	Hs.270799	EST	1	1.95
	126395	N70192	Hs.278956	Hypothetical protein FLJ12929	1	1.35
70	126645	A167942	Hs.61635	STEAP1 (Homo sapiens BAC clone RG041D11	1	2.23
	127221	A1354332	Hs.72365	ESTs	0.73	3.27
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaph	0.51	1.94
	128192	A1204246		KIAA1085 protein	1.8	3.16
75	128610	L38608	Hs.10247	activated leucocyte cell adhesion molecu	0.89	0.97
	128777	U46006	Hs.10526	Cysteine and glycine-rich protein 2	1	1
	128924	AA234962	Hs.26557	Plakophilin 3	1.3	2.97
	129041	H58873	Hs.169902	*Solute carrier family 2 (facilitated gl	0.84	2.04
	129099	H50398	Hs.108660	*ATP-binding cassette, sub-family C (CFT	0.87	1.04
80	129404	AA172056	Hs.111128	ESTs	1	1
	129466	L42583		*Genbank Homo sapiens keratin 6 isoform	0.72	12.67
	129605	S72493	Hs.115947	Keratin 16 (focal non-epidermolytic palm	0.92	1.5
	129628	U26727	Hs.1174	*Cyclin-dependant kinase inhibitor 2A (m	0.85	1.93
	130023	X13461	Hs.239600	Calmodulin-like 3	0.84	1.22
	130080	X14850	Hs.147097	*H2A histone family, member X*	0.98	1.96
85	130385	AA126474	Hs.155223	stanniocalcin 2	1	1

	130410	V01514	Hs.155421	Alpha-fetoprotein	0.63	0.63
	130441	U35835	Hs.301387	*Human DNA-PK mRNA, partial cds*	1.15	3.65
	130482	L32866	Hs.1578	Baculoviral IAP repeat-containing 5 (sur	1	1.88
5	130553	AA430032	Hs.252587	Pituitary tumor-transforming 1	0.92	1.96
	130577	M35410	Hs.162	Insulin-like growth factor binding prote	1.17	4.7
	130827	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage	0.69	4.05
	130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subu	1.13	2.41
	130939	AA598689	Hs.21400	ESTs	0.8	0.89
10	131046	X02530	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	0.8	1.15
	131244	D38076	Hs.24763	RAN binding protein 1	1.13	1.85
	131877	J04088	Hs.156346	Topoisomerase (DNA) II alpha (170kD)	1	1
	131927	AA461549	Hs.34780	*Doublecortin; lissencephaly, X-linked (0.81	0.62
	131965	W90146	Hs.35962	ESTs	0.74	3.27
	131978	D80008	Hs.36232	KIAA0186 gene product	1	1
15	132354	L05187	Hs.211913	Small proline-rich protein 1A	0.69	1.43
	132543	AA417152	Hs.5101	ESTs; Highly similar to protein regulati	0.79	4.27
	132632	N59764	Hs.5398	guanine-monophosphate synthetase	1	1.08
	132653	U31201	Hs.54451	*laminin gamma2 chain gene (LAMC2), exon	1	1
20	132659	Z75190	Hs.54481	*Low density lipoprotein receptor-relate	0.89	0.89
	132710	W93726	Hs.55279	*Serine (or cysteine) proteinase inhibit	0.64	4.41
	132758	W52432	Hs.56105	*ESTs, Weakly similar to WDNM RAT WDNM1	1.55	2.08
	132767	L05188	Hs.231622	Small proline-rich protein 2B	0.83	1.66
	132816	M74542	Hs.575	Aldehyde dehydrogenase 3	0.55	0.55
25	132990	AA458761	Hs.18387	transcription factor AP-2 alpha (activat	1	3.53
	133070	U69611	Hs.64311	*A disintegrin and metalloproteinase dom	1.16	2
	133282	U52960	Hs.285145	*SRB7 (suppressor of RNA polymerase B, y	1	2.7
	133317	AA215299	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	0.95	1.42
	133370	AA156897	Hs.72157	Homo sapiens mRNA; cDNA DKFZp564H1922	1.12	2.55
30	133391	X57579	Hs.727	H.sapiens activin beta-A subunit (exon 2	1.65	1.76
	133832	H03387	Hs.241305	estrogen-responsive B box protein (EBBP)	1.02	1.39
	134032	Z81326	Hs.78589	*Serine (or cysteine) proteinase inhibit	1	1
	134168	AA398908	Hs.181634	*Homo sapiens cDNA: FLJ23602 fis, clone	0.95	1.53
	134218	AA227480	Hs.80205	Pim-2 oncogene	1.36	2.48
35	134405	R67275	Hs.82772	***collagen, type XI, alpha 1***	0.76	2.86
	134453	X70683	Hs.83484	SRX (sex determining region Y)-box 4	1.89	3.78
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.82	4.11
	134645	U87459	Hs.167379	*Cancer/testis antigen (NY-ESO-1, CTAG1,	0.82	0.83
	134781	M17183	Hs.89626	Parathyroid hormone-like hormone	1	1
40	135002	U19147	Hs.272484	G antigen 6	1	1
	100040	M97935		AFFX control: STAT1	0.92	1.25
	101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin;	2.92	8.5
	101664	M60752	Hs.121017	H2A histone family; member A	1	1
	102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer;	0.8	1.61
45	102031	U04898	Hs.2156	RAR-related orphan receptor A	1	1
	102221	U24576		LIM domain only 4	1	1
	102270	U30255	Hs.75888	phosphogluconate dehydrogenase	1.08	1.43
	102339	U37022	Hs.95577	cyclin-dependent kinase 4	0.88	1.32
	102391	U41668	Hs.77494	deoxyguanosine kinase	1.07	1.58
50	103000	X51956	Hs.146580	enolase 2; (gamma; neuronal)	0.91	1.49
	103395	X94754	Hs.119503	methionine-IRNA synthetase	0.89	1.32
	105638	AA281599	Hs.20418	Homo sapiens mRNA for for histone H2B; c	0.91	1.25
	105726	AA292328	Hs.9754	activating transcription factor 5	0.94	1.48
	114841	AA234722	Hs.55408	ESTs; Moderately similar to CALCIUM-DEPE	0.78	1.56
55	115206	AA262491	Hs.186572	ESTs	1	1
	115908	AA435616	Hs.82302	ESTs	0.74	2.52
	119132	R49046	Hs.107911	ATP-binding cassette; sub-family B (MDR/	1.1	1.51
	124163	H30539	Hs.189838	ESTs	1	1
	126487	AA482505	Hs.184601	solute carrier family 7 (cationic amino	1.01	1.46
60	127141	AA307980	Hs.75478	KIAA0956 protein	0.85	1.4
	128034	AA905754	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-mo	1	1.18
	128609	AA234365	Hs.102458	survival of motor neuron protein Interac	1	1.5
	128895	R37753	Hs.106985	ESTs	1.7	2
	130199	Z48579	Hs.172028	a disintegrin and metalloprotease domain	1	1
65	130524	U89995	Hs.159234	forkhead box E1	1	1
	133000	U24152	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	1	1
	133658	M25756	Hs.75426	secretogranin II (chromogranin C)	1	1
	135047	AA460466	Hs.93597	ESTs	1	1
	100053	M27830		AFFX control: 28S ribosomal RNA	0.88	1.53
70	100114	D00596	Hs.82962	thymidylate synthetase	0.68	1.86
	100128	D11094	Hs.61153	proteasome (prosome; macropain) 26S subu	1.29	2.03
	100154	D14657	Hs.81892	KIAA0101 gene product	0.71	4.26
	100161	D14694	Hs.77329	phosphatidylserine synthase 1	1.02	1.55
	100168	D14874	Hs.394	adrenomedullin	0.46	1.17
75	100187	D17793	Hs.78183	aldo-keto reductase family 1; member C3	1	1
	100188	D21063	Hs.57101	minichromosome maintenance deficient (S.	0.97	1.4
	100217	D26600	Hs.89545	proteasome (prosome; macropain) subunit;	1.13	1.9
	100220	D28364		***Human mRNA for annexin II, 5'UTR (seq	1.11	1.53
	100287	D43950	Hs.1800	chaperonin containing TCP1; subunit 5 (e	1.13	2.09
80	100297	D49489	Hs.182429	protein disulfide isomerase-related prot	0.92	1.78
	100330	D55716	Hs.77152	minichromosome maintenance deficient (S.	1.07	1.61
	100355	D78129		***Homo sapiens mRNA for squalene epoxid	0.96	1.87
	100364	D78586	Hs.154868	carbamoyl-phosphate synthetase 2; aspart	1.49	2.46
	100368	D79987	Hs.153479	extra spindle poles; S. cerevisiae; homo	0.59	1.32
	100398	D84557	Hs.155462	minichromosome maintenance deficient (ml	1.08	1.9
85	100438	D87448	Hs.91417	topoisomerase (DNA) II binding protein	1	2.15

	100455	D87953	Hs.75789	N-myc downstream regulated	0.91	1.48
	100491	HG1153-HT1153		Nucleoside Diphosphate Kinase Nm23-H2s	0.99	1.41
	100518	HG174-HT174		Desmoplakin I	1.28	3.17
5	100528	HG1828-HT1857		***Nexin, Glia-Derived***	0.68	1.9
	100661	HG2874-HT3018		Ribosomal Protein L39 Homolog	1.1	5.44
	100667	HG2981-HT3127		***Epican, Alt. Splice 11***	0.8	1.97
	100830	HG4074-HT4344		Rad2	1.01	2.12
	101081	K03515	Hs.944	glucose phosphate isomerase	0.91	1.79
10	101131	L10838	Hs.167460	splicing factor; arginine/serine-rich 3	1.23	1.87
	101162	L14595	Hs.174203	solute carrier family 1 (glutamate/neutr	1.35	2.73
	101181	L19686	Hs.73798	macrophage migration inhibitory factor (1.03	1.78
	101183	L19779	Hs.795	H2A histone family; member O	0.57	1.3
	101216	L25876	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	0.7	2.2
15	101228	L27706	Hs.82916	chaperonin containing TCP1; subunit 6A (0.99	1.99
	101233	L29008	Hs.878	sorbitol dehydrogenase	0.82	2.11
	101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	1.2	1.91
	101332	L47276		***Homo sapiens (cell line HL-6) alpha 1	0.69	2.78
	101342	L76191	Hs.182018	Interleukin-1 receptor-associated kinase	1.04	1.84
20	101396	M15796	Hs.78996	proliferating cell nuclear antigen	0.95	3.55
	101423	M18391	Hs.89839	EphA1	1	1.5
	101445	M21259	Hs.1065	small nuclear ribonucleoprotein polypept	1.21	1.96
	101505	M27398	Hs.75692	asparagine synthetase	0.93	1.6
	101525	M29536	Hs.12163	eukaryotic translation initiation factor	1.19	1.93
25	101535	M30448	Hs.251669	casein kinase 2; beta polypeptide	0.96	1.42
	101607	M38690	Hs.1244	CD9 antigen (p24)	1.11	1.25
	101624	M55998		***Human alpha-1 collagen type I gene, 3	1.17	1.98
	101758	M77836	Hs.79217	pyrroline-5-carboxylate reductase 1	1.77	3.45
	101839	M93036	Hs.692	membrane component; chromosomal 4; surfa	0.71	1.45
30	101853	M94362	Hs.76084	lamin B2	0.84	1.19
	101977	S83364		***putative Rab5-interacting protein (cl	0.89	1.9
	101992	U01038	Hs.77597	polo (Drosophila)-like kinase	0.65	1.46
	102009	U02680	Hs.82643	protein tyrosine kinase 9	1.23	3.35
	102012	U30057	Hs.118400	singed (Drosophila)-like (sea urchin fas	0.85	1.88
35	102039	U05861	Hs.201967	aldo-keto reductase family 1; member C1	0.93	2.32
	102123	U14518	Hs.1594	centromere protein A (17kD)	1	4.28
	102130	U15009	Hs.1575	small nuclear ribonucleoprotein D3 polyp	0.89	1.42
	102148	U16954	Hs.75823	ALL1-fused gene from chromosome 1q	0.8	2.95
	102210	U23028	Hs.2437	eukaryotic translation initiation factor	1.01	1.34
40	102220	U24389	Hs.65436	lysyl oxidase-like 1	1.15	2.34
	102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; impor	1.14	2.69
	102330	U35451	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta	1.05	1.7
	102423	U44754	Hs.179312	small nuclear RNA activating complex; po	1.14	2.99
	102455	U48705	Hs.75562	discoidin domain receptor family; member	1.05	2.01
45	102499	U51478	Hs.76941	ATPase; Na+/K+ transporting; beta 3 poly	1.27	1.92
	102522	U53347	Hs.183556	solute carrier family 1 (neutral amino a	0.84	1.31
	102590	U82136		***Homo sapiens enterocyte differentiall	1.11	1.6
	102676	U72514	Hs.12045	putative protein	1.04	2.17
	102687	U73379	Hs.93002	ubiquitin carrier protein E2-C	0.86	2.28
50	102704	U76638	Hs.54089	BRCA1 associated RING domain 1	1.12	1.63
	102781	U83843		***Human HIV-1 Nef interacting protein (0.9	1.39
	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat	0.98	2.16
	102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (b	0.96	1.62
	102935	X13482	Hs.80506	small nuclear ribonucleoprotein polypept	1.21	4.2
55	102972	X16662	Hs.87268	annexin A8	1.25	2.32
	102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A)	1.03	1.83
	103023	X53793	Hs.117950	multifunctional polypeptide similar to S	1.58	5.44
	103038	X54941	Hs.77550	CDC28 protein kinase 1	1.32	3.79
	103075	X59543	Hs.2934	ribonucleotide reductase M1 polypeptide	1.11	2.58
60	103168	X68314	Hs.2704	glutathione peroxidase 2 (gastrointestin	0.75	3.05
	103185	X69910	Hs.74368	transmembrane protein (63kD); endoplasm	1.01	1.97
	103212	X73874	Hs.2393	phosphorylase kinase; alpha 1 (muscle)	0.95	1.72
	103223	X74801	Hs.1708	chaperonin containing TCP1; subunit 3 (g	0.97	1.77
	103260	X78416	Hs.3155	casein; alpha	1	1
65	103262	X78555	Hs.204133	hexabrachion (tenascin C; cytactin)	1.23	3.09
	103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypept	1.12	2.25
	103364	X90872	Hs.75854	SULT1C1 sulfotransferase	2.85	4.62
	103375	X91868	Hs.54416	sine oculis homeobox (Drosophila) homolo	1	2.48
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	1	1.53
70	103404	X95586	Hs.78596	proteasome (prosome; macropain) subunit;	0.92	1.53
	103437	X98260	Hs.82254	M-phase phosphoprotein 11	0.92	1.54
	103448	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	0.55	0.96
	103605	Z35402	Hs.194657	cadherin 1; E-cadherin (epithelial)	1.32	2.51
	103646	Z68228	Hs.2340	junction plakoglobin	0.88	1.28
75	103658	Z74615	Hs.172928	collagen; type I; alpha 1	1.06	2.98
	103774	AA092898	Hs.92918	ESTs; Weakly similar to R07G3.8 [C.elega	1.88	4.66
	104261	AF008442	Hs.5409	RNA polymerase I subunit	0.87	2.17
	104276	C02193	Hs.85222	ESTs; Weakly similar to R27090_2 [H.sapi	1.4	2.49
	104289	C16281	Hs.75478	KIAA0956 protein	1.15	1.68
	104434	L02870	Hs.1640	collagen; type VII; alpha 1 (epidermolys	1.04	1.49
80	104453	M19169	Hs.123114	cystatin SN	0.38	0.76
	104611	R98280	Hs.125845	ribulose-5-phosphate-3-epimerase	1.08	2.25
	104758	AA024661	Hs.7010	ESTs; Weakly similar to ACYL-COA DEHYDRO	1.14	1.65
	105114	AA156532	Hs.11801	adenosine A2b receptor pseudogene	0.91	1.38
	105132	AA159501	Hs.247280	HBV associated factor	1.08	1.7
85	105174	AA186613	Hs.34744	ESTs	0.95	2.05

	105280	AA232215	Hs.14600	ESTs	1	1.4
	105344	AA235303	Hs.8645	ESTs	0.72	2.02
	105516	AA257971	Hs.21214	ESTs	1.35	3.56
5	105621	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564K0222 (f	1.23	1.82
	105698	AA287393	Hs.15202	ESTs; Weakly similar to oligodendrocyte-	0.98	1.28
	105705	AA290767	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (fr	0.92	1.32
	105724	AA292098	Hs.22934	ESTs; Weakly similar to ZINC FINGER PROT	0.99	1.41
	105782	AA350215	Hs.21580	ESTs	1	1
10	105799	AA372018	Hs.24743	ESTs	1.08	1.78
	105807	AA393803	Hs.16869	ESTs; Moderately similar to COLLAGEN ALP	0.95	1.34
	105891	AA400768	Hs.26662	ESTs; Weakly similar to tumor necrosis f	0.87	2.25
	105936	AA404338		ESTs	1.14	1.46
	106069	AA417741	Hs.29899	ESTs; Weakly similar to ZINC FINGER PROT	1	1
	106103	AA421104	Hs.12094	ESTs	1.04	1.44
15	106140	AA424524	Hs.14912	KJAA0286 protein	1.23	2.11
	106149	AA424881	Hs.256301	ESTs	0.83	1.48
	106154	AA425304	Hs.6994	ESTs	0.77	2.05
	106182	AA426609	Hs.10862	ESTs	0.74	2.23
20	106220	AA428582	Hs.32196	ESTs; Moderately similar to metargidin p	0.97	1.99
	106228	AA429290	Hs.17719	ESTs	0.99	1.54
	106318	AA436570	Hs.9605	pre-mRNA cleavage factor Im (25kD)	0.95	2.09
	106341	AA441798	Hs.5243	ESTs; Moderately similar to p11.2 hypothe	0.98	2.66
	106432	AA448850	Hs.17138	ESTs	0.95	1.93
25	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (fr	1	1
	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	1.4	2.29
	106599	AA457235	Hs.12842	ESTs; Moderately similar to non-function	1	1.82
	106611	AA458904	Hs.26267	ESTs; Weakly similar to torsinA [H.sapie	1.49	2.78
	106654	AA460449	Hs.3784	ESTs; Highly similar to phosphoserine am	1	1.4
30	107076	AA609145	Hs.21143	ESTs; Weakly similar to fos39554_1 [H.s	1.11	1.49
	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein	1	1.03
	107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	1.13	3.63
	107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.c	1.05	2.09
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	1.18	1.9
35	107481	W58247	Hs.27437	Homo sapiens kinesin superfamily motor K	0.99	2.74
	107516	X56597	Hs.99853	fibrillarin	0.94	1.77
	107529	Y12065	Hs.5092	nuclear protein (KKE/D repeat)	1.05	2.29
	107531	Y13936	Hs.17883	protein phosphatase 1G (formerly 2C); ma	1.06	1.62
	107801	AA019433	Hs.173100	ESTs	1.03	1.4
40	107957	AA031948	Hs.57548	ESTs	0.95	1.46
	108565	AA085342	Hs.1526	ATPase; Ca++ transporting; cardiac muscl	0.69	1.35
	108780	AA128561	Hs.117938	collagen; type XVII; alpha 1	1	7.63
	108828	AA131584	Hs.71435	DKFZP564O0463 protein	1.33	2.56
	109060	AA160879	Hs.241551	chloride channel; calcium activated; fam	0.67	1.42
45	109112	AA169379	Hs.72865	ESTs	1.03	2.31
	109344	AA213696	Hs.86559	poly(A)-binding protein-like 1	0.97	1.55
	109412	AA227145	Hs.209473	ESTs; Weakly similar to REGULATOR OF MIT	0.76	1.87
	110780	N23174	Hs.22891	solute carrier family 7 (cationic amino	0.9	0.95
	110958	N50550	Hs.24587	signal transduction protein (SH3 contain	1.17	2.26
50	111018	N54067	Hs.3628	mitogen-activated protein kinase kinase	1.21	1.85
	111337	N78612	Hs.16607	ESTs; Highly similar to Myosin heavy cha	1	1.45
	112305	R54822	Hs.26244	ESTs	1	1
	112401	R61279	Hs.237536	ESTs; Weakly similar to F25B5.3 [C.elega	1.24	1.64
	112853	T02843	Hs.4351	EST	1.56	1.96
55	112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	1.03	1.57
	112992	T23513	Hs.7147	ESTs	1	1
	113048	T25895	Hs.184008	ESTs; Weakly similar to RNA-binding prot	1.37	2.26
	113063	T32438	Hs.5027	ESTs	1	1
	113179	T55182	Hs.152571	ESTs; Highly similar to IGF-II mRNA-bind	1.33	2.7
60	113573	T91166	Hs.15990	ESTs	0.76	1.47
	113811	W44928	Hs.4878	ESTs	0.79	1.51
	114086	Z38266	Hs.12770	Homo sapiens PAC clone DJ0777023 from 7p	0.9	1.34
	114587	AA070827	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEM	1.02	1.76
	114846	AA234929	Hs.44343	ESTs	1.32	2.36
65	114964	AA243873	Hs.82184	ring finger protein 3	1.1	1.84
	115047	AA252627	Hs.22554	homeo box B5	1.01	2.38
	115166	AA258409	Hs.198907	myelin protein zero-like 1	1.05	2.31
	115167	AA258421	Hs.43728	hypothetical protein	1.52	2.52
	115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the b	0.7	2.67
70	115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.m	1.14	2.12
	115652	AA405098	Hs.38178	ESTs	0.82	4.67
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity	1.2	1.98
	116004	AA449122	Hs.76086	ESTs; Highly similar to small zinc finge	0.98	1.31
	116121	AA459254	Hs.48855	ESTs	0.97	1.55
75	116129	AA459956	Hs.49163	ESTs; Highly similar to putative ribonuc	1.08	2.73
	116190	AA464963	Hs.67776	ESTs	0.8	1.57
	116312	AA490494	Hs.65403	ESTs	1.37	2.65
	116732	F13779	Hs.165909	ESTs	0.92	1.8
	117602	N35020	Hs.44685	ESTs; Weakly similar to GOLIATH PROTEIN	1.15	1.84
80	117950	N51394	Hs.75478	KJAA0956 protein	1.04	2.36
	117992	N52000	Hs.172069	Homo sapiens mRNA; cDNA DKFZp586B0222 (f	0.62	1.29
	118785	N75386	Hs.111867	GLI-Kruppel family member GLI2	1	1
	119717	W69134	Hs.57987	ESTs	1	1.4
	119814	W74069	Hs.58350	ESTs	0.78	1.77
85	120128	Z38499	Hs.91448	MKP-1 like protein tyrosine phosphatase	0.86	1.46
	120242	Z98443	Hs.86366	ESTs	0.83	2.01

	120483	AA252994	Hs.1578	apoptosis inhibitor 4 (survivin)	0.74	1.64
	121054	AA398604	Hs.97387	ESTs	1.05	1.93
	121326	AA404246	Hs.97031	ESTs; Weakly similar to Similar to phyto	0.98	1.3
	121376	AA405699	Hs.166232	ESTs; Moderately similar to SODIUM- AND	0.91	1.83
5	121457	AA411448	Hs.208985	ESTs	0.91	1.59
	121780	AA422086	Hs.124660	ESTs	0.46	0.55
	121781	AA422150	Hs.98370	cytochrome P540 family member predicted	1.07	1.54
	121844	AA425732	Hs.98485	gap junction protein; beta 2; 26kD (conn	0.94	1.4
10	122059	AA431737	Hs.98749	EST	1.93	2.33
	122338	AA443311	Hs.98998	ESTs	1	1
	122354	AA443772	Hs.186692	ESTs	0.88	1.39
	122591	AA453265	Hs.99311	ESTs; Weakly similar to MRJ (H.sapiens)	2.28	2.93
	122790	AA460156	Hs.99556	ESTs	0.88	1.3
15	123398	AA521265	Hs.105514	ESTs	1	1.93
	123518	AA608531	Hs.170313	ESTs	1	1
	123673	AA609471	Hs.112712	ESTs	1	1.15
	124000	D57317	Hs.74861	activated RNA polymerase II transcriptio	0.74	1.12
	124367	N24006	Hs.99348	distal-less homeo box 5	0.67	1.1
20	124447	NA8000	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	1.19	1.7
	125756	W25498	Hs.81634	ATP synthase; H+ transporting; mitochond	0.93	1.59
	125769	AI382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.65	6.76
	125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	0.72	2.26
	125924	AA526849	Hs.82109	syndecan 1	1.22	2.25
25	126037	M85772	Hs.6066	KIAA1112 protein	1.36	1.63
	126214	N29455	Hs.74316	desmoplakin (DPI; DPLI)	1.93	3.55
	126414	N78770	Hs.223439	ESTs	1.21	1.66
	126737	AA488132	Hs.62741	ESTs	1	1
	126743	AA179253	Hs.172182	poly(A)-binding protein; cytoplasmic 1	1.3	2.16
30	126928	AA179546	Hs.832	ESTs; Highly similar to INTEGRIN BETA-8	2.53	2.8
	127432	AA501734	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.57	2.12
	128218	H02682	Hs.99189	ESTs; Moderately similar to recombinatio	1.24	2.09
	128527	M31523	Hs.101047	transcription factor 3 (E2A immunoglobul	1.08	1.78
	128568	X60673	Hs.247568	adenylate kinase 3	1.23	3.48
35	128584	M11433	Hs.101850	retinol-binding protein 1; cellular	0.87	2.42
	128628	C14037	Hs.251978	EST	1.22	1.9
	128691	W27939	Hs.103834	ESTs	1.1	1.73
	128714	V00599	Hs.179661	Homo sapiens clone 24703 beta-tubulin mR	0.92	1.17
	128733	AA328993	Hs.104558	ESTs	1.34	1.94
40	128781	X85372	Hs.105465	small nuclear ribonucleoprotein polypept	0.9	1.34
	129052	AA496297	Hs.182740	ribosomal protein S11	2.59	3.19
	129095	L12350	Hs.108623	thrombospondin 2	1.04	3.2
	129241	AA435665	Hs.109706	ESTs; Moderately similar to HN1 (M.muscu	0.95	1.61
	129665	M88458	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.28	2.63
45	129703	AA401348	Hs.179999	ESTs	0.97	1.63
	129720	AA476582	Hs.12152	ESTs; Moderately similar to SIGNAL RECOG	1.09	1.79
	129850	N20593	Hs.56845	GDP dissociation inhibitor 2	0.74	1.68
	129896	AA043021	Hs.13225	UDP-Gal:betaGlcNAc beta 1;4- galactosyl	1.43	4.19
	130069	AA055896	Hs.146428	collagen; type V; alpha 1	1.17	1.98
50	130405	H88359	Hs.155396	nuclear factor (erythroid-derived 2)-lik	1.26	1.79
	130541	X05608	Hs.211584	neurofilament; light polypeptide (68kD)	1	1
	130599	M91670	Hs.174070	ubiquitin carrier protein	1.07	1.66
	130867	J04093	Hs.2056	UDP glycosyltransferase 1	1	4.8
	131009	AA063596	Hs.22142	ESTs; Weakly similar to NADH-CYTOCHROME	0.93	1.05
55	131028	U20240	Hs.2227	CCAAT/enhancer binding protein (C/EBP);	1	1.23
	131083	U66661	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.1	1.8
	131091	T35341	Hs.22880	ESTs; Highly similar to dipeptidyl pept	1.28	1.98
	131144	C14412	Hs.23528	ESTs; Highly similar to HSPC038 protein	1.43	2.06
	131148	C00038	Hs.23579	ESTs	0.88	3.38
60	131164	Y00503	Hs.182265	keralin 19	1.19	2.77
	131185	M25753	Hs.23960	cyclin B1	0.86	3.84
	131219	C00476	Hs.24395	small inducible cytokine subfamily B (Cy	0.66	2.96
	131454	AA455896	Hs.2699	glypican 1	0.99	1.54
	131687	L11066	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1	1.18
65	131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix	1	1.95
	131692	D50914	Hs.30736	KIAA0124 protein	1.55	2.39
	131786	AA135554	Hs.32125	ESTs	1	1.33
	131843	AA195893	Hs.184062	ESTs; Moderately similar to putative Rab	0.83	1.63
	131860	U02082	Hs.334	Oncogene TIM	1.08	2.2
70	131884	H90124	Hs.3463	ribosomal protein S23	1.23	1.24
	131903	AA481723	Hs.3436	deleted in oral cancer (mouse; homolog)	0.91	1.18
	131945	M87339	Hs.35120	replication factor C (activator 1) 4 (37	1	2.8
	131958	AA093998	Hs.3566	ESTs; Highly similar to phosphorylation	0.87	1.36
	131964	W42508	Hs.3583	ESTs	1	1.25
75	132001	J00277	Hs.37003	v-Ha-ras Harvey rat sarcoma viral oncoge	1.12	1.43
	132040	AA146843	Hs.172894	BH3 interacting domain death agonist	1	1.55
	132065	D82226	Hs.211594	proteasome (prosome; macropain) 26S subu	0.89	1.27
	132109	AA599801	Hs.40098	ESTs	1	1.05
	132112	AA150661	Hs.40154	jumonji (mouse) homolog	0.99	1.44
80	132123	AA447123	Hs.250705	ESTs	1.06	2.46
	132162	H89551	Hs.41241	ESTs	1.08	2.46
	132180	AA405569	Hs.418	fibroblast activation protein; alpha; se	1.02	4.56
	132309	AA460917	Hs.2780	jun D proto-oncogene	1.16	1.8
	132371	AA235448	Hs.46677	ESTs	0.8	1.26
85	132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma	0.5	1.49
	132738	U68019	Hs.211578	MAD (mothers against decapentaplegic; Dr	1.21	1.81

5	132771	AA488432	Hs.56407	phosphoserine phosphatase	1	1.3
	132833	U78525	Hs.57783	eukaryotic translation initiation factor	0.91	1.43
	132922	T23641	Hs.6066	KIAA1112 protein	1.16	1.53
	132959	AA028103	Hs.61472	ESTs; Weakly similar to unknown [S.cerev	1.02	1.88
	132994	AA505133	Hs.7594	solute carrier family 2 (facilitated glu	0.72	2.97
	133005	C21400	Hs.103329	KIAA0970 protein	0.88	1.34
	133065	X62535	Hs.172690	diacylglycerol kinase; alpha (80kD)	0.93	1.23
	133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (b	1.14	1.76
10	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso	0.97	1.43
	133134	T89703	Hs.65648	RNA binding motif protein 8	1.1	1.8
	133195	AA350744	Hs.181409	KIAA1007 protein	2.29	2.69
	133313	AA249427	Hs.70704	ESTs	1.07	1.68
	133331	T62039	Hs.158675	ribosomal protein L14	0.85	1.18
15	133438	D13370	Hs.73722	APEX nuclease (multifunctional DNA repa	0.91	1.45
	133445	T99303	Hs.73797	guanine nucleotide binding protein (G pr	0.94	1.68
	133483	X52426	Hs.74070	keratin 13	0.85	1.14
	133492	L40397	Hs.74137	transmembrane trafficking protein	1.1	1.69
	133504	W95070	Hs.74316	desmoplakin (DP1; DP11)	0.7	6.21
20	133517	X52947	Hs.74471	gap junction protein; alpha 1; 43kD (con	0.95	1.3
	133540	D78151	Hs.74619	proteasome (prosome; macropain) 26S subu	0.91	1.25
	133594	L07758	Hs.172589	nuclear phosphoprotein similar to S. cer	0.84	1.29
	133627	U09587	Hs.75280	glycyl-tRNA synthetase	1.09	1.99
	133671	T25747	Hs.75471	zinc finger protein 146	1.02	1.5
25	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	1.11	3.33
	133865	F09315	Hs.170290	disca; large (Drosophila) homolog 5	1.84	6.7
	133913	W84712	Hs.7753	calumenin	1.15	1.86
	133963	L34587	Hs.184693	transcription elongation factor B (SIII)	1.3	1.91
	133982	U47621	Hs.207251	nucleolar autoantigen (55kD) similar to	1.3	1.99
30	134100	L07540	Hs.171075	replication factor C (activator 1) 5 (36	0.72	1.65
	134110	U41060	Hs.79136	LIV-1 protein; estrogen regulated	1.04	1.62
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	1	1.55
	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	0.82	1.95
	134193	F09570	Hs.7980	ESTs	0.98	1.48
35	134367	X54199	Hs.82285	phosphoribosylglycinamide formyltransfer	1	2.8
	134402	U25165	Hs.82712	fragile X mental retardation; autosomal	1.26	2
	134457	D86963	Hs.174044	dishevelled 3 (homologous to Drosophila	1	1.47
	134469	X17567	Hs.83753	small nuclear ribonucleoprotein polypept	0.94	1.57
	134498	M63180	Hs.84131	threonyl-tRNA synthetase	1.2	2.64
40	134501	W84870	Hs.211568	eukaryotic translation initiation factor	0.84	1.36
	134507	M63488	Hs.84318	replication protein A1 (70kD)	1.7	2.93
	134548	U41515	Hs.85215	Deleted in split-hand/split-foot 1 regio	1.46	2.73
	134599	X99226	Hs.86297	Fanconi anemia; complementation group A	1.36	2.22
	134692	R73567	Hs.8850	a disintegrin and metalloproteinase doma	0.77	1.64
45	134693	N70361	Hs.8854	ESTs	1.09	1.82
	134806	Z49099	Hs.89718	spermine synthase	0.98	1.35
	134821	Z34974	Hs.198382	plakophilin 1 (ectodermal dysplasia/skin	0.99	1.4
	134864	Y08999	Hs.90370	actin related protein 2/3 complex; subun	0.95	1.42
	134914	U29815	Hs.91093	chitinase 1 (chitinobiosidase)	1.16	1.29
50	134953	L10678	Hs.91747	profilin 2	0.95	1.76
	134993	AA282343	Hs.9242	purine-rich element binding protein B	0.98	1.73
	135051	C15324	Hs.93668	ESTs	1.35	2.11
	135158	U51711		Human desmocollin-2 mRNA; 3' UTR	0.86	1.16

55 Table 1B shows the accession numbers for those pkays in Table 1A lacking unigenal IDs. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the Accession column.

60 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT	Accessions
65	100661 23182_1 100667 26401_3	BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655 L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 A1632506 T29068 A1783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 A1420712 BE620922 A1279161 AA992549 W47198 BE005241 A1342698 H50700 A1969974 A1863855 AA374490 AW130675 A1950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 A1673068 A1887890 AW804171 A1675961 AW804172 AA778841 AL048050 A1127757 A1095568 AW204965 AW468978 W31898 A1052595 A1278771 BE464018 A1081503 A1824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 A1280942 T27619 BE621435 N66010 AW589527 A1160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
70		
75	100668 26401_3	L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 A1632506 T29066 A1783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 A1420712 BE620922 A1279161 AA992549 W47198 BE005241 A1342698 H50700 A1969974 A1863855 AA374490 AW130675 A1950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 A1673068 A1887890 AW804171 A1675961 AW804172 AA778841 AL048050 A1127757 A1095568 AW204965 AW468978 W31898 A1052595 A1278771 BE464018 A1081503 A1824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 A1280942 T27619 BE621435 N66010 AW589527 A1160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
80		
85	101332 25130_1	J04088 NM_001067 AF071747 AJ011741 N85424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA104024 A1471482 A1970337 AA737616 A1827444 AW003286 A1742333 A1344044 A1765634

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A1948838 AW235336 AW172827 AA095289 BE046383 A1734240 W16699 A1660329 A1289433 AA933778 AW469242 AA468838 AA806983
 AA625873 W78031 BE206307 AA550803 A1743147 A1990075 AA948274 AA129533 A1635399 AA605313 A1624669 AW594319 A1221834 A1337434
 A10307706 BE550282 A1760467 A1630836 A1221521 AW674314 AW078889 A1933732 A1686969 A186928 AW074595 A1127486 A1079644
 A1910815 H17814 AA310903 AW137854 T19279 AA026682 AA306035 AW383390 AW383389 AW383422 AW383427 AW383395 H09977
 AA306247 AA352501 AW0403639 F05421 AA224473 AA305321 H93904 AA089612 AW391543 AW402915 AW173382 AW402701 AW403113
 R94438 N73126 H93466 AA090928 AA095051 T29025 AW951071 L47277 L47276 A1375913 BE384156 W24652 AA746288 AA568223 BE090591
 H93033 N57027 AA504348 AA327653 AW959913 N53767 AA843715 A1453437 AW263710 A1076594 AA583483 AW873194 AW575166 A1128799
 A1803319 AL042776 AW074313 A1887722 A1032284 AA447521 A1123885 N29334 A1354911 AW090687 AA236763 AA435535 AA236910
 AA047124 AA236734 AW514610 H93467 AA952007 A1446783 AA127259 A1613495 A1686720 A1587374 AA936731 AA702453 A1859757
 AA216786 A1251819 A1469227 AA806022 A1092324 N71868 AA968782 AA236919 AA809450 AA227220 AA765284 A1192007 AA768810
 AA805794 AA729280 AA806238 AW768817 N71879 A1050686 AA505822 AA668974 A1688160 BE045915 AW466315 AA731314 AA649568
 AA834316 AW591901 AW063876 AW294770 A100266 A1336094 A1560380 AA721755 H09978 D20305 D29165 AW821790 BE150854 F01876
 A1457474 AW466316 AA550969 AA530788
 BE561958 BE561728 BE397612 BE514391 BE269037 BE514207 BE562381 BE514256 BE514403 BE514250 BE397832 BE269598 BE559865
 BE396881 BE560031 BE514199 BE560037 BE560454
 100780 458_127
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 H42334 H38280 AA121497 AA114137 AI750938 M17783 AA383786 BE274462 AI753182 C05975 AA347404 AW069298 AI754351 AI754044
 AA188808 AA186879 AA565243 AL040655 AA456177 AI750722 AA045756 AA213580 C16936 AW578747 AW753731 H41632 N44761 R58560
 R61260 AA039902 N59721 AW992543 R68380 AA149686 T29017 H03739 BE383822 BE387105 BE408251 BE410425 H41660 AA247591
 BE389677 AI752233 AI566195 AA868004 AI424523 AW753720 AA852159 BE386803
 NM_000094 L02870 D13694 S51236 M96984 AW946290 M65158 AI285422 D29523 AL119886 AW630655 L06862 AI884355 AW168737 T29085
 AW797005 AW801340 AI355504 AW079048 AW801337 AI690455 AI972063 AW268565 W68588 AA587326 AA883498 AI033523 AW510356
 AW591998 H98463 AL043852 AI150055 AI566239 AI624803 AA844717 H40670 AA922334 AI864424 AW615094 AW451233 AI302203 F31221
 AI872170 W68589 AA904478 AI917631 AW014208 AW450759 AA847625 AI284033 AA848176 AA598507
 X00356 NM_001741 M26095 X03662 M12667 X02330 X02330 AA716058 AW296074 X04861 AI695720 AA719597
 N22401
 AL037551 AI804716 AW439811 AI569470 AA075299 AI738572 AI270388 AI816783 AW263026 AI633951 AI655285 AI990572 AI950425
 AW241533 AA916883 AA576693 AA160156 AA613783 AW078884 AI888282 AI275241 AI133467 AA164921

Tables 2A-8C were previously filed on November 9, 2001 in USSN 60/339,245 (18501-004100US)

Table 2A shows 504 genes down-regulated in lung tumors relative to normal lung and chronically diseased lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of AI for normal lung samples divided by the 80th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
 R2: median of AI for normal lung samples divided by 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
 R3: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
 R4: average of AI for normal lung samples divided by average AI for squamous cell carcinoma and adenocarcinoma lung tumors.
 R5: median of AI for normal lung samples divided by the 90th percentile of AI for adenocarcinomas.
 R6: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
 R7: average of AI for normal lung samples divided by the 90th percentile of AI for squamous cell carcinomas.
 R8: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for squamous cell carcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3	R4	R5	R6	R7	R8
100095	Z97171	Hs.78454	myocilin; trabecular meshwork inducible	40.20							
100115	NM_002084	Hs.336920	glutathione peroxidase 3 (plasma)								3.46
100138	U83508	Hs.2463	angiopoietin 1			2.30					
100299	D49493	Hs.2171	growth differentiation factor 10		11.00						
100305	U86749	Hs.80598	transcription elongation factor A (SII);						3.08		
100447	NM_014767	Hs.74583	KIAA0275 gene product								3.16
100458	S74019	Hs.247979	Vpre-B	42.40							
100862	AA005247	Hs.285754	Hepatocyte Growth Factor Receptor						4.13		
100959	AA359129	Hs.118127	actin; alpha; cardiac muscle				125.60				
101032	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	36.40							
101081	AF047347	Hs.4880	amyloid beta (A4) precursor protein-bind				34.60				
101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte				193.20				
101125	AJ250562	Hs.82749	transmembrane 4 superfamily member 2						3.10		
101180	U11874	Hs.846	Interleukin 8 receptor; beta				54.86				
101308	L41390		*Homo sapiens core 2 beta-1,6-N-acetylgl	33.20							
101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do				36.40				
101345	NM_005795	Hs.152175	Calcitonin receptor-like			2.29					
101346	AJ738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				70.55				
101397	M26380	Hs.180878	lipoprotein lipase								3.54
101414	NM_000066	Hs.38069	complement component 8; beta polypeptide				34.60			3.81	
101435	NM_001100	Hs.1288	actin; alpha 1; skeletal muscle				37.60				
101507	X16896	Hs.82112	Interleukin 1 receptor; type I								4.25
101530	M29874	Hs.1360	cytochrome P450; subfamily IIB (phenobar			2.54					
101537	AJ469059	Hs.184915	zinc finger protein; Y-linked								
101542	NM_000102	Hs.1363	cytochrome P450; subfamily XVII (steroid		5.50						
101545	BE246154	Hs.154210	EDG1; endothelial differentiation, sphin	39.40							
101554	BE207611	Hs.123078	thyroid stimulating hormone receptor		13.00						
101560	AW858272	Hs.83733	Intercellular adhesion molecule 2, exon								3.38
101574	M34182	Hs.158029	protein kinase; cAMP-dependent; catalyti						4.37		
101605	M37984	Hs.118845	troponin C; slow								3.80
101621	BE391804	Hs.62661	guanylate binding protein 1; Interferon-	30.20							
101680	AA299330	Hs.1042	Sjogren syndrome antigen A1 (52kD; ribon						3.37	2.75	
101829	AW452398	Hs.129763	solute carrier family 8 (sodium/calcium				38.20				
101842	M93221	Hs.75182	mannose receptor; C type 1								
101961	AW004056	Hs.168357	*Hs-TBX2=T-box gene (T-box region) [huma			2.32					
101994	T92248	Hs.2240	uteroglobin								6.85
102020	AU077315	Hs.154970	transcription factor CP2			2.45					
102091	BE280901	Hs.83155	aldehyde dehydrogenase 7								6.75
102112	AW025430	Hs.155591	forkhead box F1	54.60							
102190	AA723157	Hs.73769	folate receptor 1 (adult)								3.98
102202	NM_000507	Hs.574	fructose-bisphosphatase 1								3.62
102241	NM_007351	Hs.288107	Multimerin			2.32					
102310	U33839		Accession not listed in Genbank		7.00						
102397	U41898		*Human sodium cotransporter RKST1 mRNA,	29.40							
102571	U60115	Hs.239069	*Homo sapiens skeletal muscle LIM-protein								3.75
102620	AA976427	Hs.121513	Human clone W2-6 mRNA from chromosome X						3.07		
102636	U67092		*Human ataxia-telangiectasia locus prote			2.40					
102667	U70867	Hs.83974	solute carrier family 21 (prostaglandin			3.15					
102675	U72512	Hs.7771	*Human B-cell receptor associated protei						3.56		
102698	M18667	Hs.1867	progastricin (papsinogen C)								4.51
102727	U79251	Hs.99902	opioid-binding protein/cell adhesion mol					12.00			
102852	V00571	Hs.75294	corticotropin releasing hormone	37.40							
103026	X54162	Hs.79386	thyroid and eye muscle autoantigen D1 (6					13.00			
103028	X54380	Hs.74094	pregnancy-zone protein	28.80							
103098	M86361		Human mRNA for T cell receptor; clone IG					10.00			
103117	X63578	Hs.295449	parvalbumin		6.00						
103241	X76223		H.sapiens MAL gene exon 4			2.47					
103280	U84722	Hs.76206	Cadherin 5, VE-cadherin (vascular eplthe			2.69					
103360	Y16791	Hs.73082	keratin; hair; acidic; 5							2.16	

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5.97

	103496	Y09267	Hs.132821	flavin containing monooxygenase 2					
	103508	Y10141		"H.sapiens DAT1 gene, partial, VNTR"				3.27	
	103561	NM_001843	Hs.143434	contactin 1	2.40				
5	103569	NM_005512	Hs.151641	glycoprotein A repetitions predominant	2.99			4.18	
	103575	Z26256		"H.sapiens isoform 1 gene for L-type cal				3.44	
	103627	Z48513		H.sapiens XG mRNA (clone PEP6)					2.25
	103767	BE244667	Hs.296155	CGI-100 protein			48.55		
	103850	AA187101	Hs.213194	Hypothetical protein MGC10895; sim to SR					
10	104078	AA402801	Hs.303276	ESTs				3.05	
	104326	AW732858	Hs.143067	ESTs				3.54	
	104352	BE219898	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl				3.16	
	104398	AI423930	Hs.36790	ESTs; Weakly similar to putative p150 [H	64.80				
	104473	AI904823	Hs.31297	ESTs					3.38
	104493	AW960427	Hs.79059	ESTs; Moderately similar to TGF-BETA REC		2.47			
15	104495	AW975687	Hs.292979	ESTs	28.60				
	104595	AI799603	Hs.271568	ESTs				3.42	
	104597	AI364504	Hs.93967	ESTs; Weakly similar to Sliit-1 protein [6.00			
	104659	AW969769	Hs.105201	ESTs	34.00				
20	104686	AA010539	Hs.18912	ESTs		11.00			
	104691	U29690	Hs.37744	ESTs; Beta-1-adrenergic receptor	56.80				
	104764	AI039243	Hs.278585	ESTs			60.40		
	104776	AA026349		ESTs	34.20				
	104825	AA035613	Hs.141883	ESTs		3.03			
25	104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fls, clone C	41.20				3.27
	104942	NM_016348	Hs.10235	ESTs					
	104989	R65998	Hs.285243	ESTs			40.00		
	105062	AW954355	Hs.36529	ESTs					3.20
	105101	H63202	Hs.38163	ESTs	34.20				
30	105173	U54617	Hs.8364	ESTs					4.17
	105194	R06780	Hs.19800	ESTs		16.00			
	105226	R58958	Hs.26808	ESTs					
	105256	AA430650	Hs.16529	transmembrane 4 superfamily member (tet		2.34			
	105394	BE245812	Hs.8941	ESTs		2.72			
	105647	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	33.60				
35	105789	AF106941	Hs.18142	arrestin; beta 2					3.59
	105817	AA397825		synaptopodin					
	105847	AW964490	Hs.32241	ESTs			35.40		4.46
	105894	AI904740	Hs.25691	calcitonin receptor-like receptor activi		3.43			
40	105999	BE268786	Hs.21543	ESTs		7.00			
	106075	AA045290	Hs.25930	ESTs			42.60		
	106178	AL049935	Hs.301763	KIAA0654 protein	34.80				
	106381	AB040916	Hs.24106	ESTs			12.00		
	106467	AA450040	Hs.154162	ADP-ribosylation factor-like 2					3.69
45	106536	AA329648	Hs.23604	ESTs			96.40		
	106569	R20909	Hs.300741	sorcin			47.20		
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr			220.40		
	106842	AF124251	Hs.26054	novel SH2-containing protein 3		2.55			
	106844	AA485055	Hs.158213	sperm associated antigen 6	39.20				
	106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl		2.28			
50	106943	AW888222	Hs.9973	ESTs					4.28
	106954	AF128847	Hs.204038	ESTs					4.32
	107106	AA862496	Hs.28482	ESTs			10.45		
	107163	AF233588	Hs.27018	ESTs		2.57			
55	107201	D20378	Hs.30731	EST				3.84	
	107238	D59362	Hs.330777	EST		8.00			
	107376	U90545	Hs.327179	solute carrier family 17 (sodium phospho		10.67			
	107530	Y13822	Hs.85087	latent transforming growth factor beta b		2.32			
	107688	AW082221	Hs.60536	ESTs			34.60		
60	107706	AA015579	Hs.29276	ESTs	28.40				
	107723	AA015967		EST				3.29	
	107727	AA149707	Hs.173091	DKFZP434K151 protein			80.80		
	107750	AA017291	Hs.60781	ESTs			51.40		
	107751	AA017301	Hs.235390	ESTs					3.14
65	107873	AK000520	Hs.143811	ESTs		9.00			
	107899	BE019261	Hs.83869	ESTs; Weakly similar to IIII ALU SUBFAM1					3.65
	107994	AA036811	Hs.48469	ESTs			44.60		
	107997	AL049176	Hs.82223	Human DNA sequence from clone 141H5 on c			32.00		
	108041	AW204712	Hs.61957	ESTs			30.80		
70	108048	AI797341	Hs.165195	ESTs					4.75
	108338	AA070773		*zm53g11.s1 Stratagene fibroblast (#9372		2.33			2.92
	108434	AA078899		*zm94b1.s1 Stratagene colon HT29 (#93722					
	108447	AA079126		*zm92a11.s1 Stratagene ovarian cancer (#				3.06	
	108480	AL133092	Hs.68055	ESTs			34.00		
75	108499	AA083103		*zn1b12.s1 Stratagene hNT neuron (#93723					3.36
	108535	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence			19.00		
	108550	AA084867		*zn11f6.s1 Stratagene hNT neuron (#93723			12.00		
	108604	AA934589	Hs.49696	ESTs		2.33			
	108625	AW972330	Hs.283022	ESTs					5.82
	108629	AA102425		*zn24c6.s1 Stratagene neuroepithelium NT				3.42	
80	108655	AA099960		*zm65c6.s1 Stratagene fibroblast (#93721		7.00			
	108756	AA127221	Hs.117037	Homo sapiens mRNA; cDNA DKFZp564N1164 (f		6.05			
	108864	AI733852	Hs.199957	ESTs	28.80				
	108895	AL138272	Hs.62713	ESTs	32.80				
	108921	AI568801	Hs.71721	ESTs			57.80		
85	108967	AA142989	Hs.71730	ESTs	28.80				

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	109001	AI056548	Hs.72116	ESTs, Moderately similar to hedgehog-int	2.57				
	109003	AA147497	Hs.71825	ESTs				2.11	
	109004	AA156235	Hs.139077	EST	5.60				
5	109065	AA161125	Hs.252739	EST			10.00		
	109250	H83784	Hs.62113	ESTs; Weakly similar to PHOSPHATIDYLETHA				3.44	
	109490	AA233416	Hs.139202	ESTs				2.92	
	109510	AI798863	Hs.87191	ESTs	2.40				
	109578	F02208	Hs.27214	ESTs	10.00				
10	109601	F02695	Hs.311662	EST			40.80		
	109613	H47315	Hs.27519	ESTs			54.40		
	109560	R31770	Hs.23540	ESTs	31.20				
	109682	H18017	Hs.22869	ESTs	8.40				
	109724	D59899	Hs.127842	ESTs			29.40		
	109782	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene			8.00		
15	109833	R79864	Hs.29889	ESTs	10.00				
	109837	H00656	Hs.29792	ESTs	6.49				
	109977	T64183	Hs.282982	ESTs				2.75	
	109984	AI796320	Hs.10299	ESTs			107.00		
20	110146	H41324	Hs.31581	ESTs; Moderately similar to SYNTAXIN 18				2.22	
	110271	H28985	Hs.31330	ESTs				3.48	
	110280	AW874263	Hs.32468	ESTs	44.20				
	110420	R93141	Hs.184261	ESTs			32.00		
	110578	T62507	Hs.11038	ESTs	28.40				
25	110634	R98905	Hs.35592	ESTs			20.00		
	110726	AW961818	Hs.24379	polassium voltage-gated channel; shaker-					4.15
	110837	H03109	Hs.108920	ESTs; Weakly similar to semaphorin F [H.			56.80		
	110875	N35070	Hs.26401	tumor necrosis factor (ligand) superfamily	3.13				
	110894	R92356	Hs.66881	ESTs; Moderately similar to cytoplasmic	5.33				
30	110971	AI760098	Hs.21411	ESTs			44.60		
	111023	AV655386	Hs.7645	ESTs	32.40				
	111057	T79639	Hs.14629	ESTs			17.14		
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f				4.58	
	111330	BE247767	Hs.18166	KIAA0870 protein					3.42
35	111374	BE250726	Hs.283724	ESTs; Moderately similar to HYA22 [H.sap				3.91	
	111442	AW449573	Hs.181003	ESTs			33.20		
	111737	H04607	Hs.9218	ESTs			53.00		
	111747	AI741471	Hs.23666	ESTs	46.20				
	111807	R33508	Hs.18827	ESTs	16.00				
40	111862	R37472	Hs.21559	EST				3.91	
	112045	AI372588	Hs.8022	TU3A protein				2.74	
	112057	R43713	Hs.22945	EST				4.92	
	112214	AW148652	Hs.167398	ESTs			13.00		
	112263	R52393	Hs.25917	ESTs		2.43			
45	112314	AW206093	Hs.748	ESTs	9.00				
	112324	R55965	Hs.26479	limbic system-associated membrane protein			14.00		
	112362	AW300887	Hs.26638	ESTs; Weakly similar to CD20 receptor [H		2.49			
	112380	H63010	Hs.5740	ESTs		2.34			
	112425	AA324998	Hs.321677	ESTs; Weakly similar to IIII ALU SUBFAMI	8.00				
50	112473	R65993	Hs.279798	pregnancy specific beta-1-glycoprotein 9				4.53	
	112492	N51620	Hs.28694	ESTs			29.80		
	112541	AF038392	Hs.116674	ESTs				3.62	
	112620	R80652	Hs.29040	ESTs	2.37				
	112623	AW373104	Hs.25094	ESTs	2.26				
55	112867	T03264	Hs.167393	ESTs			12.00		
	112894	T08188	Hs.3770	ESTs	6.50				
	112954	AA928953	Hs.6655	ESTs	7.00				
	113029	AW081710	Hs.7369	ESTs; Weakly similar to IIII ALU SUBFAMI					4.39
	113086	AA346839	Hs.209100	DKFZP434C171 protein					4.47
60	113140	T50405	Hs.175967	ESTs			10.00		
	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	14.00				
	113257	AI821378	Hs.159367	ESTs				3.72	
	113394	T81473	Hs.177894	ESTs				3.60	
	113437	T85349	Hs.15923	EST	35.00				
65	113454	AI022166	Hs.16188	ESTs	6.00				
	113502	T89130		ESTs	39.60				
	113552	AI654223	Hs.16026	ESTs					3.88
	113645	T95358	Hs.333181	ESTs				2.58	
	113691	T96935	Hs.17932	EST			38.20		
70	113706	AA004693	Hs.269192	ESTs				3.09	
	113883	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	2.31				
	113924	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	30.40				
	114035	W92798	Hs.269181	ESTs			13.00		
	114058	AK002016	Hs.114727	ESTs					5.00
75	114084	AA708035	Hs.12248	ESTs			40.60		
	114121	H05785	Hs.25425	ESTs	2.31				
	114124	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)	7.00				
	114275	AW515443	Hs.306117	Interleukin 13 receptor; alpha 1	6.00				
	114297	AA149707	Hs.173091	DKFZP434K151 protein			48.80		
80	114427	AA017176	Hs.33532	ESTs; Highly similar to Miz-1 protein [H				3.45	
	114449	AA020736		*ze63b11.s1 Soares retina N2b4HR Homo sa			10.00		
	114452	AI369275	Hs.243010	ESTs, Moderately similar to RTC0_HUMAN G	14.00				
	114609	AA079505		*zm97a5.s1 Stratagene colon HT29 (#93722				3.13	
	114648	AA101056		*zn25b3.s1 Stratagene neuroepithelium NT			35.40		
85	114731	BE094291	Hs.155651	Homo sapiens HNF-3beta mRNA for hepatocy					3.42
	114762	AA146979	Hs.288464	ESTs	33.00				

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	114776	AA151719	Hs.95834	ESTs	34.40				
	115009	AA251561	Hs.48689	ESTs	30.20				
	115272	AW015947		ESTs; Weakly similar to hypothetical L1	32.60				
5	115279	AW964897	Hs.290825	ESTs		6.00		12.00	
	115302	AL109719	Hs.47578	ESTs					3.32
	115365	AW976252	Hs.268391	ESTs					
	115559	AL079707	Hs.207443	ESTs				48.00	
	115566	AI142336	Hs.43977	ESTs				56.20	
10	115683	AF255910	Hs.54650	ESTs; Weakly similar to (define not ava	31.40				
	115744	AA418538	Hs.43945	ESTs; Highly similar to dJ1178H5.3 [H.s.a				33.60	
	115819	AA486620	Hs.41135	Endomucin 2				74.40	
	115949	AI478427	Hs.43125	ESTs		3.18			
	115965	AA001732	Hs.173233	ESTs				388.80	
15	116035	AA621405	Hs.184664	ESTs				33.20	
	116049	AA454033	Hs.41644	ESTs				45.80	
	116081	AI190071	Hs.55278	ESTs					3.57
	116082	AB029498	Hs.59729	ESTs		3.06			
	116213	AA292105	Hs.326740	leucine rich repeat (in FLII) Interactin	50.80				
20	116228	AI767947	Hs.50841	ESTs; Weakly similar to tuftelin [M.musc		3.85			
	116250	N76712	Hs.44829	ESTs		6.00			
	116419	AI613480	Hs.47152	ESTs; Weakly similar to testicular tekti				30.00	
	116617	D80761	Hs.45220	EST		2.27			
	116784	AB007979	Hs.301281	tenascin R (restriclin; janusin)	47.20				
25	116835	N39230	Hs.38218	ESTs				41.20	
	116970	AB023179	Hs.9059	KIAA0962 protein				91.00	11.00
	117023	AW070211	Hs.102415	ESTs					
	117027	AW085208	Hs.130093	ESTs	49.40				
	117036	H88908	Hs.41192	EST				32.60	
30	117110	AA160079	Hs.172932	ESTs		8.67			
	117209	W03011	Hs.306881	ESTs				30.60	
	117325	N23599	Hs.43396	ESTs					9.29
	117454	N29569	Hs.44055	ESTs					3.19
	117475	N30205	Hs.93740	ESTs	44.00				
35	117543	BE219453	Hs.42722	ESTs		16.00			
	117567	AW444761	Hs.44565	ESTs				12.00	
	117570	N48649	Hs.44583	ESTs				11.00	
	117600	N34963	Hs.44676	EST					3.74
	117730	N45513	Hs.46608	ESTs		6.00			
40	117791	N48325	Hs.93958	EST		9.00			
	117929	N51075	Hs.47191	ESTs				29.20	
	117990	AA446167	Hs.47385	ESTs		8.00			
	118224	N62275	Hs.48503	EST	31.40				
	118244	N62516	Hs.48556	ESTs	32.80				
45	118357	AL109687	Hs.124154	Homo sapiens mRNA full length insert cDN		2.40			
	118446	N66361	Hs.269121	ESTs		2.28			
	118447	N66399	Hs.49193	EST	30.80				
	118530	N67900	Hs.118446	ESTs					3.10
	118549	N68163	Hs.322954	EST					3.41
50	118823	W03754	Hs.50813	ESTs; Weakly similar to long chain fatty		3.94			
	118862	W17065	Hs.54522	ESTs					3.58
	118935	AI979247	Hs.247043	KIAA0525 protein				33.00	
	118944	AI734233	Hs.226142	ESTs; Weakly similar to !!!! ALU SUBFAM					11.43
	118995	N94591	Hs.323056	ESTs		14.00			
55	119073	BE245360	Hs.279477	ERG-2/ERG-1; V-ets avian erythroblastosi				52.60	
	119268	T16335	Hs.65325	EST	31.40				
	119514	W37937		Accession not listed in Genbank					3.50
	119824	W74536	Hs.184	advanced glycosylation end product-speci		2.75			
60	119831	AL117664	Hs.58419	DKFZP586L2024 protein					3.21
	119861	W78816	Hs.49943	ESTs; Moderately similar to !!!! ALU SUB				33.80	
	119889	W84346	Hs.58671	ESTs				30.03	
	119921	W86192	Hs.58815	ESTs	29.00				
	120082	H80286	Hs.40111	ESTs					3.80
	120094	AA811339	Hs.124049	ESTs		6.00			
65	120132	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)				36.60	
	120378	AA223249	Hs.285728	ESTs		12.00			
	120404	AB023230	Hs.96427	KIAA1013 protein	39.40				
	120504	AA256837		ESTs				8.00	
70	120512	N55761	Hs.194718	ESTs	33.00				
	120667	AA287740	Hs.78335	microtubule-associated protein; RP/EB fa					4.18
	120777	AA287702	Hs.10031	KIAA0955 protein				46.60	
	121082	AA398722		ESTs				39.00	
	121191	AA400205	Hs.104447	ESTs	41.60				
	121248	AA400914	Hs.97827	EST					5.08
75	121363	AI287280	Hs.97933	ESTs				12.00	
	121366	AI743515		ESTs				20.00	
	121483	AI660332	Hs.25274	ESTs; Moderately similar to putative sev					3.32
	121518	AA412155		ESTs				30.20	
	121545	AA412442	Hs.98132	ESTs		2.29			
80	121622	AA416931	Hs.126065	ESTs		9.00			
	121665	AA416556	Hs.98234	ESTs				34.80	
	121709	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	34.80				
	121730	AI140683	Hs.98328	ESTs	38.80				
	121740	AA421138	Hs.98334	EST		7.00			
85	121772	AI590770	Hs.110347	Homo sapiens mRNA for alpha integrin bin	36.20				
	121821	AL040235	Hs.3346	ESTs					3.61

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	121835	AB033030	Hs.300670	ESTs	2.34				
	121841	AA427794	Hs.104864	ESTs	2.61				
	121885	AA934883	Hs.98467	ESTs				2.25	
	121888	AA426429	Hs.98463	ESTs				2.92	
5	121938	AA428659	Hs.98610	ESTs			46.80		
	121950	AA428515	EST				31.40		
	122030	AA431310	Hs.98724	ESTs	34.40				
	122054	AA431725	Hs.98746	EST					3.58
10	122211	AA300900	Hs.98849	ESTs; Moderately similar to bithoraxoid-	49.40				
	122233	AA436455	Hs.98872	EST	29.80				
	122247	AA436676	Hs.98890	EST			39.80		
	122253	AA436703	Hs.104938	ESTs; Weakly similar to hypothetical pro	9.00				
	122266	AA436840	Hs.98907	EST				3.60	
	122285	AA436981	Hs.121602	EST				3.14	
15	122409	AA446830	Hs.99081	ESTs	30.80				
	122485	AA524547	Hs.160318	phospholemman		2.65			
	122697	AA420683	Hs.98321	Homo sapiens cDNA FLJ14103 fis, clone MA	15.00				
	122772	AW117452	Hs.99489	ESTs	6.67				
	122831	AI857570	Hs.5120	ESTs				3.37	
20	122913	AI638774	Hs.105328	ESTs			32.20		
	123049	BE047680	Hs.211869	ESTs			41.80		
	123076	AI345569	Hs.190046	ESTs	35.80				
	123136	AW451999	Hs.194024	ESTs					2.58
	123309	N52937	Hs.102679	ESTs			19.00		
25	123455	AA353113	Hs.112497	ESTs			82.80		
	123691	AA609579	Hs.112724	ESTs				3.95	
	123756	AA609971	Hs.112795	EST	35.40				
	123802	AA620448	Homo sapiens clone 24760 mRNA sequence	58.00					
30	123837	AI807243	Hs.112893	ESTs			32.40		
	123844	AA938905	Hs.120017	olfactory receptor; family 7; subfamily	2.63				
	123936	NM_004673	Hs.241519	ESTs	29.00				
	123987	C21171	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPOR			70.60		
	124013	AI521936	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED S	28.40				
35	124160	R40290	Hs.124685	ESTs			13.00		
	124205	H77570	Hs.108136	ESTs				4.74	
	124226	AA618527	Hs.190266	ESTs		2.35			
	124246	H67680	Hs.270962	ESTs			29.40		
	124348	AI796320	Hs.10299	ESTs	17.00				
40	124358	AW070211	Hs.102415	*yw35g11.s1 Morton Fetal Cochlea Homo sa		3.07			
	124409	AI814166	Hs.107197	ESTs				3.14	
	124442	AW663632	Hs.285625	TATA box binding protein (TBP)-associate	2.48				
	124468	N51413	Hs.109284	ESTs			30.80		
	124479	AB011130	Hs.127436	calcium channel; voltage-dependent; alph					6.03
45	124519	AI870056	Hs.137274	ESTs; Weakly similar to SPLICEOSOME ASSO	2.50				
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	59.20				
	124866	AI768289	Hs.304389	ESTs	8.00				
	124874	BE550182	Hs.127826	ESTs			37.60		
	125097	AW576389	Hs.335774	ESTs			10.00		
50	125179	AW206468	Hs.103118	ESTs				3.12	
	125200	AW836591	Hs.103156	ESTs					2.79
	125299	T32982	Hs.102720	ESTs			34.20		
	125400	AL110151	Hs.128797	DKFZP586D0824 protein	29.00				
	125810	H00083		aryl hydrocarbon receptor-interacting pr	32.20				
55	126176	BE242256	Hs.2441	KIAA0022 gene product	12.00				
	126303	D78841	HUM525A05B Human placenta polyA+ (TFu)				33.60		
	126403	AW629054	Hs.125976	ESTs; Weakly similar to metalloprotease/	35.80				
	126507	AL040137	Hs.23964	ESTs; Weakly similar to HC1 ORF [M.muscu			29.80		
	126773	AA648284	Hs.187584	ESTs	39.60				
60	127307	AW962712	Hs.126712	ESTs; Weakly similar to pIL2 hypothetica	28.80				
	127462	AA760776	Hs.293977	aa59b04.s1 NCLCGAP_GCB1 Homo sapiens c			34.40		
	127486	AW002846	Hs.105468	ESTs	9.00				
	127572	AA594027	Hs.191788	ESTs		2.36			
	127609	X80031	Hs.530	ESTs			29.40		
65	127832	AW976035	Hs.292396	ESTs			37.20		
	127898	AA774725	Hs.128970	ESTs				4.42	
	128073	AW340720	Hs.125983	ESTs			38.40		
	128101	AA905730	Hs.128254	ESTs	7.33				
	128149	NM_012214	Hs.177576	mannosyl (alpha-1,3)-glycoprotein beta-					2.58
70	128212	W27411	Hs.336920	glutathione peroxidase 3 (plasma)	3.09				
	128333	W68800	Hs.12125	ESTs; Weakly similar to LR8 [H.sapiens]			34.40		
	128364	N76462	Hs.269152	ESTs; Weakly similar to ZINC FINGER PROT	10.00				
	128426	AI265784	Hs.145197	ESTs				4.31	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel; s	31.20				
75	128634	AA464918		ESTs; Moderately similar to IIII ALU SUB			41.60		
	128687	AW271273	Hs.23767	ESTs			87.00		
	128726	AI311238	Hs.104476	ESTs					4.02
	128773	NM_004131	Hs.1051	granzyme B (granzyme 2; cytotoxic T-lymp			9.00		
	128833	W26667	Hs.184581	ESTs					3.76
80	128870	H39537	Hs.75309	eukaryotic translation elongation factor	2.66				
	128878	R25513	Hs.10583	ESTs				3.10	
	128885	AF134803	Hs.180141	cofilin 2 (muscle)			11.00		
	128998	W04245	Hs.107761	ESTs; Weakly similar to PUTATIVE RHO/RAC				3.21	
	129000	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inhi					3.68
	129038	AW156903	Hs.108124	ribosomal protein L41				3.17	
85	129098	AW580945	Hs.330466	ESTs	34.60				

	129210	AL039940	Hs.202949	KIAA1102 protein					4.09
	129240	AA361258	Hs.237868	interleukin 7 receptor	2.29				
	129262	BE222198	Hs.109843	ESTs			3.30		
5	129301	AF182277	Hs.330780	Human cytochrome P450-11B (h11B3) mRNA;					4.05
	129331	AW167668	Hs.279772	ESTs; Highly similar to CGI-38 protein [4.09
	129381	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	2.93				
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1		160.80			
	129595	U09550	Hs.1154	oviductal glycoprotein 1; 120kD			10.00		
10	129613	AW978517	Hs.172847	ESTs; Weakly similar to collagen alpha 1				3.40	
	129782	AW016932	Hs.104105	EST	9.00				
	129950	F07783	Hs.1369	decay accelerating factor for complement					
	129958	R27496	Hs.1378	annexin A3		87.80			
	129959	AL036554	Hs.274463	defensin; alpha 1; myeloid-related seque		44.60			
15	130160	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1;3-galactosyltr	2.72				
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	2.54				
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic; Dr		51.60			
	130312	AF056195	Hs.15430	DKFZP586G1219 protein				3.16	
	130436	NM_001928	Hs.155597	D component of complement (adipsin)					4.11
20	130523	AA999702	Hs.214507	ESTs				4.77	
	130799	AB028945	Hs.12696	ESTs	6.00				
	130885	NM_005883	Hs.20912	adenomatous polyposis coli like				3.54	
	131002	AL050295	Hs.22039	KIAA0768 protein					3.50
	131012	AL039940	Hs.202949	KIAA1102 protein	20.00				
25	131031	NM_001650	Hs.288650	aquaporin 4	41.20				
	131061	N64328	Hs.268744	ESTs; Moderately similar to KIAA0273 [H.		31.40			
	131066	AW169287	Hs.22588	ESTs		29.60			
	131082	AI091121	Hs.246218	ESTs; Weakly similar to zinc finger prot			9.00		
	131087	AF147709	Hs.22824	ESTs; Weakly similar to p160 myb-binding					3.86
30	131161	AF033382	Hs.23735	potassium voltage-gated channel; subfami				3.14	
	131179	AA171388	Hs.184482	DKFZP586D0524 protein				3.80	
	131182	AI824144	Hs.23912	ESTs					3.67
	131205	NM_003102	Hs.2420	superoxide dismutase 3; extracellular	2.98				
	131277	AA131466	Hs.23767	ESTs	3.15				
35	131281	AA251716	Hs.25227	ESTs		32.20			
	131282	X03350	Hs.4	alcohol dehydrogenase 3 (class I); gamma					3.44
	131285	AI567943	Hs.25274	ESTs; Moderately similar to putative sev				6.40	
	131355	R52804	Hs.25955	DKFZP564D206 protein	8.00				
	131391	AW085781	Hs.26270	ESTs	10.00				
40	131461	AA992841	Hs.27263	butyrate response factor 2 (EGF-response	28.80				
	131487	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZP564O1763 (f					4.03
	131517	AB037789	Hs.263395	ESTs; Highly similar to semaphorin 1a [39.00				
	131545	AL137432	Hs.28564	ESTs			11.00		
	131583	AK000383	Hs.323092	ESTs; Weakly similar to dual specificity			10.00		
45	131647	AA359615	Hs.30089	ESTs	2.47				
	131675	HI5205	Hs.30509	ESTs				3.06	
	131676	AI126821	Hs.30514	ESTs					
	131708	S60415	Hs.30941	calcium channel; voltage-dependent; beta	45.80				
	131717	X94630	Hs.3107	CD97 antigen	2.28				
50	131756	AA443966	Hs.31595	ESTs		40.60			3.78
	131762	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inh1					3.67
	131821	AA017247	Hs.164577	ESTs	2.87				
	131839	AB014533	Hs.33010	KIAA0533 protein					3.48
	131861	AL058588	Hs.184245	KIAA0929 protein Mx2 interacting nuclea	54.00				
55	132015	AI418006	Hs.3731	ESTs		49.20			
	132070	BE622641	Hs.38489	ESTs		34.80			
	132242	AA332697	Hs.42721	ESTs	2.68				
	132334	AW080704	Hs.45033	lacritinal proline rich protein	4.66				
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regl	34.20				
60	132490	NM_001290	Hs.4980	LIM binding domain 2	2.66				
	132533	AI922988	Hs.172510	ESTs	13.00				
	132598	X80031	Hs.530	collagen; type IV; alpha 3 (Goodpasture		30.60			
	132619	H28855	Hs.53447	ESTs; Moderately similar to kinesin lig				4.02	
	132652	N41739	Hs.61260	ESTs				3.18	
65	132726	N52298	Hs.55608	ESTs; Weakly similar to cDNA EST yk484g1			11.43		
	133028	R51604	Hs.300842	ESTs	2.37				
	133071	BE384932	Hs.64313	ESTs	2.27				
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.63				
	133129	AA428580	Hs.65551	ESTs					5.49
70	133147	AA026533	Hs.66	interleukin 1 receptor-like 1	6.20				
	133151	NM_014051	Hs.94896	ESTs				3.69	
	133213	AA903424	Hs.6786	ESTs		31.40			
	133276	AW978439	Hs.69504	ESTs			9.00		
	133377	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	41.20				
75	133407	AF017987	Hs.7306	secreted frizzled-related protein 1	50.20				
	133535	AL134030	Hs.284180	protocadherin 2 (cadherin-like 2)				3.72	
	133537	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr					3.35
	133656	BE149455	Hs.75415	Accession not listed in Genbank	2.65				
	133689	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)		90.80			
80	133779	T58486	Hs.222566	ESTs				3.05	
	133978	AF035718	Hs.78061	transcription factor 21	2.92				
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec					3.45
	134000	AW175787	Hs.334841	selenium binding protein 1					4.05
	134111	AI372588	Hs.8022	TU3A protein	4.49				
85	134185	AA285136	Hs.301914	Homo sapiens mRNA; cDNA DKFZP586K1220 (f				3.27	
	134204	AI873257	Hs.7994	ESTs; Weakly similar to CGI-69 protein {		40.80			

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	134641	AI092634	Hs.156114	protein tyrosine phosphatase; non-recept					
	134677	AA251363	Hs.177711	ESTs			32.20	3.76	
	134745	NM_000685	Hs.89472	angiotensin receptor 1B	15.00				
	134749	T28499	Hs.89485	carbonic anhydrase IV		3.05			
5	134786	T29618	Hs.89640	angiotensin 1 receptor; TEK tyrosine ki			57.80		
	134825	U33749	Hs.197764	thyroid transcription factor 1					3.73
	134978	AI829008	Hs.333383	ficollin (collagen/fibrinogen domain-cont		2.52			
	135010	N50465	Hs.92927	ESTs			31.60		
	135053	AW796190	Hs.93678	ESTs				3.21	
10	135081	AF069517	Hs.173993	RNA binding motif protein 6	28.80				
	135091	AA493650	Hs.94387	ESTs					4.24
	135135	AA775910	Hs.95011	syntrophin; beta 1 (dystrophin-associate		8.00			
	135203	C15737	Hs.269386	ESTs				4.31	
	135236	AI636208	Hs.96801	ESTs	43.00				
15	135266	R41179	Hs.97393	Human mRNA for KIAA0328 gene; partial cd				6.42	
	135346	NM_000928	Hs.992	phospholipase A2; group IB (pancreas)		3.82			
	135378	AW961818	Hs.24379	potassium voltage-gated channel; shaker-		4.15			
	135387	NM_001972	Hs.99863	elastase 2; neutrophil	37.20				
	135388	W27965	Hs.99865	EST	38.80				
20	135402	L12398	Hs.99922	dopamine receptor D4				4.21	

TABLE 2B shows the accession numbers for those primekeys lacking unigene/D's for Table 2A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Key: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Key	CAT number	Accessions
	108447	43452_7 AA079126
35	108550	120073_1 AA084857 AA084996
	108655	127522_1 AA099960 AA113013
	102397	44371_1 U41898
	126303	1525933_1 D78841 D78880
40	125810	1554054_1 H00083 R81062
	103627	2615_2 Z48513 Z48512
	121366	280401_1 AI743515 AA405617 AW276706
	114609	116777_1 AA079505 AA079537
	115272	172113_1 AW015947 AA211890 AA279425
	108338	112186_1 AA070773 AA070774
45	108434	114012_1 AA078899 AA078782 AA075788
	123802	genbank_AA620448 AA620448
	102310	NOT_FOUND_entrez_U33839 U33839
	102636	entrez_U67092 U67092
	104776	genbank_AA026349 AA026349
50	120504	genbank_AA256837 AA256837
	113502	genbank_T89130T89130
	108499	genbank_AA083103 AA083103
	101308	entrez_L41390 L41390
	108629	genbank_AA102425 AA102425
55	103098	221_215 M86361 Z26593 X02850 D13070 AE000559 M17649 M87869 M87871 X61077 M16286 AF018169 X61079 S59351 X60142 AF043169
	103241	entrez_X76223 X76223
	103508	entrez_Y10141 Y10141
	103575	entrez_Z26256 Z26256
	119514	NOT_FOUND_entrez_W37937 W37937
60	121082	genbank_AA398722 AA398722
	128634	AA464918_at AA464918
	105817	genbank_AA397825 AA397825
	121518	genbank_AA412155 AA412155
	114449	genbank_AA020736 AA020736
65	114648	genbank_AA101056 AA101056
	121950	genbank_AA429515 AA429515
	107723	genbank_AA015967 AA015967

Table 3A shows 452 genes up-regulated in chronically diseased lung relative to normal lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Ecs/Affymatrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

- 5 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 10 R1: 80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of AI for normal lung samples.
 R2: 80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas
 R3: 70th percentile of AI for chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples

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	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3
20	135423	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	12.40		
	135378	AW961818	Hs.24379	MUM2 protein			2.13
	135348	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)			
	135235	AW298244	Hs.293507	ESTs	12.40		
	135057	U90268	Hs.93810	cerebral cavernous malformations 1	11.67		
25	134951	BE305081	Hs.169358	hypothetical protein		8.00	
	134789	M36821	Hs.89690	GRO3 oncogene		8.20	
	134786	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous			
	134772	NM_000829	Hs.163697	glutamate receptor, ionotropic, AMPA 4	29.80		
	134752	BE246762	Hs.89499	arachidonate 5-lipoxygenase			1.93
	134749	T28499	Hs.89485	carbonic anhydrase IV			2.07
30	134698	BE326276	Hs.8861	ESTs			
	134636	NM_005582	Hs.87205	lymphocyte antigen 64 (mouse) homolog, r	13.60		
	134627	AI018768	Hs.12482	glyceronephosphate O-acyltransferase			1.92
	134622	AW975159	Hs.293097	ESTs, Weakly similar to A55380 faciojeni			1.92
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	13.20		
35	134561	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h			1.78
	134468	NM_001772	Hs.83731	CD33 antigen (gp87)		6.20	
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci			
	134343	D50683	Hs.82028	transforming growth factor, beta recepto			
40	134323	BE170651	Hs.8700	deleted in liver cancer 1			
	134300	NM_001430	Hs.8136	endothelial PAS domain protein 1			
	134299	AW580939	Hs.97199	complement component C1q receptor			
	134253	X52075	Hs.80738	sialophorin (gpL115, leukosialin, CD43)	20.60		
	134182	D52059	Hs.7972	KIAA0871 protein	12.20		
45	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec			
	133978	AF035718	Hs.78061	transcription factor 21			
	133835	AI677897	Hs.76640	RGC32 protein			
	133651	AI301740	Hs.173381	dihydropyrimidinase-like 2			
	133633	D21262	Hs.75337	nucleolar and colloid-body phosphoprotein	15.20		
50	133565	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A			
	133548	AW946384	Hs.178112	DNA segment, single copy probe LNS-CAIL			1.77
	133488	AA335295	Hs.74120	adipose specific 2			
	133478	X83703	Hs.31432	cardiac ankyrin repeat protein			2.08
	133337	AF085983	Hs.293676	ESTs		9.60	
55	133200	AB037715	Hs.183639	hypothetical protein FLJ10210			1.77
	133153	AF070592	Hs.66170	HSKM-B protein	30.60		
	133130	AI128606	Hs.6557	zinc finger protein 161	22.60		
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein			
	132928	AW168082	Hs.169449	protein kinase C, alpha	13.80		
60	132836	AB023177	Hs.29900	KIAA0960 protein			
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,	41.60		
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	40.40		
	132548	X12830	Hs.193400	interleukin 6 receptor		7.20	
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi		4.76	
65	132439	AK001942	Hs.4863	hypothetical protein DKFZp566A1524			1.88
	132240	AB018324	Hs.42676	KIAA0781 protein	21.20		
	132210	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2			1.99
	132199	AL041299	Hs.165084	ESTs	15.20		
	131751	T96555	Hs.31562	ESTs			1.76
70	131745	AI828559	Hs.31447	ESTs, Moderately similar to A46010 X-II	27.80		
	131694	NM_000246	Hs.3076	MHC class II transactivator		4.00	
	131686	NM_012296	Hs.30687	GRB2-associated binding protein 2			
	131676	AI126821	Hs.30514	ESTs		6.20	
	131629	Z45794	Hs.238809	ESTs	21.40		
75	131589	C18825	Hs.29191	epithelial membrane protein 2			
	131536	AA019201	Hs.269210	ESTs		9.40	
	131517	AB037789	Hs.263395	sema domain, transmembrane domain (TM),		3.59	
	131355	R52804	Hs.25956	DKFZP564D206 protein		4.48	
	131253	R71802	Hs.24853	ESTs	15.00		
80	131207	AF104266	Hs.24212	latrophilin			1.75
	131156	AI472209	Hs.323117	ESTs			1.84
	131066	AW169287	Hs.22588	ESTs		3.54	
	131061	N64328	Hs.268744	KIAA1796 protein			
	131053	AA348541	Hs.296261	guanine nucleotide binding protein (G pr			1.93
85	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	16.60		
	130762	D84371	Hs.1898	paraoxonase 1	12.00		

	130657	AW337575	Hs.201591	ESTs		
	130655	AI831952	Hs.17409	cysteine-rich protein 1 (intestinal)		
	130589	AL110226	Hs.16441	DKFZP434H204 protein	2.08	
5	130562	D50402	Hs.182611	solute carrier family 11 (proton-coupled)	1.91	
	130555	R69743	Hs.116774	Integrin, alpha 1	9.60	
	130365	W56119	Hs.155103	eukaryotic translation initiation factor	11.60	
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic, Dr	6.60	
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	1.91	
10	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	21.20	
	129958	R27496	Hs.1378	annexin A3	5.05	
	129898	AI672731	Hs.13256	ESTs		
	129875	AA181018	Hs.13056	hypothetical protein FLJ13920	18.60	
	129699	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligase		
15	129626	F13272	Hs.111334	fertilin, light polypeptide		
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	22.63	
	129593	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f		
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1	2.53	
	129527	AA769221	Hs.270847	della-tubulin	39.20	
20	129402	W72062	Hs.11112	ESTs	2.11	
	129385	AA172106	Hs.110950	Rag C protein	15.20	
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	12.40	
	129312	T97579	Hs.110334	ESTs, Weakly similar to I78885 serine/th	20.83	
	129240	AA361258	Hs.237868	interleukin 7 receptor	1.95	
	129210	AL039940	Hs.202949	KIAA1102 protein		
25	129122	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	4.20	
	129057	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)		
	128946	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	5.20	
	128798	AF015525	Hs.302043	chemokine (C-C motif) receptor-like 2		
	128769	AW368576	Hs.139851	caveolin 2	2.24	
30	128778	AA504776	Hs.186709	ESTs, Weakly similar to I38022 hypothet	12.20	
	128766	AW160432	Hs.296460	craniofacial development protein 1	26.40	
	128631	R44238	Hs.155546	KIAA1080 protein; Golgi-associated, gamm		
	128624	BE154765	Hs.102647	ESTs, Weakly similar to TRHY_HUMAN TRICH	1.78	
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	2.51	
35	128603	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	16.00	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel, s	12.80	
	128458	H55864	Hs.56340	ESTs	4.00	
	128061	AF150882	Hs.186877	sodium channel, voltage-gated, type XII,	17.20	
40	127968	AA830201	Hs.124347	ESTs	21.30	
	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L		
	127944	AI557081	Hs.262476	S-adenosylmethionine decarboxylase 1	10.60	
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	13.40	
	127896	AI689586	Hs.222194	ESTs	7.00	
	127859	AA761802	Hs.291559	ESTs	14.00	
45	127817	AA836641	Hs.163085	ESTs	14.00	
	127742	AW293496	Hs.180138	ESTs	11.00	
	127628	AI240102	Hs.322430	NDRG family, member 4	11.10	
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture		
50	127582	AA908954	Hs.130844	ESTs	19.60	
	127543	AK000787	Hs.157392	Homo sapiens cDNA FLJ20780 fis, clone CO	15.40	
	127535	AA568424	Hs.164450	ESTs	17.50	
	127404	AI379920	Hs.270224	ESTs	14.60	
	127396	L31968	Hs.187991	DKFZP564A122 protein	15.40	
55	127374	AA442797	Hs.312110	ESTs, Weakly similar to I38022 hypothet	14.60	
	127346	AA203616	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	21.00	
	127340	BE047653	Hs.119183	ESTs, Weakly similar to ZN91_HUMAN ZINC	15.80	
	127307	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5		
	127242	AW390395	Hs.181301	cathepsin S	22.60	
60	127167	AA625690	Hs.190272	ESTs	21.40	
	127046	AA321948	Hs.293968	ESTs	41.20	
	126928	AA480902	Hs.137401	ESTs	11.00	
	126900	AF137386	Hs.12701	plasmolipin		
	126852	AA399961		gb:zu68c01.r1 Soares_testis_NHT Homo sap	5.60	
65	126816	AA248234		gb:csq2228.seq.F Human fetal heart, Lamb	12.20	
	126812	AB037860	Hs.173933	nuclear factor IIA	17.19	
	126666	AA648886	Hs.151999	ESTs	13.57	
	126645	AA316181	Hs.61635	slx transmembrane epithelial antigen of	15.40	
	126592	AI611153	Hs.6093	Homo sapiens cDNA: FLJ22783 fis, clone K	4.67	
70	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	18.00	
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	16.77	
	126299	AW979155	Hs.298275	amino acid transporter 2	14.60	
	126218	AL049801	Hs.13849	Novel human gene mapping to chromosome 13	3.50	
	126182	AA721331	Hs.293771	ESTs	13.40	
75	126177	AW752782	Hs.129750	hypothetical protein FLJ10546	18.20	
	126142	H86261	Hs.40558	ESTs	14.00	
	126077	M78772	Hs.210836	ESTs	16.59	
	125994	AI990529	Hs.270799	ESTs	17.40	
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	13.00	
80	125847	AW161885	Hs.249034	ESTs	49.57	
	125831	HO4043		gb:yl45c03.r1 Soares_placenta Nb2HP Homo		
	125731	R61771	Hs.26912	ESTs	13.20	
	125676	BE612918	Hs.151973	hypothetical protein FLJ23511	11.20	
	125561	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S		
85	125552	HO9701	Hs.278366	ESTs, Weakly similar to I38022 hypotheti	12.60	
	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	33.40	

	125422	AA903229	Hs.153717	ESTs		1.80
	125331	AA422996	Hs.161378	ESTs	38.00	
	125309	T12411	Hs.183745	hypothetical protein FLJ13456	18.20	
5	125167	AL137540	Hs.102541	netrin 4		1.95
	125139	AW194933	Hs.9788	hypothetical protein MGC10924 similar to		1.84
	125042	T78906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN	21.80	
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl)	10.60	
	124631	NM_014053	Hs.270594	FLVCR protein	23.20	
	124578	N68321	Hs.231500	EST	21.43	
10	124574	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2		1.77
	124472	N52517	Hs.102670	EST	37.20	
	124438	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A		
	124357	N22401		gb:zw37g07.s1 Morton Fetal Cochlea Homo	14.64	
15	124306	AW973078	Hs.293039	ESTs	4.00	
	124214	H58608	Hs.151323	ESTs		
	124097	AW298235	Hs.101689	ESTs	27.20	
	123978	T89832	Hs.170278	ESTs		2.03
	123972	T46848	Hs.70337	immunoglobulin superfamily, member 4	6.00	
	123961	AL050184	Hs.21610	DKFZP434B203 protein		1.79
20	123936	NM_004673	Hs.241519	angiotensin-like 1	15.80	
	123802	AA620448		gb:ae58c09.s1 Stratagene lung carcinoma	4.23	
	123734	AA609861	Hs.312447	ESTs	4.20	
	123619	AA602984		gb:nc97c02.s1 NCI_CGAP_Pr2 Homo sapiens	33.60	
25	123596	AA421130	Hs.112640	EST	10.93	
	123476	AA384564	Hs.108829	ESTs		2.18
	123340	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	11.20	
	123190	AA489212	Hs.105228	EST	14.20	
	123136	AW451999	Hs.194024	ESTs		7.00
	123073	AA485061	Hs.105652	ESTs	31.20	
30	123055	AA482005	Hs.105102	ESTs, Weakly similar to reverse transcri		4.80
	122699	AA456130	Hs.301721	KIAA1255 protein		5.00
	122679	AA811286	Hs.192837	ESTs, Weakly similar to ALU5_HUMAN ALU S	14.40	
	122633	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg		
35	122553	AA451884	Hs.190121	ESTs	40.00	
	122544	AW973253	Hs.292689	ESTs	15.40	
	122485	AA524547	Hs.160318	FXRD domain-containing ion transport reg		1.81
	122211	AA300900	Hs.98849	ESTs, Moderately similar to AF161511.1 H	12.10	
	122127	AW207175	Hs.106771	ESTs		1.95
40	122011	AA431082		gb:zw78a10.s1 Soares_testis_NHT Homo sap		1.89
	121992	AI860775	Hs.98506	ESTs	3.60	
	121989	W58487	Hs.193784	Homo sapiens mRNA; cDNA DKFZp586K1922 (f		2.01
	121835	AB033030	Hs.300670	KIAA1204 protein		1.85
	121726	AF241254	Hs.178098	angiotensin I converting enzyme (peptidyl	12.43	
45	121690	AV660305	Hs.110286	ESTs		1.82
	121643	AA640987	Hs.193787	ESTs		
	121633	AA417011	Hs.98175	EST	14.00	
	121622	AA416931	Hs.126065	ESTs		16.40
	121497	AA412031	Hs.97901	EST	11.20	
50	121351	AW206227	Hs.287727	hypothetical protein FLJ23132	12.20	
	121314	W07343	Hs.182538	phospholipid scramblase 4		1.83
	121242	AA400857	Hs.97509	ESTs	22.40	
	121059	AA393283		gb:z174e03.r1 Soares_testis_NHT Homo sap	14.80	
	120934	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	21.20	
55	120755	AA312934	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone		1.79
	120637	AA811804		gb:ob39a05.s1 NCI_CGAP_GCB1 Homo sapiens	20.00	
	120484	AA253170	Hs.96473	EST	40.20	
	120336	N85785	Hs.181165	eukaryotic translation elongation factor		6.60
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	16.80	
60	120132	W57554	Hs.125019	ESTs		4.73
	120041	AA830882	Hs.59368	ESTs		1.75
	119996	W88996	Hs.59134	EST	7.20	
	119970	AA767718	Hs.93581	hypothetical protein FLJ10512	11.20	
	119861	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-		3.78
65	119824	W74536	Hs.184	advanced glycosylation end product-speci		
	119740	AW021407	Hs.21068	hypothetical protein	20.20	
	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	15.20	
	119221	C14322	Hs.250700	trypsin beta 1		
	119126	R45175	Hs.117183	ESTs	12.60	
70	119073	BE245360	Hs.279477	ESTs		
	118928	AA312799	Hs.283689	activator of CREM in testis	10.00	
	118901	AW292577	Hs.94445	ESTs	3.96	
	118661	AL137554	Hs.49927	protein kinase NYD-SP15	9.60	
	118607	AI377444	Hs.54245	ESTs, Weakly similar to S65824 reverse t	10.40	
75	118449	AI813865	Hs.164478	hypothetical protein FLJ21939 similar to		1.90
	118416	N66028	Hs.49105	FKBP-associated protein	16.20	
	118379	N64491	Hs.48990	ESTs		4.00
	118329	N63520		gb:yy62i01.s1 Soares_multiple_sclerosis_	6.60	
	118320	N63451	Hs.141600	ESTs, Weakly similar to alternatively s	3.80	
80	118253	AA497044	Hs.20887	hypothetical protein FLJ10392	17.60	
	118124	N66968	Hs.46707	chromosome 21 open reading frame 37	14.00	
	118056	AB037746	Hs.42768	hypothetical protein DKFZp76100113		1.86
	118032	N52802	Hs.47544	EST	5.00	
	117840	T26379	Hs.48802	Homo sapiens clone 23632 mRNA sequence	4.00	
85	117404	N39725	Hs.15220	zinc finger protein 106		1.90
	117314	N32498	Hs.42829	ESTs	14.20	

	117209	W03011	Hs.306881	MSTP043 protein			
	117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f		2.31	
	116814	H50834		gb:yp86a10.s1 Soares fetal liver spleen	20.20		
5	116784	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific		3.51	
	116768	AI608657	Hs.95097	ESTs	16.20		
	116712	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr		6.80	
	116707	H10344	Hs.49050	ESTs, Weakly similar to A Chain A, Human	18.60		
	116351	AL133623	Hs.82501	similar to mouse Xrn1 / Dhm2 protein	19.40		
10	116279	AW971248	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S			
	116166	AL039940	Hs.202949	KIAA1102 protein		2.13	
	116152	AL040521	Hs.15220	zinc finger protein 106		1.75	
	116117	BE613410	Hs.31575	SEC63, endoplasmic reticulum translocon	13.20		
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	30.11		
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970		2.36	
15	115955	AF263613	Hs.44198	Intracellular membrane-associated calciu	18.20		
	115844	AI373062	Hs.332938	hypothetical protein MGC5370	18.57		
	115683	AF255910	Hs.54650	junctional adhesion molecule 2		23.00	
	115673	AA406341	Hs.269908	Homo sapiens cDNA FLJ11991 fls, clone HE	11.82		
	115672	AI889110	Hs.73251	ESTs	10.60		
20	115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1		1.76	
	115313	AA808001	Hs.184411	albumin	25.20		
	115279	AW984897	Hs.290825	ESTs		8.00	
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fls, clone L		1.80	
25	115110	AK001671	Hs.11387	KIAA1453 protein	14.20		
	114999	BE246481	Hs.87856	ESTs	19.20		
	114930	AA237022	Hs.188717	ESTs		5.60	
	114922	AA235672	Hs.87491	ESTs		3.60	
	114837	BE244930	Hs.166895	ESTs	43.70		
	114769	AA149060	Hs.296100	ESTs	11.00		
30	114761	AA143781	Hs.128280	hypothetical protein FLJ23393	14.00		
	114735	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN A		4.20	
	114596	AA310162	Hs.169248	cytochrome c	10.71		
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	20.40		
35	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.40		
	114452	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fls, clone HE		17.20	
	114359	NM_016929	Hs.283021	chloride intracellular channel 5		2.09	
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fls, clone OV	12.40		
	114251	H15261	Hs.21948	ESTs		2.00	
40	114138	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr		11.40	
	114124	W57554	Hs.125019	ESTs		6.04	
	113946	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fls, clone PL		1.82	
	113685	T96965	Hs.17948	ESTs, Weakly similar to ALUB_HUMAN IIII			
	113606	NM_013343	Hs.278951	NAG-7 protein		2.15	
45	113590	R49642	Hs.142447	ESTs, Weakly similar to ALU1_HUMAN ALU S		3.60	
	113560	T91015	Hs.268626	ESTs	32.00		
	113552	AI654223	Hs.16026	hypothetical protein FLJ23191			
	113540	AW152618	Hs.16757	ESTs			
	113502	T89130		gb:ye12d01.s1 Stratagene lung (937210) H		8.35	
50	113288	AI076838	Hs.12967	ESTs	12.40		
	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en		4.27	
	113238	R45467	Hs.189813	ESTs			
	113203	AA743563	Hs.10305	ESTs	21.20		
	113195	H83285	Hs.8881	ESTs, Weakly similar to S41044 chromosom		1.92	
55	113089	T40707	Hs.270862	ESTs	14.33		
	113076	AF033199	Hs.8198	zinc finger protein 204		6.00	
	113009	T23699	Hs.7246	ESTs		9.40	
	112937	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti		12.20	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	10.57		
60	112794	R97018		gb:yyq74b08.s1 Soares fetal liver spleen		26.60	
	112691	R88708	Hs.220647	ESTs	15.33		
	112602	AW004045	Hs.203365	ESTs	15.60		
	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequence	15.40		
	112210	R49645	Hs.7004	ESTs	14.00		
65	112064	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	13.00		
	111998	R42379	Hs.138283	ESTs	11.00		
	111987	NM_015310	Hs.6763	KIAA0942 protein	22.40		
	111803	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A		1.77	
	111737	H04607	Hs.9218	ESTs		1.86	
70	111605	T91061	Hs.194178	ESTs, Moderately similar to PC4259 ferri	23.00		
	111510	R07856	Hs.16355	ESTs	11.02		
	111341	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr		1.88	
	111280	AA373527	Hs.19385	CGL-58 protein	18.40		
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f			
75	111232	AI247763	Hs.16928	ESTs	27.60		
	110942	R63503	Hs.28419	ESTs	14.80		
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	24.71		
	110837	H03109	Hs.108920	HT018 protein		2.18	
	110824	AI767183	Hs.26942	ESTs	12.20		
80	110776	AB032417	Hs.19545	fizzled (Drosophila) homolog 4		1.75	
	110576	H60869	Hs.37889	ESTs	13.00		
	110369	AK000768	Hs.107872	hypothetical protein FLJ20761		5.60	
	110099	R44557	Hs.23748	ESTs		2.31	
	109984	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fls, clone PL			
85	109958	AA001266	Hs.133521	ESTs	11.25		
	109893	AA884208	Hs.30484	ESTs		2.68	

5	109842	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	23.83		
	109837	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypothet		17.20	3.91
	109796	AI800515	Hs.12024	ESTs		9.60	
	109688	R41900	Hs.22245	ESTs			
	109648	H17800	Hs.7154	ESTs	22.80		
10	109613	H47315	Hs.27519	ESTs			
	109550	AW021488	Hs.26981	ESTs			
	109523	AW193342	Hs.24144	ESTs			1.89
	109472	AK001989	Hs.91165	hypothetical protein		6.00	
	109355	AA524525	Hs.48297	DKFZP586C1620 protein	15.00		
15	109260	AW978515	Hs.131915	KIAA0863 protein	25.60		
	108781	AA128654		gb:zn98g07.s1 Stratagene fetal retina 93	14.20		
	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypothet	11.00		
	108573	AA086005		gb:zl84c04.s1 Stratagene colon (937204)	26.00		
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428			
20	108382	NM_006770	Hs.67726	macrophage receptor with collagenous str			1.83
	108174	AA055632	Hs.303070	ESTs	15.20		
	108138	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr		3.60	
	108087	AA045708	Hs.40545	ESTs	15.44		
	108048	AI797341	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT		11.40	
25	108041	AW204712	Hs.61957	ESTs			
	107997	AL049176	Hs.82223	chordin-like		4.76	
	107994	AA036811	Hs.48469	LIM domains containing 1			
	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	14.20		
	107581	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	51.80		
30	107666	AA010611	Hs.60418	EST	29.20		
	107332	T87750	Hs.183297	DKFZP566F2124 protein	10.73		
	107292	BE166479	Hs.4789	Homo sapiens serologically defined breas	32.00		
	107230	AI034467	Hs.34650	ESTs	17.40		
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	10.43		
35	107160	AA314490	Hs.27669	KIAA1663 protein	11.40		
	107054	AI076459	Hs.15978	KIAA1272 protein			
	107029	AF264750	Hs.288971	myeloid/lymphoid or mixed-lineage leukem	21.40		
	106999	H93281	Hs.10710	hypothetical protein FLJ20417	35.80		
	106954	AF128847	Hs.204038	indolethylamine N-methyltransferase			1.76
40	106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl			
	106865	AW192535	Hs.19479	ESTs	13.40		
	106844	AA485055	Hs.158213	sperm associated antigen 6		7.13	
	106820	NM_016831	Hs.12592	period (Drosophila) homolog 3		7.00	
	106818	AK002135	Hs.3542	hypothetical protein FLJ11273	13.00		
45	106797	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL			2.05
	106773	AA478109	Hs.188833	ESTs			
	106747	NM_007118	Hs.171957	triple functional domain (PTPRF) interact	12.60		
	106743	BE613328	Hs.21938	hypothetical protein FLJ12492	10.60		
	106667	AW360847	Hs.16578	ESTs			
50	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr			2.40
	106567	AW450408	Hs.88412	chromosome 9 open reading frame 5			1.78
	106562	AL031846	Hs.152151	plakophilin 4			1.76
	106536	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot			2.19
	106533	AL134708	Hs.145998	ESTs	23.20		
55	106507	AA259068	Hs.267819	protein phosphatase 1, regulatory (inhib	15.20		
	106490	AA404265	Hs.115537	putative dipeptidase			
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	10.44		
	106211	AA428240	Hs.126083	ESTs		29.80	
	105986	AB037722	Hs.8707	KIAA1301 protein		3.70	
60	105894	AI904740	Hs.25691	receptor (calcionin) activity modifying			1.84
	105847	AW864490	Hs.32241	ESTs, Weakly similar to S65857 alpha-1C-			1.75
	105803	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm			2.47
	105731	AA834664	Hs.29131	nuclear receptor coactivator 2	10.71		
	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds			
65	105688	AI299139	Hs.17517	ESTs	23.40		
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	37.20		
	105101	H63202	Hs.38163	ESTs		8.30	
	104989	R65998	Hs.285243	hypothetical protein FLJ22029		8.09	
	104986	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1			1.92
70	104969	AI670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinas		5.40	
	104903	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,		7.60	
	104896	AW015318	Hs.23165	ESTs	13.80		
	104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C			
	104825	AA035613	Hs.141883	ESTs			1.87
75	104781	AA099904	Hs.21610	DKFZP434B203 protein			1.93
	104776	AA026349		gb:zj99f01.s1 Soares_pregnant_uterus_NbH		10.20	
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor		5.69	
	104667	AI239923	Hs.30098	ESTs		3.82	
	104404	H58762		gb:EST00057 HE6W Homo sapiens cDNA clone		4.20	
80	104392	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	27.20		
	104212	AB002298	Hs.173035	KIAA0300 protein			1.91
	104074	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	11.20		
	103749	AL135301	Hs.8768	hypothetical protein FLJ10849	10.86		
	103645	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	12.00		
85	103554	AI878826	Hs.323469	caveolin 1, caveolae protein, 22kD			1.80
	103541	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, l			
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2			
	103428	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	11.20		
	103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa	19.80		

5	103295	X81479	Hs.2375	egf-like module containing, mucin-like,	3.60	
	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula		1.76
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)		2.15
	103025	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t		
	102698	M18667	Hs.1867	progastricin (papsinogen C)		
10	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	11.00	
	102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatida	25.40	
	102417	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	14.00	
	102363	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc		
	102302	AA306342	Hs.69171	protein kinase C-like 2	10.86	
15	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11		7.40
	102188	U20350	Hs.78913	chemokine (C-X3-C) receptor 1		
	102151	T27013	Hs.3132	steroidogenic acute regulatory protein	16.40	
	101957	L28824	Hs.74101	spleen tyrosine kinase	15.40	
	101842	M93221	Hs.75182	mannose receptor, C type 1		
20	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant		1.78
	101764	A198550	Hs.81256	S100 calcium-binding protein A4 (calcium		
	101718	AF050658	Hs.2563	tachykinin, precursor 1 (substance K, su	18.80	
	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a l		2.22
	101447	M21305		gb:Human alpha satellite and satellite 3	504.80	
25	101383	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co	31.00	
	101348	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N		1.75
	101345	NM_005795	Hs.152175	calcinonin receptor-like		
	101336	NM_005732	Hs.75678	FBJ murine osteosarcoma viral oncogene h		2.24
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do		
30	101277	BE297626	Hs.296049	microfibrillar-associated protein 4		
	101262	L35854		gb:Human dystrophin (dp140) mRNA, 5' end	19.00	
	101168	NM_005308	Hs.211569	G protein-coupled receptor kinase 5		2.01
	101102	NM_003243	Hs.79059	transforming growth factor, beta recepto		
	101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte	7.52	
35	101066	AW970254	Hs.889	Charot-Leyden crystal protein	19.38	
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		1.91
	100893	BE245294	Hs.180789	S164 protein	15.40	
	100770	W25797.comp	Hs.177486	amyloid beta (A4) precursor protein (pro	11.20	
	100716	X89887	Hs.172350	HIR (histone cell cycle regulation defec	14.80	
40	100555	M69181		gb:Human nonmuscle myosin heavy chain-B	33.00	
	100425	NM_014747	Hs.78748	KIAA0237 gene product	16.20	
	100408	D86640	Hs.56045	src homology three (SH3) and cysteine ri	4.00	
	100382	D83407	Hs.156007	Down syndrome critical region gene 1-lik	4.24	
	100351	D64158			6.20	
45	100299	D49493	Hs.2171	growth differentiation factor 10	21.20	
	100134	AA305746	Hs.49	macrophage scavenger receptor 1		
	100108	U09577	Hs.76873	hyaluronoglucosaminidase 2		1.79
	100095	Z97171	Hs.78454	myoclin, trabecular meshwork inducible	5.40	
	100066				11.29	

TABLE 3B shows the accession numbers for those primekeys lacking unigenal D's for Table 3A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using *Clustering and Alignment Tools (DoubleTwist, Oakland California)*. The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123619	371681_1	AA602964 AA609200
126433	127143_1	AA325606 AA099517 N89423
125831	1522905_1	H04043 D60988 D60337
126816	122973_1	AA248234 AA090985
126852	136135_1	AA399961 AA128347
121059	273450_1	AA393283 AA398526
120637	200885_1	AA811804 AA809404 AA286907 AW977624
122011	7617_-2	AA431082
120934	177521_1	AA226198 AA226513 AA383773
123802	genbank_AA620448	AA620448
116814	genbank_H50834	H50834
118329	genbank_N63520	N63520
104404	H58762_et	H58762
104776	genbank_AA026349	AA026349
113502	genbank_T89130T89130	
101262	entrez_L35854	L35854
108573	genbank_AA086005	AA086005
101447	entrez_M21305	M21305
124357	genbank_N22401	N22401
108781	genbank_AA128654	AA128654
112794	genbank_R97018	R97018
100351	entrez_D64158	D64158
100555	Ugr_HT2245	M69181 M81105 U51039

Table 4A shows 202 genes up-regulated in samples from patients treated with chemotherapy or radiotherapy. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
10	R1:	average of AI for samples from patients treated with chemotherapy or radiotherapy divided by the average of AI for normal lung samples.			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	100113	NM_001269	Hs.84746	chromosome condensation 1	27.20
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	20.60
15	100210	D26361	Hs.3104	KIAA0042 gene product	20.40
	100225	D28539	Hs.167185	glutamate receptor, metabotropic 5	20.60
	100269	NM_001949	Hs.1189	E2F transcription factor 3	29.40
	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	23.50
	100877	X80821	Hs.27973	KIAA0874 protein	35.56
20	100893	BE245294	Hs.180789	S164 protein	43.40
	101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	21.80
	101447	M21305		gb:Human alpha satellite and satellite 3	193.60
	101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	38.40
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	198.80
25	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	78.60
	101809	M68649	Hs.323733	gap junction protein, beta 2, 26kD (conn	162.20
	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	50.00
	101915	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	26.00
	101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	37.20
30	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	
	102031	U04898	Hs.2156	RAR-related orphan receptor A	32.00
	102052	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	51.20
	102391	AA296874	Hs.77494	deoxyguanosine kinase	13.90
	102420	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	28.80
35	102610	U65011	Hs.30743	preferentially expressed antigen in mela	110.60
	102829	NM_006183	Hs.80962	neurensin	116.80
	103000	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	2.30
	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	181.40
40	103507	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	49.20
	103587	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	86.60
	104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	42.60
	104896	AW015318	Hs.23165	ESTs	29.40
	105038	AW503733	Hs.9414	KIAA1488 protein	21.50
	105298	BE387790	Hs.26369	hypothetical protein FLJ20287	32.80
45	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	20.20
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	28.40
	106073	AL157441	Hs.17834	downstream neighbor of SON	25.40
	106205	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	32.00
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (40.60
50	106533	AL134708	Hs.145998	ESTs	59.80
	106575	AW970602	Hs.105421	ESTs	43.40
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	50.80
	106851	AI458623		gb:lk04g09.x1 NCL_CGAP_Lu24 Homo sapiens	53.40
	106995	AB023139	Hs.37892	KIAA0922 protein	20.88
55	107332	T87750	Hs.183297	DKFZP566F2124 protein	23.60
	107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	57.20
	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	49.00
	108609	BE409857	Hs.69499	hypothetical protein	19.67
	108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	48.17
60	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakldns	59.20
	109260	AW978515	Hs.131915	KIAA0863 protein	28.60
	109280	AK001355	Hs.279610	hypothetical protein FLJ10493	22.80
	109292	AW975746	Hs.188662	KIAA1702 protein	
	109384	AA219172	Hs.86849	ESTs	21.00
65	109415	U80736	Hs.110826	trinucleotide repeat containing 9	31.60
	109445	AA232103	Hs.189915	ESTs	24.20
	109502	AW967069	Hs.211556	hypothetical protein MGC5487	21.40
	109633	AW003785	Hs.170267	ESTs	20.40
	109786	AI989482	Hs.146286	kinesin family member 13A	19.60
70	109958	AA001266	Hs.133521	ESTs	24.00
	110920	N47224	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	28.40
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	36.00
	111084	H44186	Hs.15456	PDZ domain containing 1	61.20
	111132	AB037807	Hs.83293	hypothetical protein	24.60
75	111229	AW389845	Hs.110855	ESTs	27.20
	111337	AA837396	Hs.263925	US1-interacting protein NUDE1, rat homo	48.00
	111987	NM_015310	Hs.8763	KIAA0942 protein	37.80
	112046	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	26.80
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	63.80
80	112685	R87650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU	26.40
	112871	AL110216	Hs.12285	ESTs, Weakly similar to I55214 salivary	47.64
	112897	AW206453	Hs.3782	ESTs	22.00
	112973	AB033023	Hs.318127	hypothetical protein FLJ10201	65.00
	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	42.00
85	113073	N39342	Hs.103042	microtubule-associated protein 1B	55.40

	113494	T91451	Hs.86538	ESTs	22.80
	113560	T91015	Hs.268626	ESTs	22.80
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	51.80
5	113950	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	28.20
	114339	AA782845	Hs.22790	ESTs	20.20
	114365	H42169	Hs.18653	hypothetical protein FLJ14627	21.00
	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	25.80
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	23.60
10	114824	AA960961	Hs.305953	zinc finger protein 83 (HPF1)	27.20
	114837	BE244930	Hs.166895	ESTs	30.20
	114974	AW866931	Hs.179562	nucleosome assembly protein 1-like 1	20.80
	115075	AA814043	Hs.88045	ESTs	30.60
	115084	BE383668	Hs.42484	hypothetical protein FLJ10618	28.86
15	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	38.00
	115313	AA808001	Hs.184411	albumin	22.60
	115697	D31382	Hs.63325	transmembrane protease, serine 4	173.60
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	27.77
	116090	AI691147	Hs.61232	ESTs	20.80
20	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	164.20
	116399	AA889120	Hs.110637	homeo box A10	38.00
	117099	H93699		gb:yv16a11.s1 Soares fetal liver spleen	21.60
	117881	AF181470	Hs.260622	butyrate-induced transcript 1	49.40
	118091	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_HUMAN CALCI	22.40
25	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	22.00
	118720	N73515		gb:za49d07.s1 Soares fetal liver spleen	20.00
	118873	AI824009	Hs.44577	ESTs	19.40
	119126	R45175	Hs.117183	ESTs	111.20
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	33.00
30	119940	AL050097	Hs.272531	DKFZP586B0319 protein	31.00
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	20.20
	120515	AA258356		gb:zr59c10.s1 Soares_NhHMPu_S1 Homo sapl	25.00
	120859	AA828434	Hs.1819	achaete-scute complex (Drosophila) homol	95.40
	120983	AA398209	Hs.97587	EST	105.20
35	121054	AW976570	Hs.97387	ESTs	38.80
	121369	AW450737	Hs.128791	CGI-09 protein	41.60
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	30.80
	122612	AA974832	Hs.128708	ESTs	19.60
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	33.20
40	123440	AI733692	Hs.112488	ESTs	23.17
	123596	AA421130	Hs.112640	EST	23.00
	123619	AA602964		gb:nc97c02.s1 NCL_CGAP_Pr2 Homo sapiens	28.80
	124006	AI147155	Hs.270016	ESTs	77.60
	124169	BE079334	Hs.271630	ESTs	22.20
45	124281	AI333756	Hs.111801	arsenate resistance protein ARS2	42.20
	124472	N52517	Hs.102670	EST	32.60
	124617	AW628168	Hs.152684	ESTs	21.80
	124631	NM_014053	Hs.270594	FLVCR protein	30.40
	124839	R55784	Hs.140942	ESTs	21.20
50	125186	AA610620	Hs.181244	major histocompatibility complex, class	42.80
	125321	T86652	Hs.178294	ESTs	27.00
	125535	NM_013243	Hs.22215	secretogranin III	23.80
	125646	AA628962	Hs.75209	protein kinase (cAMP-dependent, catalyti	23.20
	125684	AW589427	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	21.20
55	125724	AL360190	Hs.295978	Homo sapiens mRNA full length insert cDN	48.80
	125847	AW161885	Hs.249034	ESTs	31.00
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	21.20
	126077	M78772	Hs.210836	ESTs	49.80
	126299	AW979155	Hs.298275	amino acid transporter 2	21.80
60	126395	AI468004	Hs.276956	hypothetical protein FLJ12929	71.00
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	23.20
	126509	R47400	Hs.23850	ESTs	23.80
	126538	AB030656	Hs.17377	coronin, actin-binding protein, 1C	23.10
	126666	AA648886	Hs.151999	ESTs	36.00
65	126812	AB037860	Hs.173933	nuclear factor I/A	20.80
	126872	AW450979		gb:U1-H-B13-ala-a-12-0-U1.s1 NCL_CGAP_Su	46.29
	127046	AA321948	Hs.293968	ESTs	22.80
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	30.00
	127489	AA650250	Hs.272076	ESTs	20.80
70	127521	AW297206	Hs.164018	ESTs	25.20
	127742	AW293496	Hs.180138	ESTs	28.00
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	21.20
	127930	AA809672	Hs.123304	ESTs	20.64
	127968	AA830201	Hs.124347	ESTs	28.20
75	127987	AI022103	Hs.124511	ESTs	19.60
	128116	H07103	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	20.40
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	34.40
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2	53.80
	128949	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	23.00
80	129168	AI132968	Hs.109052	chromosome 14 open reading frame 2	37.60
	129404	AI267700	Hs.317584	ESTs	28.60
	129527	AA769221	Hs.270847	delta-tubulin	40.80
	129574	AA026815	Hs.11463	UMP-CMP kinase	31.20
	128598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	29.60
85	129785	H19006	Hs.184780	ESTs	72.20
	129970	AV655806	Hs.296198	chromosome 12 open reading frame 4	22.20

	130149	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	29.60
	130199	Z48579	Hs.172028	a disintegrin and metalloproteinase domain	27.60
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	28.36
5	130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	20.20
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	22.40
	130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	19.60
	130703	R77776	Hs.18103	ESTs	19.40
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	21.40
10	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	110.00
	131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	25.20
	131086	AL035461	Hs.2281	chromogranin B (secretogranin 1)	40.60
	131284	NM_001429	Hs.25272	E1A binding protein p300	24.60
	131775	AB014548	Hs.31921	KIAA0648 protein	21.00
15	131860	BE383676	Hs.334	Rho guanine nucleotide exchange factor (33.40
	131945	NM_002918	Hs.35120	replication factor C (activator 1) 4 (37	60.80
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	20.40
	132084	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)	29.40
	132389	AA310393	Hs.190044	ESTs	32.40
20	132437	AA152106	Hs.4859	cyclin L an/a-6a	27.40
	132550	AW969263	Hs.170195	bone morphogenetic protein 7 (osteogenic	75.60
	132617	AF037335	Hs.5338	carbonic anhydrase XII	31.36
	132632	AU076916	Hs.5398	guanine monophosphate synthetase	32.40
	132672	W27721	Hs.54697	Cdc42 guanine exchange factor (GEF) 9	23.40
25	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	61.20
	132771	Y10275	Hs.56407	phosphoserine phosphatase	22.33
	133070	U92649	Hs.64311	a disintegrin and metalloproteinase domain	23.50
	133153	AF070592	Hs.66170	HSKM-B protein	30.00
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	23.80
30	133282	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	51.60
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	33.00
	133592	AV652066	Hs.75113	general transcription factor IIA	82.00
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 6	69.33
35	134032	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor	33.20
	134125	NM_014781	Hs.50421	KIAA0203 gene product	31.60
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	30.60
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-in	23.40
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	49.20
40	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	20.20
	134753	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	20.80
	135002	AA448542	Hs.251677	G antigen 7B	37.60
	135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase	53.40
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	31.60
45	135345	X53655	Hs.99171	neurotrophin 3	28.80

TABLE 4B shows the accession numbers for those primekeys lacking unigenelD's for Table 4A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123619	371681_1	AA602964 AA609200
126433	127143_1	AA325605 AA099517 N89423
126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359
		BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
106851	322947_1	AI458623 AA639708 AA485409 R22065 AA485570
118720	genbank_N73515	N73515
120515	genbank_AA258356	AA258356
117099	321871_1	H93699 H97976 H80036
101447	entrez_M21305	M21305
123130	genbank_AA487200	AA487200

Table 5A shows 680 genes up-regulated in squamous cell carcinoma or adenocarcinoma lung tumors relative to normal lung and chronically diseased lung. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 GeneChip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number							
	ExAccn:	Exemplar Accession number, Genbank accession number							
	UnigeneID:	Unigene number							
	Unigene Title:	Unigene gene title							
10	R1:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R2:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R3:	80th percentile of AI squamous cell carcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R4:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 80th percentile of AI for squamous cell carcinoma lung tumor samples.							
15	R5:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by 90th percentile of AI for normal and chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples							
20	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3	R4	R5
	100035			AFFX control: GAPDH					6.76
	100036			AFFX control: GAPDH					5.77
	100037			AFFX control: GAPDH					5.75
25	100071	A28102		Human GABAA receptor alpha-3 subunit		8.00			
	100114	X02308	Hs.82962	thymidylate synthetase					5.71
	100154	H60720	Hs.81892	KIAA0101 gene product	3.84				
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	3.33				
	100188	AW247090	Hs.57101	mln1 chromosome maintenance deficient (S.					4.52
	100202	BE294407	Hs.99910	phosphofructokinase, platelet					5.49
30	100216	AA489908	Hs.1390	proteasome (prosome, macropain) subunit,					5.67
	100269	NM_001949	Hs.1189	E2F transcription factor 3	2.55				
	100287	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (a					5.66
	100297	AU077258	Hs.182429	protein disulfide isomerase-related prot					3.81
	100330	AW410976	Hs.77152	mln1 chromosome maintenance deficient (S.					4.50
35	100336	AW247629	Hs.6793	platelet-activating factor acetylhydrola	5.07				
	100360	W70171	Hs.75939	uridine monophosphate kinase					4.82
	100372	NM_014791	Hs.184339	KIAA0175 gene product					3.79
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic				15.65	
	100486	T19006	Hs.10842	RAN, member RAS oncogene family					5.49
40	100491	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)					4.17
	100516	D90278	Hs.11	carcinoembryonic antigen-related cell ad		7.20			
	100522	X51501	Hs.99949	prolactin-induced protein				14.20	
	100559	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	3.10				
45	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid				9.30	
	100629	AA015693	Hs.21291	mitogen-activated protein kinase kinase				20.60	
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.85				
	100677	AA353686	Hs.57813	zinc ribbon domain containing, 1		8.60			
	100696	D14887	Hs.121686	general transcription factor IIA, 1 (37k				10.00	
50	100709	N26539	Hs.100469	myeloid/lymphoid or mixed-lineage leukem			24.80		
	100761	BE208491	Hs.295112	KIAA0618 gene product		7.60			
	100830	AC004770	Hs.4756	flap structure-specific endonuclease 1					7.99
	100867	U14622		gb:Human transketolase-like protein gene		10.20			
	100902	M16029	Hs.287270	ret proto-oncogene (multiple endocrine n		8.00			
55	100906	AU076916	Hs.5398	guanine monophosphate synthetase					5.16
	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	2.57				
	101045	J05614		gb:Human proliferating cell nuclear anti					4.69
	101061	NM_000175	Hs.180532	glucose phosphate isomerase					4.19
	101071	L02840	Hs.84244	potassium voltage-gated channel, Shab-re		12.91			
60	101124	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.12				
	101175	U82671	Hs.36980	melanoma antigen, family A, 2	3.50				
	101181	BE262621	Hs.73798	macrophage migration inhibitory factor (5.69
	101204	L24203	Hs.82237	ataxia-telangiectasia group D-associated	4.08				
	101210	L29301	Hs.2353	opioid receptor, mu 1			6.40		
65	101216	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.53				
	101228	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (7.90
	101233	AL135173	Hs.878	sorbitol dehydrogenase					4.45
	101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	8.50				
	101342	U52112	Hs.182018	interleukin-1 receptor-associated kinase					4.17
70	101346	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				21.89	
	101369	NM_000892	Hs.1901	kalikrein B, plasma (Fletcher factor) 1				12.80	
	101396	BE267931	Hs.78996	proliferating cell nuclear antigen	3.24				
	101431	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)					7.90
	101448	NM_000424	Hs.195850	keratin 5 (epidermolysis bullosa simplex	8.31				
75	101462	AL035668	Hs.73853	bone morphogenetic protein 2				38.80	
	101466	BE262660	Hs.170197	glutamic-oxaloacetic transaminase 2, mit					4.01
	101484	AA053486	Hs.20315	interferon-induced protein with tetrabir				12.00	
	101502	M26958		gb:Human parathyroid hormone-related pro	10.50				
	101505	AA307680	Hs.75692	asparagine synthetase					4.46
80	101526	NM_002197	Hs.154721	aconitase 1, soluble	4.02				
	101535	X57152	Hs.99853	fibrillarin					4.65
	101577	M34353	Hs.1041	v-ras avian UR2 sarcoma virus oncogene h				9.09	
	101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	54.00				
	101663	NM_003528	Hs.2178	H2B histone family, member Q	5.59				
	101664	AA436989	Hs.121017	H2A histone family, member A	7.00				
85	101669	L24498	Hs.80409	growth arrest and DNA-damage-inducible,		7.60			

	101695	M69136	Hs.135626	chymase 1, mast cell	4.79		
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	15.21		
	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	55.50		
5	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino		18.57	4.10
	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant			
	101804	M86699	Hs.169840	TTK protein kinase	4.50		
	101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	140.00		
	101833	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.56		
10	101842	M93221	Hs.75182	mannose receptor, C type 1		12.80	
	101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor			5.88
	102002	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	7.80		
	102039	AL134223	Hs.306098	aldo-keto reductase family 1, member C1			4.35
	102072	U09410	Hs.78743	zinc finger protein 131 (clone pHZ-10)		7.40	
	102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4			5.12
15	102111	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,		12.00	
	102123	NM_001809	Hs.1594	centromere protein A (17kD)	6.20		
	102154	U17760	Hs.75517	laminin, beta 3 (niclin (125kD), kalinin	2.62		
	102193	AL036335	Hs.313	secreted phosphoprotein 1 (osteopontin,	5.85		
	102217	AA825978	Hs.301613	JTV1 gene			6.18
20	102224	NM_002810	Hs.148495	proteasome (prosome, macropain) 26S subu			4.49
	102234	AW163390	Hs.278554	heterochromatin-like protein 1			5.80
	102251	NM_004398	Hs.41706	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.50		
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)			5.15
	102330	BE298063	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta			4.17
25	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro		9.33	
	102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	8.87		
	102368	U39817	Hs.36820	Bloom syndrome	15.91		
	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma		19.20	
30	102404	NM_005429	Hs.79141	vascular endothelial growth factor C			14.00
	102537	U57094	Hs.50477	RAB27A, member RAS oncogene family			12.00
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2			4.57
	102605	AI435128	Hs.181369	ubiquitin fusion degradation 1-like			3.98
	102610	U65011	Hs.30743	preferentially expressed antigen in meta	77.50		
35	102623	AW249285	Hs.37110	melanoma antigen, family A, 9	12.50	22.00	
	102642	AA205847	Hs.23016	G protein-coupled receptor			
	102654	AV649989	Hs.24385	Human hbc647 mRNA sequence		12.00	
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein			12.80
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.50		
40	102672	U72066	Hs.29287	retinoblastoma-binding protein 8	8.50		
	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C			9.24
	102696	BE540274	Hs.239	forkhead box M1			5.54
	102768	U82321		gb:Homo sapiens clone 14.9B mRNA sequenc	6.60		
	102781	BE258778	Hs.108809	chaperonin containing TCP1, subunit 7 (e			3.78
45	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat		14.40	4.26
	102824	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H			
	102829	NM_006183	Hs.80962	neurotensin	8.00		
	102888	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1			5.50
	102892	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin		6.70	
50	102913	NM_002275	Hs.80342	keratin 15	4.64		
	102935	BE561850	Hs.80508	small nuclear ribonucleoprotein polypept	2.93		
	102951	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol		11.40	
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)			7.26
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	3.01		
55	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	27.90		
	103038	AA926960	Hs.334883	CDC28 protein kinase 1			8.79
	103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin			4.27
	103099	AI693251	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S pro	9.80		
	103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.05		
60	103168	X53463	Hs.2704	glutathione peroxidase 2 (gastric/intestin	3.07		
	103185	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasm			5.62
	103192	M22440	Hs.170009	transforming growth factor, alpha	7.40		
	103223	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (g			4.70
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o		100.00	
65	103316	X83301	Hs.324728	SMA5			9.80
	103375	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	9.71		
	103376	AL036166	Hs.323378	coated vesicle membrane protein	14.00		
	103385	NM_007069	Hs.37189	similar to rat HREV107		11.00	
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	2.93		
70	103404	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,			5.15
	103430	BE564090	Hs.20716	translocase of inner mitochondrial membr			3.98
	103446	X98834	Hs.79971	sal (Drosophila)-like 2		21.40	
	103476	Y07701	Hs.293007	aminopeptidase puromycin sensitive	13.00		
	103477	AJ011812	Hs.119018	transcription factor NRF		6.40	
75	103478	BE514982	Hs.38991	S100 calcium-binding protein A2	5.02		
	103515	Y10275	Hs.56407	phosphoserine phosphatase	10.50		
	103558	BE816547	Hs.2785	keratin 17	6.41		
	103580	AA328046	Hs.46405	polymerase (RNA) II (DNA directed) polyp			3.84
	103587	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	78.50		
80	103594	AI368680	Hs.816	SRV (sex determining region Y)-box 2	6.51		
	103636	NM_006235	Hs.2407	POU domain, class 2, associating factor	3.50		
	103768	AF086009		gb:Homo sapiens full length insert cDNA			4.48
	103841	AA314821	Hs.38178	hypothetical protein FLJ23458	8.00		
	103847	AF219946	Hs.102237	tubby super-family protein	10.40		
85	103913	AW987500	Hs.133543	ESTs		15.60	
	104094	AA418187	Hs.330515	ESTs	6.60		

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	104150	AL122044	Hs.331633	hypothetical protein DKFZp566N034		26.00	
	104257	BE560621	Hs.9222	estrogen receptor binding site associate	6.80		
	104261	AW248364	Hs.5409	RNA polymerase I subunit			3.98
5	104331	AB040450	Hs.279862	cdk inhibitor p21 binding protein	6.80		
	104415	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha	10.29		
	104558	R56578	Hs.88959	hypothetical protein MGC4816	4.21		
	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m		15.79	
	104658	AA350954	Hs.27268	Homo sapiens cDNA: FLJ21933 fis, clone H		17.40	
10	104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	6.40		
	104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr			6.55
	104754	AI206234	Hs.155924	cAMP responsive element modulator		10.00	
	104758	BE560269	Hs.7010	NPD002 protein			4.47
	104971	BE311926	Hs.15830	hypothetical protein FLJ12691	2.87		
15	105011	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.83		
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.86		
	105026	AA809485	Hs.124219	hypothetical protein FLJ12934	11.00		
	105076	AI598262	Hs.37810	hypothetical protein MGC14833			5.01
	105132	AA148164	Hs.247280	HBV associated factor			3.99
20	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti		11.00	
	105158	AW976357	Hs.234545	hypothetical protein NUF2R	16.00		
	105175	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	4.32		
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	3.00		
	105264	AA227934		gb:zr57e08.s1 Soares_NhHMPu_S1 Homo sapi		10.00	
25	105298	BE387790	Hs.26369	hypothetical protein FLJ20287	3.69		
	105409	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8		9.20	
	105460	AW296078	Hs.271721	Homo sapiens, clone IMAGE:4179986, mRNA,		7.80	
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.12		
	105743	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	3.82		
30	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro		27.00	
	105848	AW954054	Hs.24951	ESTs		7.60	
	105891	U55984	Hs.289088	heat shock 90kD protein 1, alpha			4.14
	106019	AF221993	Hs.46743	McKusick-Kaufman syndrome		16.80	
	106069	BE586623	Hs.29899	ESTs, Weakly similar to G02075 transcrip		23.40	
35	106073	AL157441	Hs.17834	downstream neighbor of SON	9.50		
	106126	AA576953	Hs.22972	hypothetical protein FLJ13352	6.00		
	106159	AK001301	Hs.3487	hypothetical protein FLJ10439			3.95
	106220	D61329	Hs.32196	mitochondrial ribosomal protein L36			6.04
40	106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S		13.20	
	106300	Y10043	Hs.19114	high-mobility group (nonhistone chromoso			5.02
	106307	AA436174	Hs.37751	ESTs, Weakly similar to putative p150 (6.60		
	106318	AA025610	Hs.9605	cleavage and polyadenylation specific fa			5.04
	106341	AF191020	Hs.5243	hypothetical protein, estradiol-induced			7.25
	106440	AA448553	Hs.151393	glutamate-cysteine ligase, catalytic sub		13.80	
45	106481	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.75		
	106586	AA243837	Hs.57787	ESTs		10.84	
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr		45.60	
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	28.00		
	106785	Y15227	Hs.20149	deleted in lymphocytic leukemia, 1	3.00		
50	106813	C05766	Hs.181022	CGI-07 protein		11.40	
	106895	AK001826	Hs.25245	hypothetical protein FLJ11269		6.00	
	106913	AI219346	Hs.86178	M-phase phosphoprotein 9	6.56		
	106919	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S			4.27
	107054	AI076459	Hs.15978	KIAA1272 protein		34.80	
55	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	4.71		
	107098	AI823593	Hs.27688	ESTs		24.80	
	107104	AU076640	Hs.16243	nucleolar protein 1 (120kD)			7.05
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.60		
	107198	AV657225	Hs.9846	KIAA1040 protein		19.20	
60	107203	D20426	Hs.41639	programmed cell death 2		7.60	
	107217	AL080235	Hs.35861	DKFZP586E1621 protein	9.50		
	107284	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	2.71		
	107318	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence		8.71	
	107516	X57152	Hs.99853	fibrillarin			4.33
65	107529	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)			4.00
	107728	AA019551	Hs.294151	Homo sapiens, clone IMAGE:3603836, mRNA,	10.80		
	107851	AA022953	Hs.61172	EST		8.00	
	107901	L42612	Hs.335952	keratin 6B	3.40		
	107922	BE153865	Hs.61460	Ig superfamily receptor LNIR	2.88		
70	107932	AW392555	Hs.18878	hypothetical protein FLJ21620	7.50		
	108015	AW298357	Hs.49927	protein kinase NYD-SP15			23.40
	108056	AA043675	Hs.62633	ESTs			12.80
	108075	AI867370	Hs.139709	hypothetical protein FLJ12572			12.60
	108187	BE245374	Hs.27842	hypothetical protein FLJ11210	7.00		
75	108296	N31256	Hs.161623	ESTs	6.60		
	108305	AA071391		gb:zm61a06.r1 Stratagene fibroblast (937			11.80
	108393	AA075211		gb:zm86a08.r1 Stratagene ovarian cancer			11.80
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428			20.60
	108554	AA084948		gb:zn13b09.s1 Stratagene hNT neuron (937	6.40		
80	108573	AA086005		gb:zlb4c04.s1 Stratagene colon (937204)			25.40
	108584	AA088326	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	9.60		
	108597	AK000292	Hs.278732	hypothetical protein FLJ20285			14.60
	108695	AB029000	Hs.70823	KIAA1077 protein	3.00		
	108699	AA121514	Hs.70832	ESTs			10.00
	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c		11.00	
85	108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.21		

5	108810	AW295647	Hs.71331	hypothetical protein MGC5350	8.50			
	108816	AA130884	Hs.270501	ESTs, Moderately similar to ALU2_HUMAN		7.40		
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	4.00			
	108860	AA133334	Hs.129911	ESTs	6.09			
	108937	AL050107	Hs.24341	transcriptional co-activator with PDZ-bl	3.00			
10	109010	NM_007240	Hs.44229	dual specificity phosphatase 12	2.69			
	109121	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S pro			4.53	
	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	10.58			
	109227	AA766998	Hs.85874	Human DNA sequence from clone RP11-16L21		9.00		
	109415	U80736	Hs.110826	trinucleotide repeat containing 9		51.40		
15	109418	AI866946	Hs.161707	ESTs			11.00	
	109454	AA232255	Hs.295232	ESTs, Moderately similar to A46010 X-II		17.60		
	109502	AW967069	Hs.211556	hypothetical protein MGC5487		9.49		
	109543	AA564994	Hs.222851	ESTs		12.67		
	109548	H17800	Hs.7154	ESTs			10.40	
20	109680	AB037734	Hs.4993	KIAA1313 protein		33.20		
	109700	F09609		gb:HSC33H092 normalized infant brain cDN			16.00	
	109704	AI743880	Hs.12878	ESTs		11.00		
	109792	R49625		gb:yg61f03.s1 Soares infant brain 1NIB H			12.60	
	109981	BE548208	Hs.26090	hypothetical protein FLJ20272	4.00			
25	109998	AL042201	Hs.21273	transcription factor NYD-sp10		7.80		
	110039	H11938	Hs.21907	histone acetyltransferase		7.00		
	110156	AA581322	Hs.4213	hypothetical protein MGC16207			4.24	
	110500	AA907723	Hs.36962	ESTs	4.50			
	110551	AW450381	Hs.14529	ESTs		8.60		
30	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.06			
	110854	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to		6.80		
	110886	AW274992	Hs.72249	three-PDZ containing protein similar to		8.80		
	110916	BE178102	Hs.24349	ESTs		6.80		
	111003	N52980	Hs.83765	dihydrofolate reductase			16.80	
35	111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	2.54			
	111434	R01608	Hs.142736	ESTs			9.80	
	111439	AI476429	Hs.19238	ESTs			10.40	
	111540	U82670	Hs.9786	zinc finger protein 275		15.40		
	111597	R11499	Hs.189716	ESTs			9.20	
40	111895	T80581	Hs.12723	Homo sapiens clone 25153 mRNA sequence		6.80		
	111929	AF027208	Hs.112360	prominin (mouse)-like 1			14.67	
	112054	R43590		gb:yc85g02.s1 Soares infant brain 1NIB H		10.80		
	112210	R49645	Hs.7004	ESTs			10.20	
	112244	AB029000	Hs.70823	KIAA1077 protein	2.99			
45	112382	R59804		gb:yh07g12.s1 Soares infant brain 1NIB H		6.60		
	112392	R60763	Hs.193274	ESTs, Moderately similar to I57588 HSrel		7.10		
	112442	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regl	3.00			
	112539	R70318	Hs.339730	ESTs			37.20	
	112772	AI992283	Hs.35437	ESTs, Moderately similar to I38026 MLN 6			14.60	
50	112869	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin				4.83
	112935	R71449	Hs.268760	ESTs	2.73			
	112970	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence			12.00	
	112973	AB033023	Hs.318127	hypothetical protein FLJ10201	11.50			
	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		10.89		
55	113063	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	15.00			
	113073	N39342	Hs.103042	microtubule-associated protein 1B		15.31		
	113078	T40444	Hs.118354	CAT56 protein		7.00		
	113238	R45467	Hs.189813	ESTs			41.20	
	113591	T91881	Hs.200597	KIAA0583 gene product			9.40	
60	113702	T97307		gb:ye53h05.s1 Soares fetal liver spleen	25.00			
	113844	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE			13.91	
	113984	R96696	Hs.35588	ESTs		7.80		
	114073	R44953	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f	3.42			
	114162	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase		7.20		
65	114208	AL049466	Hs.7859	ESTs		6.74		
	114251	H15261	Hs.21948	ESTs			33.20	
	114285	R44338	Hs.22974	ESTs			13.20	
	114313	H18456	Hs.27946	ESTs			10.00	
	114339	AA782845	Hs.22790	ESTs		7.80		
70	114407	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f				4.14
	114560	AI452469	Hs.165221	ESTs			9.80	
	114699	AA127386		gb:zn90d09.r1 Stratagene lung carcinoma		7.60		
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S	3.21			
	114793	AA158245		gb:zo76c03.s1 Stratagene pancreas (93720		6.00		
75	114833	AI417215	Hs.87159	hypothetical protein FLJ12577			11.40	
	115047	BE270930	Hs.82916	chaperonin containing TCP1, subunit 6A (4.31
	115060	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3				4.03
	115097	AA256213	Hs.72010	ESTs			35.40	
	115113	AA256460		gb:zr81a04.s1 Soares_NhHMPu_S1 Homo sapi			15.20	
80	115123	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m				4.19
	115134	AW968073	Hs.194331	ESTs, Highly similar to A55713 inositol			12.40	
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	25.00			
	115347	AA356792	Hs.334824	hypothetical protein FLJ14825		7.00		
	115414	AA662240	Hs.283099	AF15q14 protein	3.25			
85	115522	BE614387	Hs.333893	c-Myc target JPO1	3.68			
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	10.50			
	115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1			24.40	
	115645	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.17			
	115648	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H		6.00		

	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	3.81				
	115697	D31382	Hs.63325	transmembrane protease, serine 4	62.14				
	115793	AA424883	Hs.70333	hypothetical protein MGC10753				11.80	
	115816	BE042915	Hs.287588	Homo sapiens cDNA FLJ13675 fis, clone PL				9.71	
5	115892	AA291377	Hs.50831	ESTs		27.40			
	115906	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fs, clone NT	2.53				
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	11.82				
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970				34.29	
	115978	AL035864	Hs.69517	cDNA for differentially expressed CO16 g				8.23	
10	115985	AA447709	Hs.268115	ESTs, Weakly similar to T08599 probable	3.00				
	116090	AI591147	Hs.61232	ESTs	5.17				
	116096	AA682382	Hs.59982	ESTs		8.20			
	116127	AF126743	Hs.279884	DNAJ domain-containing		10.60			
	116157	BE439838	Hs.44298	mitochondrial ribosomal protein S17				5.82	
15	116190	AI949095	Hs.87776	ESTs, Weakly similar to T22341 hypotheti				4.08	
	116278	NM_003686	Hs.47504	exonuclease 1	9.50				
	116335	AK001100	Hs.41690	desmocollin 3	3.67				
	116496	AW450634	Hs.21433	hypothetical protein DKFZp547J036		7.00			
20	116503	AI925316	Hs.212617	ESTs				12.60	
	116674	AI768015	Hs.92127	ESTs		32.00			
	116929	AA586922	Hs.80475	polymerase (RNA) II (DNA directed) polyp	7.60				
	116973	AI702054	Hs.166982	phosphatidylinositol glycan, class F	9.80				
	116993	AI417023	Hs.40478	ESTs				10.20	
25	117079	H92325		gb:ys85f05.s1 Soares retina N2b4HR Homo				15.20	
	117317	AI263517	Hs.43322	ESTs				13.40	
	117326	N23629	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,				20.60	
	117396	W20128	Hs.296039	ESTs				10.60	
	117412	N32536	Hs.42645	ESTs				16.00	
	117519	N32528	Hs.146286	kinesin family member 13A				9.11	
30	117693	AW179019	Hs.112110	mitochondrial ribosomal protein L42				4.01	
	117721	N46100	Hs.93939	EST				19.80	
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	2.71				
	117903	AA768283	Hs.47111	ESTs				17.80	
35	117992	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586i2022 (f				10.60	4.17
	118013	AI674126	Hs.94031	ESTs					
	118017	AI813444	Hs.42197	ESTs			8.82		
	118186	N22886	Hs.42380	ESTs		7.00			
	118325	AI868065	Hs.166184	Intersectin 2				13.80	
40	118367	N84269	Hs.48946	EST			6.14		
	118368	N64339	Hs.48956	gap junction protein, beta 6 (connexin 3	3.14				
	118472	AL167545	Hs.42179	bromodomain and PHD finger containing, 3		12.40			
	118709	AA232970	Hs.293774	ESTs				12.20	
	119025	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	4.50				
45	119027	AF086161	Hs.114611	hypothetical protein FLJ11808	3.22				
	119052	R10889		gb:yf38d02.s1 Soares fetal liver spleen		9.60			
	119164	AF221993	Hs.46743	McKusick-Kaufman syndrome			6.60		
	119186	AI979147	Hs.101265	hypothetical protein FLJ22593				10.80	
	119243	T12603		gb:CHR90123 Chromosome 9 exon II Homo sa				9.44	
50	119490	AA195276	Hs.263858	ESTs, Moderately similar to B34087 hypot				11.80	
	119499	AI918906	Hs.55080	ESTs			14.80		
	119599	W45552		gb:zc26d03.s1 Soares_senescent_fibroblas		12.60			
	119780	NM_016625	Hs.191381	hypothetical protein	17.00				
	119845	W79123	Hs.58561	G protein-coupled receptor 87	13.50				
55	119941	AA699485	Hs.58896	ESTs		8.00			
	119994	AA642402	Hs.59142	ESTs	7.73				
	120102	W67353	Hs.170218	KIAA0251 protein			39.60		
	120104	AK000123	Hs.180479	hypothetical protein FLJ20118	2.91				
	120294	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par			8.20		
60	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.73				
	120599	AA804448	Hs.104463	ESTs		7.00			
	120699	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos				10.00	
	120715	AA292700		gb:zs59a06.s1 NCL_CGAP_GCB1 Homo sapiens		9.40			
	120821	Y19062	Hs.96870	staufer (Drosophila, RNA-binding protein				13.80	
65	120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol					
	120880	AA360240	Hs.97019	EST		15.60			
	120983	AA398209	Hs.97587	EST			27.66		
	121034	AL389951	Hs.271623	nucleoporin 50kD			20.80		
	121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like		22.80			
70	121313	AA402713	Hs.97872	ESTs				10.00	
	121369	AW450737	Hs.128791	CGI-09 protein	25.71				
	121376	AA448103	Hs.187958	solute carrier family 6 (neurotransmitte				5.42	
	121476	AA412311	Hs.97903	ESTs		8.30			
	121509	AA868939	Hs.97888	ESTs		8.59			
75	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associat	18.50				
	121753	AK000552	Hs.323518	WD repeat domain 5	7.00				
	121838	AA425680	Hs.98441	ESTs				10.40	
	121857	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.00				
	121991	AA430058	Hs.98649	EST				12.20	
80	122089	AW016543	Hs.98682	hypothetical protein FKSG32			8.60		
	122105	AW241685	Hs.98699	ESTs			6.14		
	122163	AA435702	Hs.98829	EST				10.40	
	122318	AA429743		gb:zv60b05.r1 Soares_testis_NHT Homo sap				18.20	
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	13.50				
	122338	AA443311	Hs.98998	ESTs	4.80				
85	122414	AK13473	Hs.99087	ESTs, Weakly similar to S47073 finger pr		8.00			

	122512	AF053305	Hs.98658	budding uninhibited by benzimidazoles 1	8.80		
	122516	AA449352	Hs.99217	ESTs		9.40	
	122702	AI220089	Hs.99439	ESTs	9.20		
	122852	AI580056	Hs.98992	ESTs		10.40	
5	122925	AW268962	Hs.111335	ESTs	6.80		
	123005	AW369771	Hs.52620	integrin, beta 8		12.60	
	123044	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro			5.35
	123160	AA488687	Hs.284235	ESTs, Weakly similar to 138022 hypothe		6.06	
	123315	AA496369		gb:zv37d10.s1 Soares ovary tumor NbHOT H		12.40	
10	123329	Z47542	Hs.179312	small nuclear RNA activating complex, po		11.80	
	123497	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	12.00		
	123518	AL035414	Hs.21068	hypothetical protein		13.00	
	123519	AW015887	Hs.112574	ESTs	12.20		
	123814	AK000492	Hs.98806	hypothetical protein		7.80	
15	123616	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L		10.60	
	123673	BE550112	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	23.00		
	123727	AI083986	Hs.282977	hypothetical protein FLJ13490	7.00		
	123731	AA609839		gb:ae62f01.s1 Stratagene lung carcinoma		9.80	
20	123752	AA227714	Hs.179703	KIAA0129 gene product	3.50		
	123900	AA621223	Hs.112953	EST		12.80	
	124006	AI147155	Hs.270016	ESTs	97.00		
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	3.02		
	124069	AF134160	Hs.7327	claudin 1		27.80	
25	124191	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha		35.80	
	124273	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	7.20		
	124297	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFp586J0323 (f		11.00	
	124305	AW963221		gb:EST375294 MAGe resequences, MAGH Homo		16.00	
	124676	AI360119.comp	Hs.181013	phosphoglycerate mutase 1 (brain)			6.08
	124874	BE550182	Hs.127826	RaiGEF-like protein 3, mouse homolog		21.00	
30	124904	AK000483	Hs.93872	KIAA1682 protein	9.40		
	124969	AI650360	Hs.100256	ESTs		10.80	
	125000	T58615	Hs.110640	ESTs		9.80	
	125201	AA693960	Hs.103158	ESTs, Weakly similar to T33296 hypothe	7.60		
35	125266	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO	6.59		
	125299	T32982	Hs.102720	ESTs		9.57	
	125356	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC		14.00	
	125370	AA256743	Hs.134158	Homo sapiens, Similar to KIAA0092 gene p	8.20		
	125418	AA777690	Hs.188501	ESTs		13.20	
40	125433	AL162066	Hs.54320	hypothetical protein DKFp762D096	21.40		
	125437	AI609449	Hs.140197	ESTs	6.98		
	125446	BE219987	Hs.166982	phosphatidylinositol glycan, class F	8.80		
	125711	AA305800	Hs.5672	hypothetical protein AF140225		11.20	
	125756	BE174587	Hs.289721	growth arrest specific transcript 5			4.31
45	125757	AI274906	Hs.166835	ESTs, Highly similar to 1814480A p53-ass		15.60	
	125769	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	3.20		
	125839	AW836261	Hs.337717	ESTs	8.20		
	125850	W85858	Hs.99804	ESTs	2.65		
	125875	H14480		gb:ym18b09.r1 Soares infant brain 1N1B H	7.40		
50	125924	BE272506	Hs.82109	syndecan 1			4.23
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein		3.98	
	126034	H60340		gb:yr39b04.r1 Soares fetal liver spleen		10.60	
	126327	AA432266	Hs.44648	ESTs	11.60		
	126345	N49713		gb:yy23f05.s1 Soares fetal liver spleen	6.67		
55	126435	AW614529	Hs.285847	CGI-19 protein		10.60	
	126487	AA283809	Hs.184601	solute carrier family 7 (cationic amino			4.38
	126521	AI475110	Hs.203933	ESTs	6.60		
	126522	W31912		gb:zc76d03.s1 Pancreatic Islet Homo sapi		14.80	
	126543	AL035864	Hs.69517	cDNA for differentially expressed CO16 g			4.01
60	126567	AA058394	Hs.57887	ESTs, Weakly similar to KIAA0758 protein	7.80		
	126605	AA676910		gb:zj65h07.s1 Soares_fetal_liver_spleen_		11.60	
	126627	AA497044	Hs.20887	hypothetical protein FLJ10392		14.60	
	126628	N49776	Hs.170994	hypothetical protein MGC10946	8.00		
	126737	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.92		
65	126795	AW976076	Hs.172589	nuclear phosphoprotein similar to S. cer	7.50		
	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	11.60		
	126892	AF121856	Hs.284291	sorting nexin 6	3.50		
	126928	AA480902	Hs.137401	ESTs		22.83	
	126979	AA210954		gb:zq89h10.r1 Stratagene hNT neuron (937		11.80	
70	126986	AI279892	Hs.46801	sorting nexin 14		11.60	
	126992	AI809521		gb:wf30e03.x1 Soares_NFL_T_GBC_S1 Homo s		20.80	
	127066	R25066		gb:yg42c07.r1 Soares Infant brain 1N1B H		27.60	
	127099	AA347668		gb:EST54026 Fetal heart II Homo sapiens		21.60	
	127139	AA830233	Hs.293585	ESTs		11.20	
75	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil	3.10		
	127221	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.76		
	127225	AA315933	Hs.120879	ESTs		16.80	
	127313	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	14.00		
	127444	AW978474	Hs.7560	Homo sapiens mRNA for KIAA1729 protein,		13.60	
80	127500	AW971353	Hs.162115	ESTs	11.20		
	127524	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin		7.80	
	127540	N45572	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	3.53		
	127599	AA613204	Hs.150399	ESTs		13.80	
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture		28.00	
85	127662	W80755	Hs.8294	KIAA0195 gene product		19.80	
	127668	AI343257	Hs.139993	ESTs		11.20	

	127746	AI239495	Hs.120189	ESTs			14.18
	127812	AA741368	Hs.291434	ESTs	4.50		
	127817	AA836841	Hs.163085	ESTs			24.60
5	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L			9.20
	127960	AI613226	Hs.41569	phosphatidic acid phosphatase type 2A			16.83
	127969	F06498	Hs.93748	Homo sapiens cDNA FLJ14676 fis, clone NT	13.60		
	128015	Z21169	Hs.334659	hypothetical protein MGC14139	7.00		
	128027	AI433721	Hs.164153	ESTs			37.40
	128077	AI310330	Hs.128720	ESTs			9.60
10	128168	NM_008147	Hs.11801	interferon regulatory factor 6			9.24
	128226	AI284940	Hs.289082	GM2 ganglioside activator protein	19.00		
	128305	AI954968	Hs.279009	matrix Gla protein			10.40
	128341	AA191420	Hs.185030	ESTs	9.00		
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul			4.30
15	128539	R46163	Hs.258618	ESTs	12.60		
	128568	H12912	Hs.274691	adenylate kinase 3			4.56
	128572	AA933022	Hs.256583	interleukin enhancer binding factor 3, 9		10.00	
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2		16.80	
	128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypept			4.48
20	128796	AJ000152	Hs.105924	defensin, beta 2	8.12		
	128920	AA622037	Hs.166468	programmed cell death 5			4.62
	128924	BE279383	Hs.26557	plakophilin 3			4.04
	128971	H05132	Hs.107510	ESTs	12.60		
	129008	AL079648	Hs.301088	ESTs	8.80		
25	129041	BE382756	Hs.169902	solute carrier family 2 (facilitated glu			6.05
	129075	BE250162	Hs.83765	dihydrofolate reductase	2.59		
	129105	AI769160	Hs.108681	Homo sapiens brain tumor associated prot		6.67	
	129189	AB023179	Hs.9059	KIAA0962 protein		8.00	
	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	4.00		
30	129241	AI878857	Hs.109706	hematological and neurological expressed			4.06
	129300	W94197	Hs.110165	ribosomal protein L26 homolog	2.55		
	129404	AI267700	Hs.317584	ESTs	18.00		
	129457	X61959	Hs.207776	aspartylglucosaminidase	6.50		
	129466	L42583	Hs.334309	keratin 6A	12.94		
35	129494	AI148976	Hs.112062	ESTs			11.00
	129605	AF061812	Hs.115947	keratin 16 (focal non-epidermolytic palm			4.46
	129641	AI911527	Hs.11805	ESTs			12.00
	129665	AW163331	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic			4.70
40	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA			4.02
	129720	AA156214	Hs.12162	APMCF1 protein			5.71
	129748	M16707	Hs.123053	H4 histone, family 2	3.50		
	129890	AI868872	Hs.282804	hypothetical protein FLJ22704			4.21
	129896	BE295568	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosyl	2.56		
45	129945	BE514376	Hs.165998	PAI-1 mRNA-binding protein			4.03
	130010	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34		7.00	
	130026	T40480	Hs.332112	EST		6.40	
	130080	X14850	Hs.147097	H2A histone family, member X			4.65
	130149	AW067805	Hs.172665	methyleneletrahydrofolate dehydrogenase	2.74		
50	130285	AA063546	Hs.75981	ubiquitin specific protease 14 (IRNA-gua		7.40	
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic			3.91
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.87		
	130500	AB007913	Hs.158291	KIAA0444 protein			9.60
	130524	U89995	Hs.159234	forkhead box E1 (thyroid transcription f		13.40	
	130541	X05608	Hs.211584	neurofilament, light polypeptide (68kD)		8.20	
55	130553	AF062649	Hs.252587	pituitary tumor-transforming 1			6.06
	130567	AA383092	Hs.1608	replication protein A3 (14kD)		7.00	
	130577	M69241	Hs.162	insulin-like growth factor binding prote	3.04		
	130627	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	3.87		
60	130648	AI458165	Hs.17296	hypothetical protein MGC2376			16.20
	130697	L29472	Hs.1802	major histocompatibility complex, class			17.80
	130744	H59698	Hs.18747	POP7 (processing of precursor, S. cerevi			5.28
	130800	AI187292	Hs.19574	hypothetical protein MGC5469			4.43
	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	16.84		
65	130869	J03626	Hs.2057	uridine monophosphate synthetase (orotat			4.92
	130925	AF093419	Hs.169378	multiple PDZ domain protein			9.60
	130994	W17044	Hs.327337	ESTs		12.40	
	131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	10.21		
	131031	NM_001650	Hs.288650	aquaporin 4			9.80
70	131041	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,			9.60
	131058	W28545	Hs.101514	hypothetical protein FLJ10342			17.00
	131090	AI143139	Hs.2288	visinin-like 1	2.74		
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f		8.80	
	131148	AW953575	Hs.303125	p53-induced protein PIGPC1	3.12		
75	131185	BE280074	Hs.23960	cyclin B1	3.07		
	131200	BE540516	Hs.293732	hypothetical protein MGC3195	3.07		
	131219	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.87		
	131257	AW339037	Hs.24908	ESTs			14.67
	131375	AW293165	Hs.143134	ESTs		19.20	
80	131460	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.50		
	131476	AI521663	Hs.334644	hypothetical protein FLJ14668	15.00		
	131510	BE245374	Hs.27842	hypothetical protein FLJ11210		7.80	
	131646	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom		7.00	
	131786	BE000971	Hs.306083	Novel human gene mapping to chromosome 22	2.65		
85	131839	AB014533	Hs.33010	KIAA0633 protein			35.20
	131843	AA192315	Hs.184062	putative Rab5-interacting protein			4.11

	131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	19.00			
	131885	BE502341	Hs.3402	ESTs	6.48			
	131921	AA456093	Hs.34720	ESTs		8.40		
5	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	56.00			
	131958	NM_014062	Hs.3556	ART-4 protein			3.82	
	131965	W79283	Hs.35962	ESTs	3.03			
	132000	AW247017	Hs.36978	melanoma antigen, family A, 3		9.80		
	132040	NM_001196	Hs.315589	Homo sapiens cDNA: FLJ22373 fis, clone H	3.30			
10	132109	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	21.00			
	132114	NM_006152	Hs.40202	lymphoid-restricted membrane protein		8.40		
	132162	AA315805	Hs.94560	desmoglein 2			12.25	
	132164	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	2.70			
	132180	NM_004460	Hs.418	fibroblast activation protein, alpha	2.71			
	132181	AW961231	Hs.16773	Homo sapiens clone TCCCA00427 mRNA sequ	3.83			
15	132182	NM_014210	Hs.70499	ecotropic viral integration site 2A			13.20	
	132231	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	9.50			
	132277	AK001745	Hs.184628	hypothetical protein FLJ10883	4.50			
	132328	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe			9.20	
	132394	AK001680	Hs.30488	DKFZP434F091 protein			19.80	
20	132424	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A		8.60		
	132528	T78736	Hs.50758	SMC4 (structural maintenance of chromoso		27.40		
	132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.38			
	132544	L19778	Hs.51011	H2A histone family, member P		7.00		
25	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.64			
	132552	BE621985	Hs.296922	thiopurine S-methyltransferase			15.83	
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624		6.60		
	132617	AF037335	Hs.5338	carbonic anhydrase XII	4.95			
	132638	AI798870	Hs.54277	DNA segment on chromosome X (unique) 992		8.20		
30	132653	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalni	4.38			
	132669	W38586	Hs.293981	guanine nucleotide binding protein (G pr			4.36	
	132710	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	4.60			
	132771	Y10275	Hs.56407	phosphoserine phosphatase	3.71			
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,			9.48	
35	132833	U78525	Hs.57783	eukaryotic translation initiation factor			5.83	
	132892	AW834050	Hs.9973	tensin			12.00	
	132906	BE613337	Hs.234896	germinin	3.09			
	132959	AW014195	Hs.61472	ESTs, Weakly similar to YAE6_YEAST HYPOT			3.87	
	132962	AA576635	Hs.6153	CGI-48 protein	3.50			
40	132990	X77343	Hs.334334	transcription factor AP-2 alpha (activat	6.18			
	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.19			
	133000	AL042444	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	2.96			
	133050	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	2.55			
	133083	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b			4.00	
45	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso			8.96	
	133134	AF198620	Hs.65648	RNA binding motif protein 8A			4.28	
	133155	M58583	Hs.662	cerebellin 1 precursor			10.60	
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.00			
	133204	BE267696	Hs.254105	enolase 1, (alpha)			4.63	
50	133412	U41493	Hs.73112	guanine nucleotide binding protein (G pr		12.50		
	133421	AF134160	Hs.7327	claudin 1	2.85			
	133451	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p			4.66	
	133453	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept		6.80		
	133504	NM_004416	Hs.74316	desmoplakin (DPI, DPII)	6.14			
55	133506	BE562958	Hs.74346	hypothetical protein MGC14353			4.55	
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,			17.80	
	133627	NM_002047	Hs.75280	glycyl-tRNA synthetase			4.85	
	133649	U25849	Hs.75393	acid phosphatase 1, soluble			6.34	
	133669	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5			14.00	
60	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		6.11		
	133776	BE268649	Hs.177766	ADP-ribosyltransferase (NAD+; poly (ADP-			4.91	
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	3.07			
	133946	AJ001259	Hs.173878	NIPSINAP, C. elegans, homolog 1			4.60	
	133973	N55540	Hs.78026	ESTs, Weakly similar to similar to ankyr			13.00	
65	134047	BE262529	Hs.78771	phosphoglycerate kinase 1			3.85	
	134098	BE513171	Hs.79086	mitochondrial ribosomal protein L3	2.56			
	134107	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte		8.20		
	134112	AW449809	Hs.79150	chaperonin containing TCP1, subunit 4 (d			4.08	
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	31.00			
70	134160	T98152	Hs.79432	fibrillin 2 (congenital contractual ara		24.60		
	134168	AA398908	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone L			6.71	
	134185	AA285136	Hs.301914	neuronal specific transcription factor D			14.74	
	134201	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5		8.40		
	134272	X76040	Hs.278614	protease, serine, 15	4.50			
75	134276	BE083936	Hs.80976	antigen identified by monoclonal antibod		9.00		
	134353	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m			16.40	
	134367	AA339449	Hs.82265	phosphoribosylglycinamide formyltransfer	2.80			
	134380	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.68			
	134423	H53497	Hs.83006	CGI-139 protein			3.84	
	134469	AA279661	Hs.83753	small nuclear ribonucleoprotein polypept			5.81	
80	134470	X54942	Hs.83758	CDC28 protein kinase 2			4.21	
	134498	AW246273	Hs.84131	threonyl-tRNA synthetase			7.30	
	134502	BE148534	Hs.84168	UV-B repressed sequence, HUR 7		13.60		
	134510	NM_002757	Hs.250870	mitogen-activated protein kinase kinase			9.70	
85	134548	N95406	Hs.333495	Deleted in split-hand/split-foot 1 regio			4.63	
	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	6.00			

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	134724	AF045239	Hs.321576	ring finger protein 22			12.00
	134743	AA044163	Hs.89463	potassium large conductance calcium-acti	4.00		
	134781	AA374372	Hs.89626	parathyroid hormone-like hormone		25.20	
5	134806	AD001628	Hs.89718	spermine synthase			4.58
	134853	BE268326	Hs.90280	5-aminimidazole-4-carboxamide ribonucle			4.79
	134859	D26488	Hs.90315	KIAA0007 protein		6.20	
	134891	R51083	Hs.90787	ESTs		7.40	
	134960	BE246400	Hs.285178	acetyl-Coenzyme A transporter	4.00		
10	134993	BE409809	Hs.301005	purine-rich element binding protein B			4.48
	135047	AL134187	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.50		
	135080	AI761180	Hs.94211	cd1 (required for cell differentiation,	5.00		
	135103	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)		11.00	
	135145	AW014729	Hs.95282	nuclear factor related to kappa B bindin			4.01
15	135184	U13222	Hs.96028	forkhead box D1		7.00	
	135242	AI583187	Hs.9700	cyclin E1	13.50		
	135286	AW023482	Hs.97849	ESTs	6.46		
	135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to		8.80	
	135355	AK001652	Hs.99423	ATP-dependent RNA helicase	10.00		
20	135371	NM_006025	Hs.997	protease, serine, 22	8.00		
	135393	L11244	Hs.99886	complement component 4-binding protein,			14.60

TABLE 5B shows the accession numbers for those primekeys lacking unigenelD's for Table 5A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Play: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Play	CAT number	Accessions
35	117079	1621717_1 H92325 T97125
	124305	242183_1 AW963221 AA344870 AA344871 H93331
	101502	18202_-6 M26958
	109792	754958_1 R49625 F10674
	126034	1598157_1 H60340 N91637
40	102768	44641_1 U82321 H66077
	126345	1653833_1 N49713 N49819 W03810
	127066	1703458_1 R25066 R20144 R20145 Z43845
	127099	244301_1 AA347668 AW956810 Z44271 F07065 F07064 R13506
	119243	1774795_1 T12603 T12604
45	125875	1566433_1 H14480 N98295
	112054	1638292_1 R43590 F10439
	126979	171411_1 AA210954 AA211007
	126992	880655_1 AI809521 H12174 Z42556
	122318	292419_1 AA429743 AA442754
	114699	135322_1 AA127386 R15644 AA127404
50	114793	150742_1 AA158245 AA158235
	108305	111550_1 AA071391 AA069892 AA069891
	108393	113411_1 AA075211 AA075245 AA075126 AA074946
	100867	Ugr_HT4586 U14622
55	123731	genbank_AA609839 AA609839
	109700	genbank_F09609 F09609
	120715	genbank_AA292700 AA292700
	113702	genbank_T97307 T97307
	115113	genbank_AA256460 AA256460
60	101045	entrez_J05814 J05814
	108554	genbank_AA084948 AA084948
	108573	genbank_AA086005 AA086005
	119052	149538_1 R10889 R10888
	126522	416020_1 W31912 AI167491
65	126605	439280_1 AA676910 AA778853 AA778865 W86800
	103768	46922_1 W42667 AI580740 AI690440 AI561350 AW467906 AW151450 AI825927 AL041716 AI885600 AI742213 AW248624 AI955498 AA033947
		AA845593 AI623711 N68583 C00064 AA193567 AW083868 AW163216 AA191595 AA522778 AI628008 AI915518 AA843508 AI926195
		AA176265 AW167963 AA992115 W93647 AW103572 AI862994 AI342059 AA911719 AA176155 AA024712 AA089988 AA205591 AI591107
		AI199673 AI811766 AI275832 AI422233 AI191852 AI096682 AI580124 AI683612 AA582453 AA927559 AA486415 T32414 AI084978 H44849
		H44848 H20477 T91695 W47039 AA070055 AA024795 AA328855 AA379248 AA379330 AA385580 W25920 W03688 AA448359 AA093881
70		AW362477 AA089997 AI350265 W93479 N99688 AA932257 AW351469 H68590 AA663402 AA069771 AW087986 AI858420 AA600214
		AI970774 AI857712 AI683081 AI885584 AW131150 AI567981 AW002714 AW189973 AW075495 AW168303 AA953714 AW516881 AI357375
		AI566663 AW512676 AI570580 AI023690 AA448216 AI079853 AI422707 AA779516 AW026972 AW130082 AW162307 AW438646 AA709332
		AW192394 AI167350 AI217879 AI129152 AA719509 AI350480 AA663418 AI003634 AW118546 AA180261 AA442833 AI268625 AA888881
75		AI038759 AA846723 AI248770 AA993694 AI280335 AI885107 AW518649 AA641563 AA995835 AA582521 AI276744 AA436478 AI017360
		AI620763 AI859887 N73926 AI076327 AI741615 AI160617 AW172819 AI492005 AA677429 AA996334 AI693771 AI950039 AI245629 AI288515
		AI866188 T93293 AA173262 AA599779 AI690092 AW439316 AI084555 AI272672 AI583507 AW473219 AA738132 AW473283 AI367492
		AA995410 AI689624 AA206353 AI033095 AI040382 AA873630 AI221074 AI934840 AI418680 AA844306 R94503 AA773520 AA843169
		AA219425 AA629658 AI811719 AW411275 AI590981 W37907 AI591178 AI684051 AA983238 AA669347 AA976239 AA704570 AI628339
80		AI884391 AI241580 AI003539 AW176687 AA009650 N34566 AI333493 AI186070 AA070827 AA411683 AI280884 AA872023 AA207255
		AA021576 N71953 AI885888 AW076039 T15777 AI537673 AW248048 H09554 W93480 W47001 AW079114 AA063160 AA757453 R60788
		AI859431 H20478 AA218882 AA757465 AA100995 AI864135 AI934209 AA070503 H47008 AA219646 W61039 W93907 AW385050 W37967
		W78028 AA189007 AA479136 R93650 AA442312 T30287 AA847628 AA180262 AA009649 C03892 AW149464 AA310963 AA219693
		AA069747 R29207 AA094784 AA293615 AA447848 AI984167 N90393 C05097 N56499 AW292351 AW149681 AW473258 AA629322 AI004409
85		AW105577 AI954937 AI811070 AA902422 AW514437 AA535460 AA916877 AW517122 AA974657 AA975649 AW517130 AW517129 F31737
		W07688 AA193645 AA378994 AA489273 F32267 W39303 AA021181 N86810 AA406524 AA062553 AA436801 H08985 H15979 N40310

AA436789 AA232172 AW360778 W25862 R60282 AA436530 AA378894 AA187461 AI940535 AA604210 AA089514 AA360421 N88243 N84281
 AA209340 N56174 N88374 AA191088 AW247691 AA249013 AA093111 AA972536 AW298594 AA375893 T12139 W28186 AW243849
 A1286629 AA843996 W15260 A1188286 AW248079 R15836

5 119599 genbank_W45552 W45552
 112382 genbank_R59904 R59904
 105264 genbank_AA227934 AA227934
 100071 entrez_A28102 A28102
 123315 714071_1 AA496369 AA496646

10

Table 6A shows 99 genes up-regulated nonsmokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Atfy matrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

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Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

20

R1: average of AI for samples from non-smokers with adenocarcinoma divided by the 90th percentile of AI for samples from smokers with adenocarcinoma
 R2: average of AI for samples from non-smokers with squamous cell carcinoma divided by the 90th percentile of AI for samples from smokers with squamous cell carcinoma

	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
25	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		3.64
	101174	L17330	Hs.280	pre-T/NK cell associated protein	15.00	
	101296	Y12490	Hs.85092	thyroid hormone receptor interactor 11		2.46
	101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8		12.00
30	101806	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias)		2.68
	101972	S82472		gb:beta-pol=DNA polymerase beta (exon a		2.11
	102274	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	7.50	
	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.50	
	102832	U92015		gb:Human clone 143789 defective mariner	13.50	
	103010	X52509	Hs.161640	tyrosine aminotransferase	9.50	
35	103439	X98266		gb:H.sapiens mRNA for ligase like protel		2.50
	103563	L02911	Hs.150402	activin A receptor, type I	9.00	
	103857	AI076795	Hs.45033	lacrimal proline rich protein		3.94
	104239	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.50	
40	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m		12.66
	104907	AA055829	Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU	16.50	
	106131	BE514788	Hs.296244	SNARE protein		2.17
	106872	H47233	Hs.30643	ESTs	7.00	
	106872	T66887	Hs.18282	KIAA1134 protein	11.50	
45	106960	AA156238	Hs.32501	ESTs		2.38
	106971	Z43845	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f	9.50	
	107982	AA035375	Hs.57887	ESTs, Weakly similar to KIAA0758 protel		2.95
	108562	AA100796		gb:zm26c06.s1 Stratagene pancreas (93720	16.50	
	108599	AB018549	Hs.69328	MD-2 protein	13.00	
50	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypothel		2.40
	109247	AA314907	Hs.85950	ESTs	7.00	
	109630	R44607	Hs.22672	ESTs		5.00
	110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	12.50	
	110234	H24458	Hs.32085	EST	16.50	
55	110644	R94207	Hs.268889	ESTs, Highly similar to type II CALM/AF1	8.00	
	110886	AW274992	Hs.72249	three-PDZ containing protein similar to	17.00	
	111057	T79639	Hs.14629	ESTs	16.50	
	111850	AF071594	Hs.110457	Wolf-Hirschhorn syndrome candidate 1	11.00	
	112291	R53972	Hs.26026	ESTs		3.00
60	112956	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)		2.79
	113009	T23699	Hs.7246	ESTs		4.50
	113060	BE564162	Hs.250820	hypothetical protein FLJ14827	9.79	
	113073	N39342	Hs.103042	microtubule-associated protein 1B	32.50	
	113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t		3.82
65	113121	T48011	Hs.8764	EST		2.21
	113125	AA968672	Hs.8929	hypothetical protein FLJ11362	19.50	
	113757	AA703095	Hs.18631	ESTs		2.65
	113848	W52654	Hs.27099	hypothetical protein FLJ23293 similar to	6.00	
	113884	AI333076	Hs.28529	chromosome 12 open reading frame 2		6.00
70	113936	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m		4.63
	114875	AA235609	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (7.00
	114987	AA251016	Hs.87808	EST		6.00
	115460	AW958439	Hs.38613	ESTs		2.27
	115722	W91892	Hs.59609	ESTs		9.00
75	116261	AA481788	Hs.190150	ESTs	9.50	
	116830	H61037	Hs.70404	ESTs, Weakly similar to ALU2_HUMAN ALU	8.50	
	116970	AB023179	Hs.9059	KIAA0962 protein	7.50	
	117178	H98675	Hs.269034	ESTs		2.68
	117757	AF088019	Hs.46732	EST	7.50	
80	118283	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	16.50	
	118384	AF217525	Hs.49002	Down syndrome cell adhesion molecule		2.50
	118657	AI822108	Hs.49902	ESTs		2.39
	120328	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi		3.50
	120404	AB023230	Hs.96427	KIAA1013 protein	7.00	
85	120524	AA261852	Hs.192905	ESTs	6.00	
	120688	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fis, clone L	17.92	

	121558	AA412497	gb:z185g12.s1 Soares_testis_NHT Homo sap		2.95
	121676	H56037	Hs.108146 ESTs	10.00	
	121936	AI024600	Hs.98612 ESTs	15.00	
5	121938	AA428659	Hs.98610 ESTs	14.00	
	122177	AA435789	Hs.98833 EST	8.93	
	123442	AA299652	Hs.111496 Homo sapiens cDNA FLJ11643 fis, clone HE	13.04	
	123551	AA608837	gb:af03h12.s1 Soares_testis_NHT Homo sap	11.50	
	123756	AA609971	Hs.112795 EST	11.00	
10	123861	AA620840	gb:af89g01.s1 Soares_testis_NHT Homo sap		2.50
	124371	N24924	Hs.188601 ESTs	6.50	
	127477	BE328720	Hs.280651 ESTs		4.33
	127591	AI190540	Hs.131092 ESTs		3.02
	128252	AA455924	Hs.192228 ESTs	7.00	
	128426	AI265784	Hs.145197 ESTs		2.08
15	128925	R67419	Hs.21851 Homo sapiens cDNA FLJ12900 fis, clone NT		2.11
	128945	AI990506	Hs.8077 Homo sapiens mRNA; cDNA DKFp547E184 (fr	10.00	
	129105	AI769160	Hs.108681 Homo sapiens brain tumor associated prot	15.50	
	129235	AW977238	Hs.126084 KIAA1055 protein		4.25
	129506	AB020684	Hs.11217 KIAA0877 protein	6.50	
20	129595	U09550	Hs.1154 oviducal glycoprotein 1, 120kD (mucin 9		10.00
	130160	AA305688	Hs.267695 UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	20.00	
	130340	D82326	Hs.239106 solute carrier family 3 (cystine, dibasi	11.50	
	131220	AB023194	Hs.300855 KIAA0977 protein	17.50	
	131430	AI879148	Hs.26770 fatty acid binding protein 7, brain	6.10	
25	132114	NM_006152	Hs.40202 lymphoid-restricted membrane protein		6.15
	132458	AA935315	Hs.48965 Homo sapiens cDNA: FLJ21693 fis, clone C		5.58
	132647	NM_006927	Hs.54432 sialyltransferase 4B (beta-galactosidase	7.50	
	132655	D49372	Hs.54460 small inducible cytokine subfamily A (Cy		2.53
	132682	AI077500	Hs.54900 serologically defined colon cancer antig		2.50
30	132747	AA345241	Hs.55950 ESTs, Weakly similar to KIAA1330 protein		2.83
	132812	R50333	Hs.92186 Leman coiled-coil protein		3.82
	133337	AF085983	Hs.293676 ESTs		5.00
	133876	AL134908	Hs.771 phosphorylase, glycogen; liver (Hers dis		3.00
	134119	AW157837	Hs.79226 fasciculation and elongation protein zet		2.05
35	134464	AA302983	Hs.239720 CCR4-NOT transcription complex, subunit		2.27
	134542	M14156	Hs.85112 insulin-like growth factor 1 (somatomedi		11.50
	135002	AA448542	Hs.251677 G antigen 7B	87.00	
	135305	AA203555	Hs.98288 Homo sapiens cDNA FLJ14903 fis, clone PL		6.50

TABLE 6B show the accession numbers for those primekeys lacking unigenelD's for Table 6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
108562	36375_1	AA100796 AF020589 AA074629 AA075946 AA100849 AA085347 AA126309 AA079311 AA079323 AA085274
103439	35330_1	X98266 N41124
123551	genbank_AA608837	AA608837
123861	genbank_AA620840	AA620840
102832	entrez_U92015	U92015
101972	entrez_S82472	S82472
121558	genbank_AA412497	AA412497

Table 7A shows 98 genes down-regulated in non-smokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
10	R1:	90th percentile of AI for samples from smokers with adenocarcinoma divided by the average of AI for samples from non-smokers with adenocarcinoma.			
	R2:	90th percentile of AI for samples from smokers with squamous cell carcinoma divided by the average of AI for samples from non-smokers with squamous cell carcinoma.			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
15	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	164.10
	100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	77.40
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	102.40
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	463.80
	101046	K01160		(NONE)	672.00
20	101066	AW970254	Hs.889	Charot-Leyden crystal protein	66.00
	101175	U82671	Hs.36980	melanoma antigen, family A, 2	77.20
	101497	W05160	Hs.37034	homeo box A5	62.80
	101663	NM_003528	Hs.2178	H2B histone family, member Q	78.00
	101677	NM_000715	Hs.1012	complement component 4-binding protein,	186.20
25	101745	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino acid	80.08
	101941	S77583		gb:HERVK10/HUMMTV reverse transcriptase	99.20
	102125	NM_006456	Hs.288215	sialyltransferase	103.10
	102242	U27185	Hs.82547	retinoic acid receptor responder (tazaro	67.00
	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro	71.60
30	102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	69.70
	102457	NM_001394	Hs.2359	dual specificity phosphatase 4	153.00
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	65.70
	102796	AL079848	Hs.107019	sympleskin; Huntingtin interacting protei	58.80
	102829	NM_006183	Hs.80962	neurotensin	268.80
35	103207	X72790		gb:Human endogenous retrovirus mRNA for	70.00
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	212.10
	103260	X78416	Hs.3155	casein, alpha	130.70
	103351	X89211		gb:H.sapiens DNA for endogenous retrovir	64.60
	104212	AB002298	Hs.173035	KIAA0300 protein	66.80
40	104252	AF002246	Hs.210863	cell adhesion molecule with homology to	63.80
	104258	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	94.40
	105024	AA126311	Hs.9879	ESTs	68.20
	106260	AI097144	Hs.5260	ESTs, Weakly similar to ALU1_HUMAN ALU S	74.60
	106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	71.10
45	106566	BE298210		gb:601118016F1 NIH_MGC_17 Homo sapiens c	73.20
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	83.80
	106614	AA648459	Hs.335951	hypothetical protein AF301222	62.30
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	202.40
	106999	H93281	Hs.10710	hypothetical protein FLJ20417	89.60
50	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c	66.40
	108810	AW295647	Hs.71331	hypothetical protein MGCS350	95.50
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	63.40
	109597	AA989362	Hs.293780	ESTs	85.00
	109691	T65568	Hs.12860	ESTs	58.70
55	109704	AI743880	Hs.12876	ESTs	60.60
	110942	R63503	Hs.28419	ESTs	76.40
	111722	R23924	Hs.23596	EST	74.60
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-II	64.80
60	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	76.70
	113073	N39342	Hs.103042	microtubule-associated protein 1B	120.20
	114251	H15261	Hs.21948	ESTs	127.20
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fls, clone L	174.00
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	91.00
	115815	AW905328	Hs.180842	ribosomal protein L13	66.40
65	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	226.60
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970	82.80
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	361.60
	116552	D20508	Hs.164649	hypothetical protein DKFZp434H247	69.00
	116571	D45652		gb:HUMGS02848 Human adult lung 3' direct	64.20
70	118466	N66741		gb:yz33g08.s1 Morton Fetal Cochlea Homo	63.50
	120484	AA253170	Hs.96473	EST	81.60
	120983	AA398209	Hs.97587	EST	81.10
	121034	AL389951	Hs.271623	nucleoporin 50kD	66.20
	121423	AW973352	Hs.290585	ESTs	64.40
75	122553	AA451884	Hs.190121	ESTs	60.40
	122946	AI718702	Hs.308026	major histocompatibility complex, class	188.60
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	80.20
	124472	N52517	Hs.102670	EST	71.00
	124526	N62096	Hs.293185	ESTs, Weakly similar to J7328 amino acid	104.90
80	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	72.00
	125731	R61771	Hs.26912	ESTs	69.90
	125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	69.00
	126020	H79863	Hs.114243	ESTs	62.40
	126547	U47732	Hs.84072	transmembrane 4 superfamily member 3	62.80
85	126956	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	60.10

	127472	AA761378	Hs.192013	ESTs	70.20	
	127610	AA960867	Hs.150271	ESTs, Highly similar to unnamed protein	64.00	
	127742	AW293496	Hs.180138	ESTs	85.20	
	127987	AI022103	Hs.124511	ESTs	96.60	
5	128233	AW889132	Hs.11916	ribokinase		78.90
	128420	AA650274	Hs.41296	fibronectin leucine rich transmembrane p		106.90
	128766	AW160432	Hs.296460	craniofacial development protein 1	66.80	
	129014	AW935187	Hs.170162	KIAA1357 protein		58.53
	129215	AB040930	Hs.126085	KIAA1497 protein	64.20	
10	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	63.80	
	130385	AW067800	Hs.155223	stanniocalcin 2		139.60
	130732	AW890487	Hs.63994	cadherin 13, H-cadherin (heart)		64.60
	131025	AB040900	Hs.6189	KIAA1467 protein	64.40	
	131241	BE501914	Hs.24654	Homo sapiens cDNA FLJ11640 fis, clone HE	76.20	
15	131775	AB014548	Hs.31921	KIAA0648 protein	97.80	
	132240	AB018324	Hs.42676	KIAA0781 protein		71.00
	132856	NM_001448	Hs.58367	glypican 4		88.40
	132977	AA093322	Hs.301404	RNA binding motif protein 3	133.20	
	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		69.30
20	133818	AI110584	Hs.7645	fibrinogen, B beta polypeptide	341.00	
	134264	AF149297	Hs.8087	NAG-5 ptplein		64.30
	134265	M83772	Hs.80876	flavin containing monooxygenase 3		232.53
	134346	X84002	Hs.82037	TATA box binding protein (TBP)-associate	66.00	
	134395	AA456539	Hs.8262	lysosomal-associated membrane protein 2		75.80
25	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su		108.30
	135056	N75765	Hs.93765	lipoma HMGIC fusion partner	71.40	
	135309	AI564123	Hs.42500	ADP-ribosylation factor-like 5	70.40	

30 TABLE 7B shows the accession numbers for those primekeys lacking unigenelD's for Table 7A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

35 Pkey: Unique Ecos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT number	Accessions
40	103207	30635_4	X72790
	106566	120358_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 AI039658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
45	116571	genbank_D45652	D45652
	118466	genbank_N66741	N66741
	101046	entrez_K01160 K01160	
	101941	entrez_S77583 S77583	
	103351	entrez_X89211 X89211	
50	123130	genbank_AA487200	AA487200

Table 8A shows 1720 genes either up or down-regulated in lung tumors or chronically diseased lung relative to a broad collection of over 40 distinct normal body tissues. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 39494 probesets on the Eos/Affymetrix Hu02 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey:		Unique Eos probeset identifier number			
ExAccn:		Exemplar Accession number, Genbank accession number			
UnigeneID:		Unigene number			
Unigene Title:		Unigene gene title			
R1:		70th percentile of AI for lung tumors divided by 90th percentile of AI for normal lung			
R2:		70th percentile of AI for chronically diseased lung divided by 90th percentile of AI for normal lung			
Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
15	300097	AI916973	Hs.213603	ESTs	5.46
	300117	AW189787	Hs.147474	ESTs	0.58
	300197	AI686661	Hs.218286	ESTs	4.26
	300201	AI308300	gb:ta90c06.x1 NCI_CGAP_Bm20 Homo sapien	0.62	0.83
	300225	AI989963	Hs.197505	ESTs	1.68
20	300247	AW274682	Hs.161394	ESTs	1.08
	300256	AI468095	Hs.298241	Transmembrane protease, serine 3	0.86
	300337	AI707881	Hs.202090	ESTs	5.80
	300362	Z42308	gb:HSC0FB121 normalized infant brain cDN	4.18	12.78
	300374	AI859947	Hs.314158	ESTs	2.99
25	300387	AW270150	Hs.254516	ESTs	1.50
	300440	AI421541	Hs.146164	ESTs	3.98
	300441	R10387	Hs.307921	EST, Weakly similar to Z232_HUMAN ZINC F	3.18
	300449	AI362967	Hs.132221	hypothetical protein FLJ12401	0.43
	300469	AW135830	Hs.233955	hypothetical protein FLJ20401	0.16
30	300552	X85711	Hs.21838	hypothetical protein FLJ11191	4.10
	300627	W27363	gb:ab37d01.r1 Stratagene HeLa cell s3 93	4.60	12.60
	300630	AW118822	Hs.128757	ESTs	2.91
	300716	AI216113	Hs.126280	hypothetical protein FLJ23393	1.00
	300738	AI623332	Hs.130541	KIAA1542 protein	1.82
35	300777	AA235361	Hs.96840	KIAA1527 protein	4.48
	300790	AI492471	Hs.188270	ESTs	1.29
	300832	AI688147	Hs.220615	ESTs, Weakly similar to T03829 transcrip	5.51
	300836	Z44942	Hs.22958	calcium channel alpha2-delta3 subunit	4.90
	300838	AI582897	Hs.192570	hypothetical protein FLJ22028	1.70
40	300878	AW449802	Hs.285901	Homo sapiens cDNA FLJ20428 fis, clone KA	4.56
	300897	AI890356	Hs.127804	ESTs, Weakly similar to T17233 hypotheti	2.23
	300926	AA504860	gb:ab03a10.s1 Stratagene fetal retina 93	2.13	3.50
	300960	AI041019	Hs.152454	ESTs	2.74
	300961	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein	1.00
45	300962	AA593373	Hs.293744	ESTs	1.46
	300967	AA565209	Hs.269439	ESTs	0.39
	300987	AW450840	Hs.148590	ESTs, Weakly similar to AF208846 1 BM-00	1.49
	300988	AI927208	Hs.208952	ESTs	0.16
	301050	AW136973	Hs.288518	ESTs, Weakly similar to S69890 mitogen I	3.23
50	301098	AA677570	Hs.185918	ESTs	6.76
	301157	AA729905	Hs.231916	ESTs	3.16
	301162	AI142118	Hs.129004	ESTs	1.68
	301170	AA737594	Hs.247606	ESTs	4.40
	301192	AI808751	Hs.121188	ESTs	6.38
55	301193	AA758115	Hs.128350	ESTs, Weakly similar to JC5423 2-hydroxy	4.35
	301267	AW297782	Hs.255690	ESTs	1.56
	301281	AA843986	Hs.190586	ESTs	2.19
	301341	AI819198	Hs.208229	ESTs	0.76
	301382	AA912839	Hs.163369	ESTs	1.00
60	301407	AW450466	Hs.126830	ESTs	1.48
	301452	AA975688	Hs.159955	ESTs	0.51
	301483	AW272467	Hs.254655	Untitled	2.40
	301494	AI678034	Hs.131099	ESTs	2.79
	301521	AI733621	Hs.133011	zinc finger protein 117 (HPF9)	0.67
65	301531	AI077462	Hs.134084	ESTs	2.52
	301580	AI878959	Hs.73737	splicing factor, arginine/serine-rich 1	7.41
	301676	Z43570	Hs.27453	ESTs, Moderately similar to G01251 Rar p	8.31
	301690	F05865	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	2.70
	301718	F07744	Hs.7987	DKFZP434F162 protein	4.20
70	301799	AA384252	Hs.286132	D15F37 (pseudogene)	5.93
	301804	AA581004	Hs.62180	anillin (Drosophila Scraps homolog), act	1.70
	301822	X17033	Hs.271986	Integrin, alpha 2 (CD49B, alpha 2 subunl	1.58
	301846	R20002	Hs.6823	hypothetical protein FLJ10430	1.00
	301868	T71508	Hs.13861	ESTs, Weakly similar to pH sensitive max	2.88
75	301882	T78054	Hs.13861	gb:yc97g09.r1 Soares infant brain 1N18 H	2.28
	301905	AI991127	Hs.117202	ESTs	1.00
	301948	AA344647	Hs.116724	aldo-keto reductase family 1, member B11	5.28
	301960	AW070252	Hs.27973	KIAA0874 protein	5.38
	302011	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	3.03
80	302016	N40834	Hs.23495	hypothetical protein FLJ11252	1.00
	302041	NM_001501	Hs.129715	gonadotroph-releasing hormone 2	0.71
	302072	AJ238381	Hs.132575	paired box gene 9	1.60
	302094	AI286176	Hs.6786	ESTs	0.52
	302095	AW044300	Hs.137506	Homo sapiens BAC clone RP11-120J2 from 7	2.75
85	302148	AW269618	Hs.23244	ESTs	3.04

	302155	AI088485	Hs.144759	ESTs	0.45	1.15
	302201	AJ006276	Hs.159003	transient receptor potential channel 6	0.33	0.84
	302202	AF097159	Hs.159140	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	0.52	0.94
5	302206	AI937193	Hs.41143	phosphoinositide-specific phospholipase	2.76	3.65
	302209	AF047445	Hs.159297	killer cell lectin-like receptor subfam1	1.00	1.00
	302235	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.68	1.50
	302290	AL117607	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	1.00	2.11
	302328	AA354849	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	9.38	13.08
10	302346	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	3.27	7.24
	302360	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.54	1.88
	302384	Y08982	Hs.202678	synaptonemal complex protein 2	1.00	0.91
	302406	U86751	Hs.211956	CD3-epsilon-associated protein; antisens	2.63	2.67
	302409	AF155156	Hs.218028	adaptor-related protein complex 4, epsil	5.82	9.34
	302423	AB028977	Hs.225974	KIAA1054 protein	3.66	3.18
15	302432	AL080068	Hs.272534	Homo sapiens mRNA; cDNA DKFZp564J062 (fr	2.44	6.77
	302435	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	0.44	0.84
	302437	AB024730	Hs.227473	UDP-N-acetylglucosamine:alpha-1,3-D-mannosid	4.18	6.64
	302456	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	1.85	0.92
	302472	AA317451	Hs.6335	SWI/SNF related, matrix associated, acti	2.04	2.13
20	302476	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	1.44	1.89
	302489	T80660	Hs.230424	Homo sapiens cDNA FLJ13540 fis, clone PL	0.51	1.10
	302490	AA885502	Hs.187032	ESTs	2.64	4.87
	302562	AJ005585	Hs.48956	gap junction protein, beta 6 (connexin 3	5.34	2.68
25	302566	AA085996	Hs.248572	hypothetical protein FLJ22965	1.00	1.21
	302630	AB029488	Hs.272100	SMS3 protein	0.52	1.24
	302634	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1.00	1.00
	302638	AA463798	Hs.102696	MCT-1 protein	1.58	1.02
	302647	X57723	Hs.198273	NADH dehydrogenase (ubiquinone) 1 beta s	2.72	6.85
	302655	AJ227892	Hs.146274	ESTs	1.00	4.32
30	302656	AW293005	Hs.70704	Homo sapiens, clone IMAGE:2823731, mRNA,	2.97	0.93
	302668	AA580691	Hs.180789	S164 protein	0.80	0.95
	302679	H65022		gb:yu66g11.r1 Weizmann Olfactory Epithel	1.68	5.04
	302680	AW192334	Hs.38218	ESTs	2.70	7.98
35	302697	AJ001408		gb:Homo sapiens mRNA for immunoglobulin	4.25	8.13
	302705	U09060		gb:Human immunoglobulin heavy chain, V-r	3.91	8.68
	302711	L08442		gb:Human autonomously replicating sequen	2.20	2.73
	302719	W69724	Hs.288959	hypothetical protein FLJ20920	0.54	1.02
	302742	L12069		gb:Homo sapiens (clone WR4.10VH) anti-th	4.28	11.57
40	302755	AW384815	Hs.149208	KIAA1555 protein	1.57	2.38
	302771	H98476	Hs.42522	ESTs	2.94	4.68
	302789	AJ245067		gb:Homo sapiens mRNA for immunoglobulin	3.49	6.31
	302795	AJ245313	Hs.272838	hypothetical protein FLJ10494	0.80	2.74
	302802	Y08250		gb:H.sapiens mRNA for variable region of	1.13	0.77
45	302803	AA442824	Hs.293961	ESTs, Moderately similar to putative DNA	3.14	10.68
	302812	N31301	Hs.162664	hypothetical protein FLJ20051	3.04	8.24
	302847	X98940		gb:H.sapiens rearranged Ig heavy chain (1.80	1.92
	302885	AL137763	Hs.132127	hypothetical protein LOC57822	1.00	1.00
	302943	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothell	0.53	0.67
	302977	AW263124	Hs.315111	hypothetical protein FLJ12894	2.45	2.62
50	303006	AF078950	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	4.88	8.61
	303011	AF090405		gb:Homo sapiens clone 2A1 scFv antibody	1.41	1.86
	303013	F07898	Hs.288968	RAB22A, member RAS oncogene family	1.51	1.19
	303061	AF151882	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	0.72	0.76
55	303077	AF163305		gb:H.sapiens T-cell receptor mRNA	1.17	3.90
	303090	AA443259	Hs.146288	kinesin family member 13A	4.08	6.46
	303091	AF192913	Hs.130683	zinc finger protein 180 (HHZ168)	2.50	4.37
	303094	AF195513	Hs.278953	Pur-gamma	5.38	8.38
	303095	AF202051	Hs.134079	NM23-H8	3.26	4.08
60	303131	AW081061	Hs.103180	DC2 protein	2.02	1.83
	303195	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	1.32	3.95
	303196	AA082298	Hs.59710	ESTs	0.77	0.53
	303216	AA581439	Hs.152328	ESTs	0.24	0.63
	303222	AA333538	Hs.204501	hypothetical protein FLJ10534	3.56	6.22
65	303234	AA132255	Hs.143951	ESTs	2.28	3.17
	303251	AW340037	Hs.115897	protocadherin 12	0.38	1.02
	303295	AA205625	Hs.208067	ESTs	2.30	1.00
	303297	T80072	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.86	4.48
	303316	AF033122	Hs.14125	p53 regulated PA26 nuclear protein	0.10	0.80
70	303467	AA398801	Hs.323397	ESTs	4.54	9.65
	303506	AA340805	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	0.09	0.04
	303552	AA359799	Hs.224662	ESTs, Weakly similar to unnamed protein	1.00	1.72
	303598	AA382814		gb:EST96097 Testis I Homo sapiens cDNA 5	4.96	9.14
	303637	AF056083	Hs.24879	phosphatidic acid phosphatase type 2C	2.06	2.02
75	303655	AA504702	Hs.258802	ATPase, (Na+)/K+ transporting, beta 4 po	1.00	1.24
	303756	AI738488	Hs.115838	ESTs	1.08	1.43
	303858	AA968589	Hs.180532	glucose phosphate isomerase	1.76	1.31
	303893	N88597	Hs.113503	karyopherin (importin) beta 3	2.30	2.57
	303907	AW467774	Hs.171880	polymerase (RNA) II (DNA directed) polyp	3.10	5.79
80	303946	AW474196	Hs.306637	Homo sapiens cDNA FLJ12363 fis, clone MA	5.06	11.86
	303978	AW513315		gb:xa43c12.x1 NCI_CGAP_U11 Homo sapiens	5.14	7.31
	303981	AW513804	Hs.278834	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.83	4.06
	303990	AW515465		gb:xu71a11.x1 NCI_CGAP_Kd8 Homo sapiens	1.15	2.35
	303998	AW516449		gb:xt68f05.x1 NCI_CGAP_U12 Homo sapiens	2.20	9.35
	303999	AW516611		gb:xp70b11.x1 NCI_CGAP_Ov39 Homo sapiens	4.85	6.28
85	304006	AW517947		gb:xt66h02.x1 NCI_CGAP_U12 Homo sapiens	3.21	4.07

	304008	AW518198	Hs.3297	ribosomal protein S27a	6.50	11.08
	304009	AW518206	Hs.181165	eukaryotic translation elongation factor	1.88	3.27
	304024	T03036		gb:FB2187 Fetal brain, Stratagene Homo s	2.15	3.55
5	304026	T03160		gb:FB26F2 Fetal brain, Stratagene Homo s	5.88	11.80
	304028	T03266		gb:FB7C1 Fetal brain, Stratagene Homo sa	5.59	13.46
	304036	T16855	Hs.244621	ribosomal protein S14	6.55	14.43
	304046	T54803		gb:yb42d06.s1 Stratagene fetal spleen (9	6.18	12.19
	304061	T61521		gb:yb73g01.s1 Stratagene ovary (937217)	2.64	8.23
10	304063	T62536		gb:yc04c12.s1 Stratagene lung (937210) H	0.53	1.61
	304097	R25376	Hs.177592	ribosomal protein, large, P1	6.49	11.67
	304114	R78946		gb:yi87g02.s1 Soares placenta Nb2HP Homo	2.90	4.18
	304122	H28966		gb:ym31a06.s1 Soares Infant brain 1NIB H	1.00	2.76
	304155	H68696		gb:yr78b06.s1 Soares fetal liver spleen	0.79	1.18
	304203	N56929		gb:yy82d08.s1 Soares_multiple_sclerosis_	4.28	11.34
15	304234	W81608		gb:zd88h06.s1 Soares_fetal_heart_NbHH19W	6.47	11.03
	304267	AA064862	Hs.73742	ribosomal protein, large, P0	1.34	1.16
	304270	AA069711	Hs.297753	vimentin	3.40	5.40
	304287	AA079286	Hs.78466	proteasome (prosome, macropain) 26S sub	2.93	4.42
20	304348	AA179868		gb:zp38g12.s1 Stratagene muscle 937209 H	3.98	10.96
	304415	AA290747	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	3.32	5.99
	304430	AA347682		gb:EST54044 Fetal heart II Homo sapiens	1.00	1.00
	304455	AA411240		gb:zv26g05.s1 Soares_NhHMPu_S1 Homo sapi	1.42	3.33
	304521	AA464716		gb:zx82c11.s1 Soares ovary tumor NbHOT H	2.18	1.15
25	304526	AA476427		gb:zx02c05.s1 Soares_total_fetus_Nb2HF8_	5.38	14.11
	304542	AA482602	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.16	8.23
	304546	AA486074	Hs.297681	serine (or cysteine) proteinase inhibitor	0.55	1.20
	304607	AA513322		gb:nh85e08.s1 NCL_CGAP_Br1.1 Homo sapien	1.95	2.10
	304640	AA524440	Hs.111334	ferritin, light polypeptide	2.10	2.83
30	304650	AA527489	Hs.3463	ribosomal protein S23	3.33	12.62
	304735	AA576453		gb:nm75h11.s1 NCL_CGAP_Co9 Homo sapiens	1.33	0.88
	304760	AA580401		gb:nn13g09.s1 NCL_CGAP_Co12 Homo sapiens	3.68	8.14
	304849	AA588157	Hs.13801	KIAA1695 protein	2.77	3.70
	304917	AA602685	Hs.284138	PRO2047 protein	7.16	11.01
35	304921	AA603092	Hs.297753	vimentin	2.47	4.24
	304968	AA613893	Hs.282435	ESTs	6.78	11.66
	304987	AA618044	Hs.300697	immunoglobulin heavy constant gamma 3 (G	0.90	1.23
	305016	AA626876		gb:zu89h06.s1 Soares_testis_NHT Homo sap	6.46	10.17
	305034	AA630128		gb:ab99c04.s1 Stratagene lung (937210) H	1.00	1.00
40	305072	AA641012		gb:nr72a12.s1 NCL_CGAP_Pr24 Homo sapiens	6.68	11.59
	305111	AA644187	Hs.303405	ESTs	1.48	1.37
	305148	AA654070		gb:nt01g08.s1 NCL_CGAP_Lym3 Homo sapiens	1.76	4.61
	305159	AA659166	Hs.275668	EST, Weakly similar to EF1D_HUMAN ELONG	1.00	2.15
	305190	AA665955		gb:ag57d12.s1 Gessler Wilms tumor Homo s	5.31	8.14
45	305232	AA670052	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	0.78	1.18
	305235	AA670480		gb:ag37e01.s1 Jla bone marrow stroma Hom	3.11	8.66
	305245	AA676695	Hs.81328	nuclear factor of kappa light polypeptid	4.38	7.53
	305312	AA700201		gb:zj44f07.s1 Soares_fetal_liver_spleen_	2.13	2.66
	305322	AA701597	Hs.163019	EST	1.20	1.40
50	305394	AA720942	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.16	0.68
	305413	AA724659		gb:al10f08.s1 Soares_parathyroid_tumor_N	5.86	9.87
	305447	AA737856		gb:mx10c08.s1 NCL_CGAP_GC3 Homo sapiens	2.21	2.86
	305476	AA745664	Hs.287445	hypothetical protein FLJ11726	3.36	6.54
	305483	AA748030	Hs.303512	EST	1.00	2.02
55	305528	AA769156		gb:nz12e05.s1 NCL_CGAP_GCB1 Homo sapiens	6.44	9.10
	305612	AA782347	Hs.272572	hemoglobin, alpha 2	0.19	0.79
	305614	AA782866		gb:aj09h02.s1 Soares_parathyroid_tumor_N	1.00	1.00
	305616	AA782884	Hs.275865	ribosomal protein S18	7.57	10.20
	305637	AA806124		gb:oe29a12.s1 NCL_CGAP_Pr25 Homo sapiens	4.78	12.42
60	305639	AA806138		gb:oe29c12.s1 NCL_CGAP_Pr25 Homo sapiens	0.89	0.70
	305650	AA807709		gb:nw31e04.s1 NCL_CGAP_GC80 Homo sapiens4.49	4.91	8.71
	305690	AA813477		gb:af67a05.s1 Soares_testis_NHT Homo sap	4.91	9.40
	305726	AA828156	Hs.73742	ribosomal protein, large, P0	0.19	0.81
	305728	AA828209		gb:of34a02.s1 NCL_CGAP_Kid6 Homo sapiens	5.12	9.29
65	305759	AA835353		gb:ak72b06.s1 Barslead spleen HPLRB2 Hom	1.66	4.11
	305792	AA845256		gb:ak84a08.s1 Barslead spleen HPLRB2 Hom	2.34	4.25
	305864	AA845374	Hs.73742	ribosomal protein, large, P0	0.30	1.40
	305901	AA872968		gb:oh63h08.s1 NCL_CGAP_Kid5 Homo sapiens	2.10	5.21
	305910	AA875981		gb:nx21h02.s1 NCL_CGAP_GC3 Homo sapiens	0.32	1.01
70	306015	AA897116		gb:am08b07.s1 Soares_NFL_T_GBC_S1 Homo s1.56	1.12	1.12
	306017	AA897221	Hs.109058	ribosomal protein S6 kinase, 90kD, poly	5.21	7.90
	306020	AA897630	Hs.130027	EST	1.96	6.59
	306063	AA906316		gb:ok03g03.s1 Soares_NFL_T_GBC_S1 Homo s	7.38	20.69
	306065	AA906725		gb:ok78g02.s1 NCL_CGAP_GC4 Homo sapiens	7.19	13.48
75	306104	AA910956		gb:ok85h11.s1 NCL_CGAP_Kid3 Homo sapiens	6.50	9.13
	306109	AA911861		gb:og21a07.s1 NCL_CGAP_PNS1 Homo sapiens	4.21	5.25
	306148	AA917409	Hs.288036	tRNA isopentenylpyrophosphate transferas	2.20	2.70
	306242	AA932805		gb:oe60g04.s1 NCL_CGAP_Lu5 Homo sapiens	2.84	5.35
	306288	AA936900		gb:of53h05.s1 NCL_CGAP_HN3 Homo sapiens	1.60	1.12
80	306325	AA953072	Hs.210546	interleukin 21 receptor	1.65	2.26
	306353	AA961382	Hs.275865	ribosomal protein S18	3.78	6.32
	306375	AA968650	Hs.276018	EST, Moderately similar to JC4562 ribos	4.30	5.74
	306396	AA970223		gb:op09d05.s1 NCL_CGAP_Kid6 Homo sapiens	0.95	2.45
	306428	AA975110	Hs.191228	hypothetical protein FLJ20284	3.19	4.10
85	306442	AA976899		gb:og35e09.s1 NCL_CGAP_GC4 Homo sapiens	4.67	7.44
	306446	AA977348		gb:og72e12.s1 NCL_CGAP_Kid6 Homo sapiens	3.92	6.27

5	306458	AA978186		gb:op33c06.s1 Soares_NFL_T_GBC_S1 Homo s	3.35	5.77
	306467	AA983508	Hs.163593	ribosomal protein L18a	3.72	5.37
	306510	AA988546		gb:cr84d07.s1 NCI_CGAP_Lu5 Homo sapiens	1.00	1.00
	306555	AA994304	Hs.276083	EST, Weakly similar to RL23_HUMAN 60S R	6.61	10.91
	306557	AA994530		gb:rou57e08.s1 NCI_CGAP_Br2 Homo sapiens	16.20	31.83
10	306572	AA995686		gb:os25c12.s1 NCI_CGAP_Kid5 Homo sapiens	2.51	6.52
	306582	AA996248		gb:os18c10.s1 NCI_CGAP_Kid5 Homo sapiens	1.42	3.13
	306598	AI000320	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.91	8.68
	306605	AI000497	Hs.119500	ribosomal protein, large P2	1.96	8.60
	306656	AI004024		gb:cou11b07.x1 Soares_NFL_T_GBC_S1 Homo s	0.11	0.45
15	306676	AI005603	Hs.284136	PRO2047 protein	9.56	17.28
	306686	AI015615		gb:ov29f10.x1 Soares_testis_NHT Homo sap	1.86	3.60
	306702	AI022565	Hs.307670	EST	1.47	1.19
	306728	AI027359	Hs.272572	hemoglobin, alpha 2	1.28	2.83
	306751	AI032589		gb:cw70h12.s1 Soares_fetal_liver_spleen_	3.91	5.21
20	306767	AI038963	Hs.249118	ESTs	3.33	6.06
	306892	AI092465		gb:qa75h12.x1 Soares_fetal_heart_NbHH19W	3.77	7.46
	306897	AI093967		gb:qa33c06.s1 Soares_NhHMPu_S1 Homo sapi	2.12	2.85
	306956	AI125111		gb:am66f03.s1 Barstead spleen HPLRB2 Hom	6.10	10.52
	306958	AI125152		gb:am55e09.x1 Johnston frontal cortex Ho	1.72	1.56
25	307035	AI142774	Hs.119122	ribosomal protein L13a	2.00	4.70
	307041	AI144243		gb:qb85b12.x1 Soares_fetal_heart_NbHH19W	9.12	12.56
	307091	AI167439		gb:cx70h06.s1 Soares_NhHMPu_S1 Homo sapi	4.88	8.52
	307181	AI189251		gb:qc99g06.x1 Soares_pregnant_uterus_NbH	3.55	6.44
	307297	AI205798	Hs.111334	ferritin, light polypeptide	2.46	4.65
30	307317	AI208303	Hs.147333	EST	5.64	10.13
	307327	AI214142	Hs.246381	CD68 antigen	3.18	5.15
	307382	AI223158	Hs.147885	ESTs	2.02	3.73
	307410	AI241715	Hs.77039	ribosomal protein S3A	0.72	0.48
	307415	AI242118		gb:qh92b02.x1 Soares_NFL_T_GBC_S1 Homo s	2.38	3.51
35	307423	AI243206	Hs.179573	collagen, type I, alpha 2	2.60	5.44
	307428	AI243364		gb:qh30g11.x1 Soares_NFL_T_GBC_S1 Homo s	3.18	7.67
	307517	AI275055		gb:qx72d03.x1 Soares_NhHMPu_S1 Homo sapi	1.00	1.00
	307551	AI281556		gb:qu52f11.x1 NCI_CGAP_Lym6 Homo sapiens	3.40	11.20
	307561	AI282207		gb:qp65a12.x1 Soares_fetal_lung_NbHL19W	4.74	15.51
40	307608	AI290295		gb:qm01f02.x1 Soares_NhHMPu_S1 Homo sapi	3.50	7.19
	307657	AI306428	Hs.298262	ribosomal protein S19	1.76	2.44
	307691	AI318285		gb:tb17b01.x1 NCI_CGAP_Ov37 Homo sapiens	1.59	1.31
	307701	AI318583	Hs.276672	EST, Weakly similar to RL6_HUMAN 60S RI	1.90	2.13
	307718	AI333406	Hs.83753	small nuclear ribonucleoprotein polypept	0.45	0.99
45	307730	AI336092		gb:ql43b07.x1 Soares_fetal_lung_NbHL19W	1.51	0.99
	307760	AI342387		gb:ql27f07.x1 Soares_pregnant_uterus_NbH	1.00	1.00
	307764	AI342731		gb:qo26a07.x1 NCI_CGAP_Lu5 Homo sapiens	4.52	12.58
	307783	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	1.42	1.00
	307796	AI350556		gb:xt18f09.x1 NCI_CGAP_GC4 Homo sapiens	6.57	9.61
50	307807	AI351799		gb:xl09d02.x1 NCI_CGAP_GC4 Homo sapiens	3.38	7.68
	307808	AI351826		gb:xl09g03.x1 NCI_CGAP_GC4 Homo sapiens	0.33	0.86
	307820	AI355761		gb:xl94a11.x1 NCI_CGAP_Co14 Homo sapiens	7.94	21.57
	307830	AI358722	Hs.276737	EST, Weakly similar to R5HU22 ribosomal	2.05	3.32
	307852	AI365541		gb:qx20g05.x1 NCI_CGAP_CLL1 Homo sapiens	3.18	5.21
55	307902	AI380462		gb:tg02h05.x1 NCI_CGAP_CLL1 Homo sapiens	3.13	4.99
	307997	AI434512	Hs.181165	eukaryotic translation elongation factor	1.00	3.01
	308002	AI435240	Hs.283442	ESTs	5.86	12.64
	308011	AI439473		gb:ti60a08.x1 NCI_CGAP_Lym12 Homo sapien	3.79	5.83
	308023	AI452732	Hs.251577	hemoglobin, alpha 1	0.38	0.88
60	308041	AI458824	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.36	6.06
	308059	AI468938	Hs.276877	EST, Weakly similar to RL10_HUMAN 60S R	1.80	1.98
	308085	AI474135	Hs.181165	eukaryotic translation elongation factor	3.38	4.14
	308101	AI475950	Hs.181165	eukaryotic translation elongation factor	1.30	3.87
	308106	AI476803		gb:jl77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S238		8.72
65	308122	AI480123	Hs.308411	EST	2.70	3.86
	308154	AI500600		gb:tn93d08.x1 NCI_CGAP_UI2 Homo sapiens	0.66	1.33
	308171	AI523632	Hs.298766	ESTs, Weakly similar to schlafen4 [M.mu	2.48	4.86
	308211	AI557029	Hs.278572	anaplastic lymphoma kinase (K1-1)	2.43	2.14
	308213	AI557041		gb:PT2.1_12_E04.r tumor2 Homo sapiens cD	3.34	3.79
70	308216	AI557135		gb:PT2.1_13_H06.r tumor2 Homo sapiens cD	4.61	4.78
	308219	AI557246		gb:PT2.1_15_D07.r tumor2 Homo sapiens cD	4.87	7.94
	308271	AI567844	Hs.252259	ribosomal protein S3	2.40	6.35
	308319	AI583983	Hs.181165	eukaryotic translation elongation factor	2.45	3.33
	308362	AI613519	Hs.105749	KIAA0553 protein	1.24	1.41
75	308413	AI636253	Hs.198511	ESTs	3.16	4.82
	308450	AI660860	Hs.96840	KIAA1527 protein	1.79	2.68
	308464	AI672425	Hs.277117	EST, Moderately similar to I38055 myosi	4.87	8.27
	308588	AI718299		gb:as51g12.x1 Barstead aorta HPLRB6 Homo	3.90	5.64
	308599	AI719893		gb:as47d07.x1 Barstead aorta HPLRB6 Homo	3.32	6.12
80	308615	AI738593	Hs.101774	hypothetical protein FLJ23045	3.11	2.36
	308643	AI745040		gb:tr19a12.x1 NCI_CGAP_Ov23 Homo sapiens	3.98	3.69
	308673	AI760864		gb:wi09c10.x1 NCI_CGAP_CLL1 Homo sapiens	0.82	0.99
	308697	AI767143		gb:wi97a07.x1 NCI_CGAP_Kid12 Homo sapien	2.76	5.59
	308762	AI807405	Hs.259408	ESTs	3.17	6.30
85	308778	AI811109		gb:tr04c11.x1 NCI_CGAP_Ov23 Homo sapiens	1.00	1.00
	308782	AI811767	Hs.2186	eukaryotic translation elongation factor	2.94	5.15
	308808	AI818289		gb:wk52c01.x1 NCI_CGAP_Pr22 Homo sapiens	4.41	8.34
	308823	AI824118	Hs.217493	annexin A2	1.85	1.92
	308875	AI832332		gb:at48g03.x1 Barstead colon HPLRB7 Homo	2.52	3.80

	308879	AI832763	Hs.75968	thymosin, beta 4, X chromosome	3.38	7.96
	308886	AI833240		gb:al76d10.x1 Barstead colon HPLRB7 Homo	3.06	2.65
	308898	AI858845		gb:w32d10.x1 NCL_CGAP_U11 Homo sapiens	2.45	3.44
5	308934	AI865023	Hs.177	phosphatidylinositol glycan, class H	4.14	6.76
	308966	AI870704		gb:w47h01.x1 NCL_CGAP_U11 Homo sapiens	1.00	1.00
	308979	AI873111		gb:w52h05.x1 NCL_CGAP_Bm25 Homo sapien	7.15	11.10
	309045	AI910902		gb:tg39f01.x1 NCL_CGAP_U11 Homo sapiens	0.61	0.59
	309051	AI911975		gb:wd78d01.x1 NCL_CGAP_Lu24 Homo sapiens	1.78	4.42
10	309069	AI917366	Hs.78202	SWI/SNF related, matrix associated, act	3.27	5.88
	309083	AI922426	Hs.119598	ribosomal protein L3	2.39	3.34
	309105	AI925503	Hs.265884	ESTs	5.54	17.78
	309122	AI928178		gb:wo95a11.x1 NCL_CGAP_Kld11 Homo sapien	1.00	2.92
	309128	AI928816	Hs.180842	ribosomal protein L13	1.38	5.55
15	309164	AI937761		gb:wp84b09.x1 NCL_CGAP_Bm25 Homo sapien	2.43	3.11
	309177	AI951118		gb:wx63g05.x1 NCL_CGAP_Br18 Homo sapiens	0.81	0.97
	309288	AI991525	Hs.299426	ESTs	4.86	7.46
	309299	AW003478		gb:wq66c06.x1 NCL_CGAP_GC6 Homo sapiens	4.36	9.43
	309303	AW004823		gb:ws93a08.x1 NCL_CGAP_Co3 Homo sapiens	2.88	7.54
20	309411	AW085201	Hs.244144	EST	4.30	7.14
	309437	AW090702	Hs.278242	tubulin, alpha, ubiquitous	2.49	3.11
	309459	AW117645	Hs.65114	keratin 18	2.88	4.55
	309476	AW129368		gb:xe14b05.x1 NCL_CGAP_U14 Homo sapiens	2.08	6.60
	309499	AW136325	Hs.279771	Homo sapiens clone PP1596 unknown mRNA	2.82	3.55
25	309529	AW150807	Hs.181357	laminin receptor 1 (67kD, ribosomal pro	4.78	3.95
	309532	AW151119		gb:xg33e10.x1 NCL_CGAP_U11 Homo sapiens	1.18	4.40
	309626	AW192004	Hs.297681	serine (or cysteine) proteinase inhibi	4.46	12.06
	309641	AW194230	Hs.253100	EST, Moderately similar to GHU Ig gamm	1.47	1.39
	309675	AW205681	Hs.253506	EST, Moderately similar to ATPN_HUMAN A	5.68	15.20
30	309693	AW237221	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	1.00	1.00
	309695	AW238011	Hs.295605	mannosidase, alpha, class 2A, member 2	5.45	9.61
	309700	AW241170	Hs.179661	tubulin, beta polypeptide	1.41	1.25
	309747	AW264889		gb:xq36h02.x1 NCL_CGAP_Lu28 Homo sapiens	5.00	8.35
	309769	AW272346		gb:xs13c10.x1 NCL_CGAP_Kld11 Homo sapien	5.76	11.90
35	309782	AW275156	Hs.156110	immunoglobulin kappa constant	0.42	0.69
	309783	AW275401	Hs.254798	EST	1.00	4.11
	309799	AW276964		gb:xp58h01.x1 NCL_CGAP_Ov39 Homo sapiens	1.68	1.44
	309866	AW299916		gb:xs44c01.x1 NCL_CGAP_Kld11 Homo sapien	3.02	5.04
40	309903	AW339071	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.05	1.18
	309923	AW340684		gb:hd05g08.x1 Soares_NFL_T_GBC_S1 Homo s	2.30	3.67
	309928	AW341418		gb:hd08c03.x1 Soares_NFL_T_GBC_S1 Homo s	7.41	13.71
	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	1.20	12.70
	309933	AW341936		gb:hb73f10.x1 NCL_CGAP_U12 Homo sapiens	4.90	18.29
	309964	AW449111	Hs.257111	hypothetical protein MGC3265	1.99	3.07
45	310002	AI439096	Hs.323079	Homo sapiens mRNA; cDNA DKFZp554P116 (fr	0.20	0.47
	310096	AW136822	Hs.172824	ESTs, Weakly similar to B48013 proline-r	1.51	1.22
	310098	AI685841	Hs.161354	ESTs	0.31	0.76
	310109	AI203094	Hs.148633	ESTs	2.06	5.83
	310112	AW197233	Hs.147253	ESTs	2.92	3.55
50	310116	AI611317	Hs.223796	ESTs	1.25	0.84
	310121	AW195642	Hs.148901	ESTs	1.00	2.71
	310148	AI206614	Hs.197422	ESTs	9.50	15.31
	310193	AI627653	Hs.147562	ESTs	2.85	4.18
	310255	AW450439	Hs.153378	ESTs	4.26	10.63
55	310261	AI240483	Hs.201217	ESTs	3.28	4.40
	310264	AI915771	Hs.74170	metallothionein 1E (functional)	0.26	0.86
	310275	AI242102	Hs.213636	ESTs	5.43	8.19
	310282	AI243332	Hs.156065	ESTs	3.15	8.06
60	310290	AW013815	Hs.149103	ESTs	2.19	3.12
	310333	AI253200	Hs.145402	ESTs	1.17	1.91
	310346	AI261340	Hs.145517	ESTs	4.81	9.95
	310385	AI263392	Hs.156151	ESTs	5.96	7.79
	310443	AW119018	Hs.164231	ESTs	2.90	4.63
	310444	AW196632	Hs.252956	ESTs	0.85	1.01
65	310446	AI275715	Hs.145926	ESTs	2.18	3.85
	310468	AI984074	Hs.196398	ESTs	3.39	5.19
	310477	AI948801	Hs.171073	ESTs	1.00	1.00
	310512	AW275603	Hs.200712	ESTs	3.87	8.12
	310514	AI681145	Hs.160724	ESTs	3.30	7.33
70	310524	AW082270	Hs.12496	ESTs, Highly similar to AC004836 1 simil	0.72	1.44
	310547	AI302654	Hs.208024	ESTs	3.26	3.46
	310584	AI653007	Hs.156304	ESTs	2.39	4.08
	310608	AI962234	Hs.195102	ESTs	5.60	6.49
	310624	AI341594		gb:Human endogenous retrovirus H proteas	4.91	9.09
75	310636	AI814373	Hs.164175	ESTs	1.85	1.71
	310648	AI347863	Hs.156672	ESTs	0.17	0.69
	310694	AI654370	Hs.157752	Homo sapiens mRNA full length Insert cDN	5.40	13.22
	310695	AI472124	Hs.157757	ESTs	4.82	6.27
	310714	AI418446	Hs.157882	ESTs	1.76	3.51
80	310722	AI989803	Hs.157289	ESTs	1.14	6.85
	310756	AI916560	Hs.158707	ESTs	8.46	13.01
	310764	AI376769	Hs.167172	ESTs	4.76	7.37
	310848	AI459554	Hs.161286	ESTs	2.84	1.96
	310851	AW291714	Hs.221703	ESTs	1.00	2.32
85	310854	AI421677	Hs.161332	ESTs	6.37	7.94
	310858	AI871000	Hs.161330	ESTs	6.07	9.84

	310864	AI924558	Hs.161399	ESTs	0.87	0.78
	310875	T47764	Hs.132917	ESTs	1.00	3.63
	310896	AW157731	Hs.270982	ESTs, Moderately similar to ALU7_HUMAN A	7.07	16.68
5	310922	AW195634	Hs.170401	ESTs	1.00	1.00
	310955	AI560210	Hs.263912	ESTs	10.08	17.66
	310957	AW190974	Hs.196918	ESTs	2.18	3.18
	311000	AI521830	Hs.171050	ESTs	3.06	6.64
	311012	AW298070	Hs.241097	ESTs	1.23	3.77
10	311034	AI564023	Hs.311389	ESTs, Moderately similar to PT0375 natur	2.44	2.09
	311074	AW290922	Hs.199848	ESTs	6.04	14.19
	311134	AI990849	Hs.196971	ESTs	3.54	6.96
	311174	AW450552	Hs.205457	perixin	0.65	0.95
	311187	AI638374	Hs.224189	ESTs	2.46	2.78
15	311220	AI656040	Hs.196532	ESTs	1.10	2.52
	311230	AI989808	Hs.197663	ESTs	1.41	1.75
	311236	AI653378	Hs.197674	ESTs	2.18	2.11
	311242	AW016812	Hs.200266	ESTs	0.63	5.11
	311258	AI671221	Hs.199887	ESTs	1.00	1.41
20	311277	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	2.56	1.94
	311294	AA826425	Hs.291829	ESTs	1.04	2.69
	311308	F12664	Hs.49000	ESTs	1.96	6.70
	311351	AI682303	Hs.201274	ESTs	4.77	9.38
	311390	AW392997	Hs.202280	ESTs	2.80	6.06
25	311405	AW290961	Hs.201815	ESTs	3.80	11.66
	311409	AI698839	gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.84	6.94	
	311420	AI936291	Hs.206867	ESTs	5.30	12.56
	311443	AI791521	Hs.192206	ESTs	4.39	6.09
	311467	AI934909	Hs.175377	ESTs	1.00	1.04
30	311479	AI933672	Hs.211399	ESTs	2.76	5.61
	311488	R57390	Hs.301064	arfaplin 1	2.50	5.73
	311495	AW300077	Hs.221358	ESTs	3.63	6.09
	311511	AW444568	Hs.210303	ESTs	2.00	2.87
35	311534	AW130351	Hs.243549	ESTs	0.31	1.33
	311537	AI805121	Hs.211828	ESTs	3.69	5.85
	311543	AI681360	Hs.201259	ESTs	1.73	1.34
	311551	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.31	6.12
	311557	AI819230	Hs.211238	interleukin-1 homolog 1	1.00	1.00
	311558	Z44432	Hs.63128	KIAA1292 protein	2.25	3.41
40	311559	AW008271	Hs.265848	similar to rat myomegalin	2.68	5.90
	311563	AI922143	Hs.211334	ESTs	2.39	3.32
	311586	AI827834	Hs.211227	ESTs	2.47	3.85
	311616	AW450575	Hs.212709	ESTs	1.00	1.00
	311621	AI924307	Hs.213464	ESTs	4.16	6.74
45	311635	AI928456	Hs.213081	ESTs	2.17	3.76
	311668	AW193674	Hs.240044	ESTs	2.60	3.12
	311672	R11807	Hs.20914	hypothetical protein FLJ23056	2.79	5.18
	311683	AW183738	Hs.232644	ESTs	0.19	0.96
	311700	R49601	Hs.171495	retinoic acid receptor, beta	6.28	8.83
50	311714	AW131785	Hs.246831	ESTs, Weakly similar to CIKG_HUMAN VOLTA	5.00	8.17
	311735	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	0.96	0.72
	311743	T99079	Hs.191194	ESTs	1.00	1.95
	311783	AI682478	Hs.13528	hypothetical protein FLJ14054	0.16	0.77
	311785	AI056769	Hs.133512	ESTs	1.34	3.97
55	311799	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	8.52	13.32
	311819	AW265275	Hs.254325	ESTs	3.58	3.91
	311823	AI089422	Hs.131297	ESTs	1.40	1.72
	311877	AA349893	Hs.85339	G protein-coupled receptor 39	0.95	0.91
	311886	AA522738	Hs.132554	ESTs	0.88	0.87
60	311896	AW206447	gb:U1-H-B11-afg-g-02-0-U1.s1 NCI_CGAP_Su	1.66	1.13	
	311910	N28365	Hs.22579	Homo sapiens clone CDABP0036 mRNA sequen	1.66	2.30
	311923	T60843	Hs.189679	ESTs	0.42	2.63
	311933	AI597963	Hs.118726	ESTs	1.88	3.02
	311959	T67262	Hs.124733	ESTs	2.02	2.33
65	311960	AW440133	Hs.189690	ESTs	3.87	6.62
	311967	AI382726	Hs.182434	ESTs	5.80	8.14
	311975	AA804374	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	0.98	3.26
	312005	T78450	Hs.13941	ESTs	0.12	1.39
	312028	T78886	Hs.284450	ESTs	3.78	4.92
70	312046	AI580018	Hs.268591	ESTs	4.11	7.32
	312058	T83748	Hs.268594	ESTs	2.36	3.08
	312064	AA676713	Hs.191155	ESTs	3.34	5.28
	312088	AW303760	Hs.13685	ESTs	1.60	1.15
	312093	T91809	Hs.121296	ESTs	0.68	0.85
75	312094	Z78390	gb:HSZ78390 Human fetal brain S. Meier-E	3.05	4.48	
	312097	AI352096	Hs.112180	zinc finger protein 148 (pH2-52)	4.52	9.70
	312118	T85332	Hs.178294	ESTs	2.40	2.60
	312128	AI052609	Hs.17631	Homo sapiens cDNA FLJ20118 fis, clone CO	2.39	3.53
	312147	T89855	Hs.195648	ESTs	0.67	1.03
80	312175	AA953383	Hs.127554	ESTs	5.85	10.60
	312179	AI052572	Hs.269864	ESTs	2.41	3.32
	312201	AI928365	Hs.91139	solute carrier family 1 (neuronal/epithe	0.24	0.89
	312207	H90213	Hs.191330	ESTs	2.20	4.55
	312220	N74613	gb:za55a07.s1 Soares fetal liver spleen	4.28	11.13	
85	312252	AI128388	Hs.143655	ESTs	1.64	1.57
	312304	AA491949	Hs.269392	ESTs	0.12	2.47

	312318	AW235092	Hs.143981	ESTs	3.46	5.69
	312319	AA216698	Hs.180780	TERA protein	5.78	4.46
	312321	R66210	Hs.186937	ESTs	0.44	1.74
5	312331	AA825512	Hs.289101	glucose regulated protein, 58kD	3.73	5.96
	312339	AA524394	Hs.165544	ESTs	3.07	0.95
	312363	AI675558	Hs.181867	ESTs	10.08	16.73
	312375	AI375096	Hs.172405	cell division cycle 27	2.78	3.71
	312376	R52089	Hs.172717	ESTs	1.00	1.00
10	312389	AI863140		gb:tz43h12.x1 NCL_CGAP_Bm52 Homo sapien	2.37	3.98
	312437	AA995028		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	4.06	5.41
	312440	AI051133	Hs.133315	Homo sapiens mRNA: cDNA DKFZp761J1324 (f	1.00	1.00
	312451	R59989	Hs.176539	ESTs	4.96	10.04
	312458	AI167637	Hs.146924	ESTs	1.11	1.00
15	312507	AI168177	Hs.143653	ESTs	5.89	8.24
	312520	AI742591	Hs.205392	ESTs	3.30	8.92
	312548	AI586228	Hs.159426	hypothetical protein PRO2121	1.38	1.65
	312564	H21520	Hs.35088	ESTs	0.40	0.77
	312583	AI193122	Hs.124141	ESTs	0.13	0.94
20	312599	AI865073	Hs.125720	ESTs	3.75	5.29
	312602	AA046451	Hs.165200	ESTs	6.78	12.93
	312645	H52121	Hs.193007	ESTs	0.38	1.13
	312666	AI240682	Hs.214678	ESTs	0.98	2.03
	312689	AW450461	Hs.203965	ESTs	0.21	0.61
	312817	H75459	Hs.233425	ESTs	1.51	0.85
25	312846	AW152104	Hs.200879	ESTs	8.93	13.78
	312873	AI690071	Hs.283552	ESTs, Weakly similar to unnamed protein	4.20	6.23
	312893	AI016204	Hs.172922	ESTs	2.67	3.15
	312902	AW292797	Hs.130316	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.19	0.71
30	312925	N90888	Hs.271695	ESTs	2.50	4.25
	312936	AI681581	Hs.121525	ESTs	1.00	1.17
	312975	AI640506	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.30	4.80
	312978	N24887	Hs.292500	ESTs	0.80	1.05
	312980	AA497043	Hs.115685	ESTs	3.12	3.60
35	312984	N25871	Hs.177337	ESTs	2.03	2.13
	313000	AI147412	Hs.146657	ESTs	5.52	8.42
	313029	AA731520	Hs.170504	ESTs	0.96	1.39
	313039	AI419290	Hs.149990	ESTs, Weakly similar to unnamed protein	6.48	13.20
	313049	AW293055	Hs.119357	ESTs	6.44	10.73
40	313056	AI651930	Hs.135884	ESTs	1.51	2.04
	313058	D81015	Hs.125382	ESTs	0.25	1.50
	313070	AI422023	Hs.161338	ESTs	8.56	11.60
	313097	AI676164	Hs.204339	ESTs	3.72	4.56
	313130	AW449171	Hs.168677	ESTs	3.28	5.06
45	313136	N59284	Hs.288010	ESTs	0.49	1.36
	313153	AI240838	Hs.132750	ESTs	5.36	5.52
	313210	N74077	Hs.197043	ESTs	0.30	0.66
	313236	AW238169	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.16	8.76
	313239	W19632	Hs.124170	ESTs	1.00	3.87
50	313265	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti	0.74	2.06
	313267	AI770008	Hs.129583	ESTs	0.23	1.30
	313275	AI027604	Hs.159650	ESTs	6.68	9.57
	313290	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fls, clone NT	1.34	1.07
	313292	AI362991	Hs.202121	ESTs, Weakly similar to env protein [H.s	2.00	4.32
55	313325	AI420611	Hs.127832	ESTs	1.20	2.27
	313357	AW074848	Hs.201501	ESTs	4.02	5.33
	313393	AI674685	Hs.200141	ESTs	1.36	2.84
	313399	AW376889	Hs.194097	ESTs	2.58	5.26
	313414	AI241540	Hs.132933	ESTs	6.57	15.07
60	313417	AA741151	Hs.137323	ESTs	0.63	3.01
	313457	AA576052	Hs.193223	Homo sapiens cDNA FLJ11646 fls, clone HE	2.78	4.70
	313499	AI261390	Hs.146085	KIAA1345 protein	0.91	2.37
	313516	AA029058	Hs.135145	ESTs	3.41	7.08
	313558	AA628517	Hs.118502	ESTs	0.23	0.70
65	313569	AI273419	Hs.135146	hypothetical protein FLJ13984	1.88	1.00
	313570	AA041455	Hs.209312	ESTs	0.73	2.27
	313638	AI753075	Hs.104627	Homo sapiens cDNA FLJ10158 fls, clone HE	1.00	1.72
	313662	AA740151	Hs.130425	ESTs	0.20	1.42
	313671	W49823	Hs.104613	RP42 homolog	1.00	1.00
70	313672	AW468891	Hs.122948	ESTs	3.46	5.80
	313690	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	0.51	0.97
	313711	AA398070	Hs.133471	ESTs	0.18	1.01
	313723	AA070412		gb:zm68c10.s1 Stratagene neuroepithelium	1.08	1.03
	313726	AI744687	Hs.257806	ESTs	2.13	2.99
75	313774	AW136836	Hs.144583	ESTs	1.38	1.19
	313784	AA910514	Hs.134905	ESTs	3.88	5.78
	313790	AW078569	Hs.177043	ESTs	0.22	2.06
	313832	AW271022	Hs.133294	ESTs	1.15	0.91
	313834	AW418779	Hs.114889	ESTs	0.68	3.14
80	313835	AI538438	Hs.159087	ESTs	5.74	8.88
	313852	H18633	Hs.123641	protein tyrosine phosphatase, receptor t	0.16	1.14
	313854	AW470806	Hs.275002	ESTs	2.09	4.06
	313865	AA731470	Hs.163839	ESTs	3.41	4.09
	313871	AW471088	Hs.145950	ESTs	5.28	6.83
85	313883	AI949384		gb:nu76d01.s1 NCL_CGAP_Alv1 Homo sapiens	2.90	10.91
	313915	AI969390	Hs.183443	Homo sapiens cDNA FLJ11576 fls, clone HE	1.00	1.00

	313926	AW473830	Hs.171442	ESTs	3.40	4.11
	313948	AW452823	Hs.135268	ESTs	5.77	9.15
	313978	AI870175	Hs.13957	ESTs	0.46	0.75
5	313983	AI829133	Hs.226780	ESTs	4.10	6.40
	314035	AA164199	Hs.270152	ESTs	5.88	7.90
	314037	AW300048	Hs.275272	ESTs	1.00	3.79
	314040	AA166970	Hs.118748	ESTs	7.60	11.33
	314067	AW293538	Hs.51743	KIAA1340 protein	1.86	1.21
10	314103	AI028477	Hs.132775	ESTs	2.90	5.29
	314107	AA806113	Hs.189025	ESTs	2.00	1.66
	314113	AA218985	Hs.118854	ESTs	0.91	4.17
	314124	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.53	3.32
	314126	AA226431		gb:nc18b12.s1 NCI_CGAP_Pr1 Homo sapiens	3.13	5.08
15	314128	AA935633	Hs.194628	ESTs	2.90	6.35
	314161	AA236163	Hs.202430	ESTs	4.15	6.45
	314184	AW081795	Hs.233465	ESTs	3.44	4.65
	314192	AW290975	Hs.118923	ESTs	1.00	1.23
	314244	AL036450	Hs.103238	ESTs	2.88	3.67
20	314253	AA278679	Hs.189510	ESTs	4.98	7.16
	314262	AW086215	Hs.246096	ESTs	0.38	1.94
	314320	AA811598	Hs.275809	ESTs	3.34	5.66
	314332	AL037551	Hs.95612	ESTs	2.85	2.09
	314335	AA287443	Hs.142570	Homo sapiens clone 24629 mRNA sequence	4.35	4.78
25	314340	AW304350	Hs.130879	ESTs, Moderately similar to putative p15	0.77	0.86
	314351	AA292275	Hs.193746	ESTs	3.07	3.77
	314376	AI628633	Hs.324679	ESTs	4.10	6.11
	314443	AA827125	Hs.192043	ESTs	6.20	13.67
	314458	AI217440	Hs.143873	ESTs	0.58	2.49
30	314466	AA767818	Hs.122707	ESTs	2.53	2.62
	314478	AI521173	Hs.125507	DEAD-box protein	3.94	5.65
	314482	AL043807	Hs.134182	ESTs	1.30	1.44
	314506	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	3.28	3.47
	314519	R42554	Hs.210862	T-box, brain, 1	3.12	6.16
35	314529	AL046412	Hs.202151	ESTs	3.43	6.87
	314546	AW007211	Hs.16131	hypothetical protein FLJ12876	1.38	1.00
	314562	AI564127	Hs.143493	ESTs	2.29	5.27
	314579	AW197442	Hs.116998	ESTs	3.87	5.75
	314580	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	0.10	0.71
40	314585	AA918474	Hs.216363	ESTs	1.08	1.40
	314589	AW384790	Hs.163408	Homo sapiens cDNA FLJ10570 fis, clone NT	1.00	1.00
	314592	AA435761	Hs.192148	ESTs	0.90	2.60
	314603	AA418024	Hs.270870	ESTs	4.56	6.29
	314604	AA946582	Hs.8700	deleted in liver cancer 1	3.42	3.92
45	314606	AA418241	Hs.188767	ESTs	2.97	4.55
	314648	AA878419		gb:EST391378 MAGE resequences, MAGP Homo1.42	3.66	1.36
	314699	AI038719	Hs.132801	ESTs	0.03	4.97
	314701	AI754634	Hs.131987	ESTs	3.40	0.90
	314710	AI669131	Hs.290989	EST	2.80	7.52
50	314750	AI095005	Hs.135174	ESTs	2.80	6.54
	314767	AW135412	Hs.164002	ESTs	3.20	4.26
	314801	AA481027	Hs.109045	hypothetical protein FLJ10498	1.00	1.00
	314817	AI694139	Hs.192855	ESTs	0.91	0.99
	314835	AI281370	Hs.76064	ribosomal protein L27a	5.75	7.44
55	314852	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapien	1.68	4.34
	314853	AA729232	Hs.153279	ESTs	0.60	1.85
	314940	AW452768	Hs.162045	ESTs	10.10	16.20
	314941	AA515802	Hs.130650	ESTs	0.31	1.02
	314943	AI476797	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.18	0.37
60	314955	AA521382	Hs.192534	ESTs	2.59	3.90
	314973	AW273128	Hs.300268	ESTs	1.05	1.25
	315004	AA527941	Hs.325351	EST	5.64	13.63
	315006	AI538613	Hs.298241	Transmembrane protease, serine 3	0.52	1.78
	315033	AI493046	Hs.146133	ESTs	2.46	1.00
65	315035	AI569476	Hs.177135	ESTs	0.34	1.33
	315056	AI202703	Hs.152414	ESTs	2.10	2.64
	315069	AI821517	Hs.105866	ESTs	1.00	1.30
	315071	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	1.78	1.00
	315073	AW452948	Hs.257631	ESTs	1.17	1.52
70	315078	AA568548	Hs.190616	ESTs	3.00	3.79
	315080	AA744550	Hs.136345	ESTs	1.00	1.00
	315120	AA564991	Hs.269477	ESTs	0.64	1.44
	315175	AI025842	Hs.152530	ESTs	0.61	1.91
	315183	AI241331	Hs.131765	ESTs	1.06	0.97
75	315186	AA972756	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	0.48	1.96
	315200	AI808235	Hs.307686	EST	3.76	9.40
	315254	AI474433	Hs.179556	ESTs	5.37	9.36
	315353	AW452608	Hs.279610	hypothetical protein FLJ10493	1.00	1.30
	315397	AA218940	Hs.137516	fidgetin-like 1	3.38	2.24
80	315403	AW362980	Hs.163924	ESTs	2.04	5.23
	315431	AA622104	Hs.184838	ESTs	2.36	8.04
	315454	AI239473		gb:qh36f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.46	7.64
	315455	AW393391	Hs.156919	ESTs	3.78	5.76
	315473	AI681671	Hs.312671	ESTs, Moderately similar to OVCA1	0.89	2.15
85	315483	AW512763	Hs.222024	transcription factor BMAL2	2.32	1.96
	315526	AI193048	Hs.128685	ESTs	1.67	1.78

	315530	AI200852	Hs.127780	ESTs	1.05	1.01
	315541	AI168233	Hs.123159	sperm associated antigen 4	0.85	0.56
	315552	AW445034	Hs.255578	ESTs	1.00	2.22
5	315562	AA737415	Hs.152826	ESTs	2.68	2.48
	315577	AW513545	Hs.17283	hypothetical protein FLJ10890	2.20	2.25
	315587	AI268399	Hs.140489	ESTs	1.00	1.04
	315589	AW072387	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 f	0.14	1.05
	315623	AA364078	Hs.258189	ESTs	7.44	12.55
10	315634	AA837085	Hs.220685	ESTs	0.50	1.40
	315668	AA912347	Hs.136585	ESTs	0.43	1.22
	315677	AI932662	Hs.164073	ESTs	0.60	1.39
	315706	AW440742	Hs.155555	hypothetical protein FLJ20202	2.18	3.77
	315707	AI418055	Hs.161160	ESTs	2.88	2.63
	315730	H25899	Hs.201591	ESTs	0.11	0.60
15	315745	AI821759	Hs.191856	ESTs	3.50	7.25
	315791	AA678177		gb:J15a05.s1 Soares_fetal_liver_spleen_	1.78	2.63
	315801	AA827752	Hs.266134	ESTs	4.31	6.23
	316820	AI652022	Hs.258785	ESTs	2.35	3.01
20	315878	AA683336	Hs.189046	ESTs	2.12	2.64
	315905	AI821911	Hs.209452	ESTs	1.03	1.97
	315923	AI052789	Hs.133263	ESTs	2.63	5.06
	315954	AW276810	Hs.254859	ESTs, Moderately similar to ALU5_HUMAN A	1.21	0.85
	315978	AA830893	Hs.119769	ESTs	3.09	3.41
25	316001	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	2.20	6.82
	316011	AW516953	Hs.201372	ESTs	0.35	1.63
	316012	AA764950	Hs.119898	ESTs	6.56	8.13
	316040	AI983409	Hs.189226	ESTs	5.69	10.69
	316048	AI720759	Hs.224971	ESTs	2.84	10.45
30	316076	AW297895	Hs.116424	ESTs	0.30	1.05
	316124	AI308862	Hs.167028	ESTs	1.00	1.43
	316151	AI806016	Hs.155520	ESTs	5.80	9.03
	316187	AW518299	Hs.192253	ESTs	1.20	3.96
	316204	AA731509	Hs.120257	ESTs	4.92	6.94
35	316232	AW297853	Hs.251203	ESTs	1.48	1.60
	316275	AI671041	Hs.292811	ESTs, Moderately similar to ALU1_HUMAN A	5.86	12.14
	316291	AW375974	Hs.156704	ESTs	2.73	2.69
	316303	AA740994	Hs.209609	ESTs	1.53	1.26
	316344	AA744518	Hs.120610	ESTs	3.66	8.34
40	316346	AI028478	Hs.157447	ESTs	3.51	6.69
	316365	AI627845	Hs.210776	ESTs	2.50	4.33
	316380	AI393378	Hs.164496	ESTs	1.16	2.16
	316470	AA809902	Hs.243813	ESTs	5.40	10.34
	316509	AA767310	Hs.291766	ESTs	2.46	2.89
45	316514	AA768037	Hs.291671	ESTs	4.70	6.04
	316519	AI929097		gb:cd10c11.s1 NCI_CGAP_GCB1 Homo sapiens	4.41	9.70
	316609	AW292520	Hs.122082	ESTs	1.00	2.89
	316633	AI125586	Hs.127955	ESTs	2.61	3.72
	316700	AW172316	Hs.252961	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.46	4.64
50	316711	AI743721	Hs.285316	ESTs, Moderately similar to ALU7_HUMAN A	4.45	6.95
	316713	AI090671	Hs.134807	hypothetical protein FLJ12057	0.30	2.40
	316715	AI440266	Hs.170673	ESTs, Weakly similar to AF126780 1 retin	0.20	1.45
	316787	AW389770	Hs.130351	ESTs	4.05	5.53
	316809	AA825839	Hs.202238	ESTs	2.25	3.82
55	316811	AA922060	Hs.132471	ESTs	1.00	1.32
	316812	AW135045	Hs.232001	ESTs	3.28	4.70
	316818	AA827176	Hs.124316	ESTs	0.67	1.81
	316824	AA837416	Hs.124299	ESTs	3.53	6.00
	316827	AI380429	Hs.172445	ESTs	0.72	1.56
60	316891	AW298119	Hs.202536	ESTs	1.64	2.97
	316951	AA134365	Hs.57548	ESTs	1.45	1.08
	316970	AA860172	Hs.132406	ESTs	1.00	1.53
	316971	AA860212	Hs.170991	ESTs	1.08	1.96
	316990	AA861611	Hs.130643	ESTs	5.44	10.04
65	317001	AI627917	Hs.233694	hypothetical protein FLJ11350	3.56	4.37
	317008	AW051597	Hs.143707	ESTs	0.69	1.37
	317051	AA873253	Hs.126233	ESTs	6.18	12.72
	317128	AA971374	Hs.125674	ESTs	1.87	2.66
	317129	H12523	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone C	4.12	6.64
70	317137	AW341567	Hs.125710	ESTs	2.82	5.12
	317196	AI348258	Hs.153412	ESTs	1.98	2.51
	317212	AI866468	Hs.148294	ESTs	1.86	2.83
	317223	AW297920	Hs.130054	ESTs	0.83	1.57
	317224	D56760	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	2.74	0.86
75	317266	AA906289	Hs.203614	ESTs	1.00	1.00
	317282	AI807444	Hs.176101	ESTs	2.60	4.21
	317285	AW370882	Hs.222080	ESTs	1.96	3.49
	317302	AA908709	Hs.135564	ESTs	7.16	8.32
	317304	AW449899	Hs.130184	ESTs	1.38	2.28
80	317320	AA927151	Hs.130452	ESTs	3.53	8.13
	317413	AW341701	Hs.126622	ESTs	2.08	4.92
	317417	AA918420	Hs.145378	ESTs	3.06	4.79
	317452	AA972965	Hs.135558	ESTs	4.22	9.21
	317519	AI859895	Hs.126860	ESTs	1.88	4.15
85	317521	AI824338	Hs.126891	ESTs	3.12	4.55
	317529	AI916517	Hs.126865	ESTs	2.73	3.34

5	317570	AI733361	Hs.127122	ESTs	1.00	2.43
	317571	AA938663	Hs.199828	ESTs	5.20	11.95
	317598	AW206035	Hs.192123	ESTs	0.33	1.66
	317627	AI346110	Hs.132553	ESTs	1.50	1.39
	317650	AI733310	Hs.127346	ESTs	0.48	1.46
10	317659	AA961216	Hs.127785	ESTs	4.18	7.14
	317674	AW294909	Hs.132208	ESTs	2.92	3.20
	317686	AA969051	Hs.187319	ESTs	1.00	1.01
	317692	AI307659	Hs.174794	ESTs	5.33	9.59
	317701	AI674774	Hs.128014	ESTs	1.00	1.00
15	317711	AI733015	Hs.272189	ESTs	5.13	7.81
	317722	AI733373	Hs.128119	ESTs	2.50	6.03
	317756	AA973667	Hs.128320	ESTs	1.59	1.30
	317777	AI143525	Hs.47313	KIAA0258 gene product	1.00	2.48
	317799	AI498273	Hs.128808	ESTs	1.78	2.11
20	317803	AA983251	Hs.128899	ESTs	0.80	1.06
	317821	AI368158	Hs.70983	PTPL1-associated RhoGAP 1	0.17	0.68
	317848	AI820575	Hs.129086	Homo sapiens cDNA FLJ12007 fis, clone HE	5.30	8.16
	317850	N29974	Hs.152982	hypothetical protein FLJ13117	1.30	2.28
	317861	AW341064	Hs.129119	ESTs	2.18	5.93
25	317865	AI298794	Hs.129130	ESTs	4.48	8.20
	317869	AW295184	Hs.129142	deoxyribonuclease II beta	0.44	0.99
	317881	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.06	2.23
	317890	AI915599	Hs.129225	ESTs	4.68	7.48
	317899	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.14	3.37
30	317986	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	0.28	1.66
	318001	AW235697	Hs.130980	ESTs	5.12	9.97
	318016	AI016694	Hs.256921	ESTs	1.86	4.50
	318023	AW243058	Hs.131155	ESTs	2.92	5.22
	318054	AW449270	Hs.232140	ESTs	3.92	6.37
35	318068	AI024540	Hs.131574	ESTs	1.21	1.27
	318117	AI208304	Hs.250114	ESTs	0.86	1.17
	318187	AI792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN IIII	5.90	6.98
	318223	AI077540	Hs.134090	ESTs	1.05	0.90
	318240	AI085377	Hs.143610	ESTs	3.10	2.40
40	318255	AI082692	Hs.134662	ESTs	0.02	1.05
	318268	AI554341	Hs.271443	ESTs	6.12	10.55
	318330	AI093840	Hs.143758	ESTs	4.98	7.90
	318369	AI493501	Hs.170974	ESTs	2.48	5.62
	318428	AI949409	Hs.194591	ESTs	0.77	0.45
45	318458	AI149783	Hs.158438	ESTs	3.54	4.92
	318467	AI151395	Hs.144834	ESTs	4.56	5.62
	318473	AI939339	Hs.146883	ESTs	2.08	4.05
	318476	AI693927	Hs.265165	ESTs	4.22	8.07
	318487	AI167877	Hs.143716	ESTs	1.47	1.05
50	318488	AI217431	Hs.144709	ESTs	1.40	4.14
	318491	T26477	Hs.228893	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.84	1.90
	318499	T25451		gb:PTH188 HTCCL1 Homo sapiens cDNA 5/3	2.58	5.20
	318537	AA377908	Hs.13254	ESTs	3.26	4.18
	318538	N28625	Hs.74034	Homo sapiens clone 24651 mRNA sequence	0.35	1.07
55	318547	R20578	Hs.90431	ESTs	3.22	4.60
	318552	R18364	Hs.90363	ESTs	4.87	9.06
	318575	R55102	Hs.107761	ESTs, Weakly similar to unnamed protein	1.91	1.98
	318580	T34571	Hs.49007	poly(A) polymerase alpha	2.74	6.22
	318587	AA779704	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	0.85	2.46
60	318596	AI470235	Hs.172698	EST	4.88	4.93
	318622	T48325	Hs.237658	apolipoprotein A-II	4.80	12.51
	318629	N25163	Hs.8861	ESTs	0.39	1.04
	318637	AA243539	Hs.9196	hypothetical protein	1.72	3.57
	318648	T77141	Hs.184411	albumin	6.27	9.91
65	318650	AA393302	Hs.176626	hypothetical protein EDAG-1	3.96	8.84
	318671	AA188823	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	1.53	0.81
	318679	T58115	Hs.10336	ESTs	1.00	2.19
	318711	AI936475	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	3.05	3.18
	318725	AI962487	Hs.242990	ESTs	1.08	2.46
70	318728	Z30201	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	1.33
	318740	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.25	1.49
	318776	R24963	Hs.23766	ESTs	1.00	3.01
	318784	H00148	Hs.5181	proliferation-associated 2G4, 38kD	2.70	3.86
	318816	F07873	Hs.21273	ESTs	3.90	7.13
75	318865	H10818		gb:ym04f10.r1 Soares Infant brain 1N1B H	2.25	3.56
	318879	R56332	Hs.18268	adenylate kinase 5	1.78	5.00
	318881	Z43224	Hs.124952	ESTs	4.79	14.13
	318894	F08138	Hs.7387	DKFZP564B116 protein	5.31	7.00
	318901	AW368520	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	1.03	0.91
80	318925	Z43577	Hs.21470	ESTs	2.23	3.80
	318936	AI219221	Hs.308298	ESTs	1.86	7.16
	318982	Z44140	Hs.268622	ESTs	5.84	9.79
	318986	Z44186	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.00	1.00
	319041	Z44720	Hs.98365	ESTs, Weakly similar to weak similarity	3.38	6.11
85	319103	H05896	Hs.4993	KIAA1313 protein	1.00	1.07
	319170	R13678	Hs.285306	putative selenocysteine lyase	3.79	5.03
	319196	F07953	Hs.16085	putative G-protein coupled receptor	1.00	2.98
	319199	F07361	Hs.13306	ESTs	3.53	5.66
	319242	F11472	Hs.12839	ESTs	5.87	7.26

	319263	T65331	Hs.81360	Homo sapiens cDNA: FLJ21927 fis, clone H	1.81	1.57
	319267	F11802	Hs.6818	ESTs	1.10	4.72
	319270	R13474	Hs.290263	ESTs	4.80	10.40
5	319279	T65094	Hs.12677	CGI-147 protein	1.50	2.11
	319282	AA461358	Hs.12876	ESTs	1.00	1.00
	319289	W07304	Hs.79059	transforming growth factor, beta recepto	0.18	0.68
	319291	W86578	Hs.285243	hypothetical protein FLJ22029	0.26	0.62
	319293	F12119	Hs.12583	ESTs	3.13	4.50
10	319312	Z45481		gb:HSC2QE041 normalized Infant brain cDN	1.10	1.00
	319370	H54254	Hs.325823	ESTs, Moderately similar to ALUS_HUMAN A	0.16	0.73
	319391	R06304	Hs.13911	ESTs	1.26	2.43
	319395	H67130	Hs.301743	ESTs	0.70	0.76
	319398	AA359754	Hs.191196	ESTs	2.45	3.59
15	319407	R05329		gb:ye91b04.r1 Soares fetal liver spleen	2.00	3.54
	319425	T82930		gb:yd39f07.r1 Soares fetal liver spleen	4.28	8.81
	319433	R06050	Hs.191198	ESTs	6.15	14.13
	319437	AA282420	Hs.111991	ESTs, Weakly similar to Y48A5A.1 [C.eleg	3.26	5.68
	319466	AI809937	Hs.116417	ESTs	1.76	5.65
20	319471	R06546	Hs.19717	ESTs	4.29	4.84
	319480	R06933	Hs.184221	ESTs	1.00	1.00
	319484	T91772		gb:yd52a10.s1 Soares fetal liver spleen	2.81	4.88
	319486	AI382429	Hs.250799	ESTs	2.08	2.82
	319508	T99898	Hs.270104	ESTs, Moderately similar to ALU8_HUMAN A	2.80	4.39
25	319523	T69499	Hs.191184	ESTs	1.55	3.25
	319545	R83716	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	1.65	1.19
	319546	R09692		gb:yf23b12.r1 Soares fetal liver spleen	5.11	8.54
	319552	AA096106	Hs.20403	ESTs	1.89	3.36
	319582	T82998	Hs.250154	hypothetical protein FLJ12973	3.48	4.82
30	319586	D78808	Hs.283683	chromosome 8 open reading frame 4	0.26	0.82
	319604	R11679	Hs.297753	vimentin	1.68	3.41
	319609	AW247514	Hs.12293	hypothetical protein FLJ21103	3.06	4.24
	319611	H14957		gb:ym19c10.r1 Soares infant brain 1N1B H	2.76	4.24
	319653	AA770183	Hs.173515	uncharacterized hypothalamus protein HTO	2.51	3.55
35	319657	R19897	Hs.106604	ESTs	5.32	7.68
	319658	R13432	Hs.167481	synaptrophin, gamma 1	3.35	5.00
	319661	H08035	Hs.21398	ESTs, Moderately similar to A Chain A, H	5.18	12.55
	319662	H06382	Hs.21400	ESTs	1.58	1.56
	319708	R15372	Hs.22664	ESTs	1.00	1.22
40	319742	T77668	Hs.21162	ESTs	2.48	3.13
	319748	R18178	Hs.295866	Homo sapiens mRNA; cDNA DKFZp434N1923 (f	3.02	4.85
	319772	R76633	Hs.22646	ESTs	4.36	11.61
	319788	AA321932	Hs.117414	KIAA1320 protein	2.56	3.68
	319805	R92857	Hs.271350	likely ortholog of mouse polydom	4.63	6.56
45	319812	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.63	1.32
	319834	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	0.30	0.94
	319878	T78517	Hs.13941	ESTs	3.99	6.44
	319882	AA258981	Hs.291392	ESTs	5.09	7.36
	319912	T77559	Hs.84109	Homo sapiens cDNA FLJ13534 fis, clone PL	3.24	3.21
50	319935	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.40	9.42
	319944	T79248	Hs.133510	ESTs	3.31	5.39
	319947	AA160967	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.80	4.95
	319962	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	1.81	1.57
	320007	AA336314		gb:EST40943 Endometrial tumor Homo sapie	3.42	6.29
55	320018	T83263		gb:yd40h09.r1 Soares fetal liver spleen	2.77	5.14
	320030	H63789	Hs.296288	ESTs, Weakly similar to KIAA0638 protein	4.10	6.69
	320032	AI699772	Hs.292664	ESTs, Weakly similar to A46010 X-linked	3.27	3.27
	320040	AA233871	Hs.87164	hypothetical protein FLJ14001	1.81	1.64
	320047	T86564	Hs.302256	EST	3.38	7.38
60	320063	AA074108	Hs.120844	FOXJ2 forkhead factor	5.90	16.73
	320096	H58138	Hs.117915	ESTs	2.08	4.47
	320099	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.00	1.00
	320112	T92107	Hs.188489	ESTs	2.27	2.06
	320140	H94179	Hs.119023	SMC2 (structural maintenance of chromoso	1.00	1.00
65	320188	AW419200	Hs.172318	ESTs	1.26	1.00
	320193	AA831259	Hs.17132	ESTs	2.58	6.23
	320195	R62203	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	2.85	4.53
	320199	R78659	Hs.29792	ESTs	0.40	0.94
	320203	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	0.84	1.18
70	320219	AA327564	Hs.127011	tubulointerstitial nephritis antigen	1.00	1.17
	320220	AF054910	Hs.127111	tektn 2 (testicular)	0.18	1.09
	320225	AF058989	Hs.128231	G antigen, family B, 1 (prostate associa	5.26	13.75
	320231	H03139	Hs.24683	ESTs	1.59	1.93
	320260	NM_003608	Hs.131924	G protein-coupled receptor 65	1.38	4.56
75	320267	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	1.00	1.92
	320268	H06019	Hs.151293	Homo sapiens cDNA FLJ10664 fis, clone NT	5.58	5.70
	320322	AF077374	Hs.139322	small proline-rich protein 3	1.41	1.01
	320325	AI167978	Hs.135851	caveolin 2	0.05	0.67
	320330	AF026004	Hs.141660	chloride channel 2	2.17	1.26
80	320339	H10807	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.81	2.32
	320388	H16065	Hs.31286	ESTs	1.00	3.22
	320402	R22291	Hs.23368	Homo sapiens clone FLC0578 PRO2852 mRNA,	1.41	1.36
	320413	AA203711	Hs.173269	ESTs	2.31	3.61
	320432	R62786	Hs.124136	ESTs	11.25	20.78
85	320436	AA253352	Hs.293663	ESTs	2.22	3.49
	320438	W24548	Hs.5669	ESTs	3.53	8.14

	320448	AI240233	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	1.42	3.46
	320451	R26944	Hs.180777	Homo sapiens mRNA; cDNA DKFZp564M0264 (f	0.87	0.81
	320484	AA094436	Hs.295267	folliculin-like 1	0.65	1.18
5	320499	R32555	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	3.44	7.15
	320514	AB007978	Hs.158278	KIAA0509 protein	6.44	13.62
	320521	N31464	Hs.24743	hypothetical protein FLJ20171	1.48	1.04
	320526	AW374205	Hs.111314	ESTs	3.66	7.87
	320527	R34672	Hs.324522	ESTs	3.16	5.63
10	320536	AA331732	Hs.137224	ESTs	2.83	5.83
	320556	AF054177	Hs.14570	hypothetical protein FLJ22530	1.28	1.00
	320564	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyc	1.22	0.81
	320587	Z44524	Hs.167456	Homo sapiens mRNA full length insert cDN	1.84	2.44
	320635	R54159	Hs.80508	small nuclear ribonucleoprotein polypept	1.00	6.25
	320639	AA243258	Hs.7395	hypothetical protein FLJ23182	2.60	2.30
15	320648	N48521	Hs.26549	Homo sapiens mRNA for KIAA1708 protein,	1.00	1.53
	320651	AA489268	Hs.111334	ferritin, light polypeptide	0.14	0.79
	320664	AI904216	Hs.91251	hypothetical protein FLJ11198	5.02	8.84
	320676	AA132650	Hs.300511	ESTs	3.63	5.37
	320683	R59291	Hs.26638	ESTs, Weakly similar to unnamed protein	0.37	1.31
20	320689	AA334609	Hs.171929	ESTs, Weakly similar to A54849 collagen	1.27	1.02
	320696	AW135016	Hs.172780	ESTs	3.53	4.60
	320714	AI445591		gb:yc04a10.r1 Soares fetal liver spleen	1.06	0.85
	320727	U96044	Hs.181125	immunoglobulin lambda locus	1.35	1.49
25	320771	AI793266	Hs.117176	poly(A)-binding protein, nuclear 1	0.04	0.82
	320794	AA281993	Hs.91226	ESTs	2.96	4.33
	320822	AF100780	Hs.194679	WNT1 Inducible signaling pathway protein	0.10	0.79
	320824	AF120274	Hs.194689	arlemn	1.16	1.11
	320830	AJ132445	Hs.266416	claudin 14	1.06	1.75
30	320843	AA317372	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.36	1.47
	320849	D60031	Hs.34771	ESTs	5.30	7.49
	320853	AI473796	Hs.135904	ESTs	1.00	1.00
	320896	AB002155	Hs.271580	uropod 1B	5.90	2.55
	320921	R94038	Hs.199538	Inhibin, beta C	2.20	1.17
35	320927	AI205786	Hs.213923	ESTs	0.18	1.46
	320957	AI878933	Hs.92023	core histone macroH2A2.2	1.67	2.18
	320997	H22544		gb:yn69f11.r1 Soares adult brain N2b5HB5	3.26	3.62
	321045	W88483	Hs.293650	ESTs	2.25	4.55
	321046	H27794	Hs.269055	ESTs	2.69	4.25
40	321052	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	2.14	2.66
	321059	AI092824	Hs.126465	ESTs	1.69	0.53
	321062	R87955	Hs.241411	Homo sapiens mRNA full length insert cDN	2.76	5.20
	321087	AF131782	Hs.241438	Homo sapiens clone 24941 mRNA sequence	4.79	7.41
	321102	AA018306		gb:ze40d08.r1 Soares retina N2b4HR Homo	1.79	4.27
45	321130	H43750	Hs.125494	ESTs	1.00	3.14
	321142	AI817933	Hs.298351	ASPL protein	8.73	15.36
	321155	AA336635	Hs.99598	hypothetical protein MGC5338	3.04	5.03
	321158	AA700289		gb:yu76f11.r1 Soares fetal liver spleen	4.62	8.39
	321170	N53742	Hs.172982	ESTs	2.21	4.46
50	321199	AW385512		gb:yy56d10.s1 Soares_multiple_sclerosis_	5.69	8.01
	321206	H54178	Hs.226469	Homo sapiens cDNA FLJ12417 fis, clone MA	4.00	7.32
	321225	AL080073	Hs.251414	Homo sapiens mRNA; cDNA DKFZp564B1462 (f	4.17	4.63
	321236	AW371941	Hs.18192	Ser/Arg-related nuclear matrix protein (1.00	1.00
	321244	AF058654		gb:Homo sapiens isolate AN.1 immunoglobu	2.18	9.13
55	321270	R83560		gb:yv76c06.s1 Soares fetal liver spleen	3.80	5.26
	321317	AI937060	Hs.6298	KIAA1151 protein	1.81	1.65
	321318	AB033041	Hs.137507	KIAA1215 protein	1.00	1.00
	321325	AB033100	Hs.300646	KIAA protein (similar to mouse paladin)	0.44	0.93
	321342	AA127984	Hs.222024	transcription factor BMAL2	4.94	4.93
60	321356	R93443	Hs.271770	ESTs	3.10	4.66
	321418	AI739161	Hs.161075	ESTs	2.28	2.54
	321420	AI368687	Hs.132743	ESTs	1.13	0.97
	321430	U05890		gb:H.sapiens (DIG3) mRNA for immunoglobu	2.42	3.35
	321453	N50080	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	1.60	3.11
65	321467	X13075		gb:Human 2a12 mRNA for kappa-immunoglobu	0.42	0.72
	321468	AA514198	Hs.38540	ESTs	2.46	6.50
	321491	H70665	Hs.292549	ESTs	1.00	1.25
	321498	AW295517	Hs.255436	ESTs	3.19	6.24
	321504	W02356	Hs.268980	ESTs	2.28	3.86
70	321510	AA703650	Hs.255748	ESTs	2.14	3.94
	321513	H84972	Hs.108651	ESTs	2.78	5.37
	321516	AI382803	Hs.159235	ESTs	3.06	7.19
	321565	AI525773	Hs.266514	hypothetical protein FLJ11342	4.89	7.82
	321577	H84260		gb:ys90g04.r1 Soares retina N2b5HR Homo	1.00	1.73
75	321581	AA019984	Hs.28803	ESTs	4.88	6.73
	321582	AA143755	Hs.21858	trinucleotide repeat containing 3	1.00	2.08
	321587	H95531		gb:ys76e02.r1 Soares retina N2b4HR Homo	2.26	4.52
	321626	AA295430	Hs.96322	hypothetical protein FLJ23560	1.95	3.83
	321628	H87064	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	0.47	1.02
80	321642	AW085917	Hs.247084	ESTs	1.52	1.38
	321669	H95404	Hs.294110	ESTs	2.17	2.45
	321687	AA625149		gb:af70c12.r1 Soares_NhHMPu_S1 Homo sapi	4.31	6.95
	321688	H97646	Hs.123158	Homo sapiens cDNA FLJ12830 fis, clone NT	2.82	3.28
	321693	AA700017	Hs.173737	ras-related C3 botulinum toxin substrate	0.51	1.08
85	321700	N55160	Hs.167260	ESTs	4.57	7.46
	321701	AW390923	Hs.42568	ESTs	1.00	1.00

	321709	N25847	Hs.108923	RAB38, member RAS oncogene family	1.00	1.00
	321710	N35682	Hs.259743	ESTs	2.97	5.26
	321775	AI694875	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.00	1.00
5	321777	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.68	0.45
	321779	N42729	Hs.163835	ESTs	0.90	0.90
	321829	D81993	Hs.8966	tumor endothelial marker 8	2.69	3.89
	321846	AA281594	Hs.87902	ESTs	5.11	7.64
	321879	AL109670	Hs.302809	ESTs	6.49	9.58
10	321883	AA426494	Hs.46901	KIAA1462 protein	0.28	0.95
	321899	N55158	Hs.29468	ESTs	0.39	0.95
	321911	AF026944	Hs.293797	ESTs	6.20	10.76
	321949	R49202	Hs.181694	EST	4.62	10.51
	321955	AI651866	Hs.195689	ESTs	2.89	5.47
	321956	AL110177	Hs.132882	ESTs	0.32	1.25
15	321987	AL133612	Hs.272759	KIAA1457 protein	1.00	1.83
	321991	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	4.00	6.47
	322002	AA328801	Hs.84522	ESTs	2.10	3.48
	322035	AL137517	Hs.306201	hypothetical protein DKFZp554O1278	1.00	1.90
20	322044	AW340926		gb:xy51b10.x1 NCI_CGAP_Lu34.1 Homo sapie	3.20	9.67
	322057	N92197	Hs.154679	synaptotagmin 1	1.55	1.07
	322060	AI341937		gb:qt10e03.x1 NCI_CGAP_GC4 Homo sapiens	4.59	7.68
	322070	U80769	Hs.210322	Homo sapiens mRNA for KIAA1766 protein,	2.78	4.52
	322083	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	3.10	5.52
	322091	AI819863	Hs.108243	ESTs	1.59	1.75
25	322125	R93901		gb:yq16c12.r1 Soares fetal liver spleen	2.06	5.27
	322130	R98978	Hs.117767	ESTs	10.12	16.49
	322147	AF085919	Hs.114176	ESTs	0.94	0.64
	322166	AF085958		gb:yr88b03.r1 Soares fetal liver spleen	4.09	6.67
30	322173	H52587		gb:y185d04.r1 Soares_pineal_gland_N3HPG	3.46	4.85
	322178	H56535		gb:y188g03.r1 Soares_pineal_gland_N3HPG	0.44	2.54
	322179	H92891		gb:y194c02.s1 Soares_pineal_gland_N3HPG	4.52	7.50
	322186	H67346	Hs.269187	ESTs	0.15	0.98
	322198	W87895	Hs.211516	ESTs	2.20	5.04
	322212	AF087995	Hs.134877	ESTs	3.42	4.84
35	322221	AI890619	Hs.179562	nucleosome assembly protein 1-like 1	0.82	2.14
	322277	AI640193	Hs.226389	ESTs	3.62	3.98
	322278	AF086283		gb:zd46f01.r1 Soares_fetal_heart_NbHH19W	1.00	1.00
	322284	AI792140	Hs.49265	ESTs	0.66	2.76
	322288	AL037273	Hs.7886	pellino (Drosophila) homolog 1	0.71	0.70
40	322320	AF086419		gb:zd76d03.r1 Soares_fetal_heart_NbHH19W	2.02	2.76
	322336	AA308526	Hs.76152	decorin	2.92	4.44
	322339	W17348		gb:zb18c07.x5 Soares_fetal_lung_NbHL19W	8.50	11.56
	322366	AW404274	Hs.122492	hypothetical protein	0.61	1.34
45	322372	W25624	Hs.153943	ESTs	7.37	12.07
	322374	AI394663	Hs.122116	ESTs, Moderately similar to Ostf2 [M.musc	4.78	10.50
	322378	AF064819	Hs.201877	DESC1 protein	1.00	1.00
	322388	AI815730	Hs.247474	hypothetical protein FLJ21032	7.09	8.49
	322416	AA223183	Hs.298442	adaptor-related protein complex 3, mu 1	3.20	5.80
50	322419	AA248987	Hs.14084	ring finger protein 7	1.64	1.57
	322425	W37943	Hs.34892	KIAA1323 protein	0.83	1.00
	322431	AA069222	Hs.141892	ESTs	3.96	5.22
	322450	AA040131	Hs.25144	ESTs	5.18	12.67
	322465	AA137152	Hs.286049	phosphoserine aminotransferase	3.41	2.23
55	322467	AF116826	Hs.180340	putative protein-tyrosine kinase	1.00	1.30
	322473	AA744286	Hs.266935	tRNA selenocysteine associated protein	1.75	2.03
	322509	T52172	Hs.302213	ESTs	1.00	2.27
	322523	W80398	Hs.193197	ESTs	2.75	5.49
	322527	AF147359		gb:Homo sapiens full length insert cDNA	1.25	1.27
60	322560	AI916847	Hs.270947	ESTs	4.57	8.81
	322566	W87285	Hs.269587	ESTs	1.00	1.42
	322585	AA837622		gb:zh69c01.r1 Soares_fetal_liver_spleen_	4.18	6.94
	322635	AA679084		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.40	4.85
	322641	AA007352	Hs.256042	ESTs	2.94	4.64
65	322653	AI828854	Hs.258538	striatin, calmodulin-binding protein	0.48	0.38
	322664	AA011522		gb:zi03g07.r1 Soares_fetal_liver_spleen_	1.92	2.18
	322687	AI110759		gb:AF074668 Human fetal liver cDNA libra	4.14	6.75
	322692	AA018117	Hs.60843	potassium voltage-gated channel, shaker-	3.50	5.00
	322694	AI110872	Hs.279812	PRO0327 protein	1.80	1.72
70	322708	AF113674	Hs.283773	clone FLB1727	1.00	3.43
	322712	AA021328	Hs.23607	hypothetical protein FLJ11109	3.28	3.86
	322766	AW068805	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.63	1.53
	322770	AA045796	Hs.122682	ESTs	1.53	1.06
	322794	AI808591	Hs.38991	S100 calcium-binding protein A2	12.05	1.94
75	322810	AI962276	Hs.127444	ESTs	4.09	6.90
	322818	AW043782	Hs.293616	ESTs	1.20	1.63
	322820	AI377755	Hs.120895	ESTs	0.21	1.93
	322872	AA827228	Hs.126943	ESTs	2.04	1.63
	322882	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	5.26	1.22
80	322887	AI986306	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.80	2.24
	322913	AI733737	Hs.68837	ESTs	2.38	6.61
	322926	AI825940	Hs.211192	ESTs	4.02	5.79
	322929	AI365585	Hs.146246	ESTs	0.30	1.14
	322958	AI905228	Hs.83484	SRY (sex determining region Y)-box 4	2.06	1.13
85	322971	C15953	Hs.212760	hypothetical protein FLJ13649	1.18	2.00
	322981	AA493252	Hs.159577	ESTs	2.28	2.61

	322988	C18727	Hs.171941	ESTs	0.39	2.00
	323003	AI733859	Hs.149089	ESTs	3.28	1.00
	323013	AA134042	Hs.191451	ESTs	3.38	5.68
5	323025	AL157565	Hs.315369	Homo sapiens cDNA: FLJ23075 fls, clone L	0.06	1.10
	323032	AW244073	Hs.145946	ESTs	10.18	21.27
	323052	R21124	Hs.85573	Homo sapiens DC29 mRNA, complete cds	1.46	1.90
	323064	AL119341	Hs.49359	Homo sapiens mRNA; cDNA DKFZp547E052 (fr	3.08	5.64
	323098	AI700025	Hs.270471	ESTs	2.31	4.49
10	323102	AL119913	Hs.163615	ESTs	5.38	11.64
	323155	AL135041		gb:DKFZp762K2310_r1 762 (synonym: hmel2)	2.38	5.56
	323176	AW071648	Hs.82101	pleckstrin homology-like domain, family	1.06	1.41
	323191	AA195600	Hs.301570	ESTs	0.73	1.24
	323225	AA205654	Hs.24790	KIAA1573 protein	5.25	11.95
15	323232	AA148722	Hs.224680	ESTs	0.45	1.35
	323266	AW003362	Hs.243885	nuclear autoantigenic sperm protein (his	1.71	1.83
	323281	AI697555	Hs.292659	ESTs	1.24	3.21
	323283	AA256014	Hs.86682	Homo sapiens cDNA: FLJ21578 fls, clone C	12.68	15.05
	323314	AA226310	Hs.191501	ESTs	4.42	9.61
20	323316	AL134620	Hs.280175	ESTs	2.98	5.93
	323334	AI336501	Hs.77273	ras homolog gene family, member A	1.98	3.30
	323338	R74219	Hs.23348	S-phase kinase-associated protein 2 (p45	1.62	1.00
	323348	AA233056	Hs.191518	ESTs	1.00	1.07
	323351	AA704103	Hs.24049	ESTs	1.43	1.68
25	323359	AA234172	Hs.137418	ESTs	0.34	1.18
	323360	AA716081	Hs.161719	ESTs	3.01	3.71
	323405	AW139550	Hs.115173	ESTs	1.90	8.81
	323420	AI672386	Hs.263780	ESTs	0.29	1.01
	323434	AW081455	Hs.120219	ESTs	2.27	1.92
30	323445	AA253103	Hs.135569	ESTs, Weakly similar to NEUROD [H.sapien	0.43	0.80
	323449	AA282865	Hs.284153	Fanconi anemia, complementation group A	3.19	3.85
	323492	H00978	Hs.20887	hypothetical protein FLJ10392	2.70	3.20
	323501	AA182461	Hs.84520	ESTs	2.04	3.31
	323505	AI652287		gb:EST382593 MAGE resequences, MAGK Homo2.21		3.08
35	323515	AA282274	Hs.256083	ESTs	2.69	3.40
	323541	AI185116	Hs.104813	RP42 homolog	1.20	1.09
	323545	AI814405	Hs.224569	ESTs	1.25	1.55
	323635	R63117	Hs.9691	Homo sapiens cDNA: FLJ23249 fls, clone C	0.27	0.72
40	323675	AA984759	Hs.272168	tumor differentially expressed 1	3.70	5.80
	323678	AL042121	Hs.20880	ESTs	3.33	5.10
	323691	AA317561	Hs.145599	ESTs	1.00	1.00
	323693	AW297758	Hs.249721	ESTs	2.01	1.54
	323746	AW298611	Hs.12808	MARK	4.11	5.53
	323774	AA329806	Hs.321056	Homo sapiens mRNA; cDNA DKFZp586F1322 (f	2.06	3.70
45	323856	AA355264	Hs.267604	hypothetical protein FLJ10450	3.42	8.13
	323857	T18988	Hs.293668	ESTs	5.97	12.51
	323870	AA341774	Hs.129212	ESTs	3.17	4.52
	323876	AL042492	Hs.147313	ESTs	0.36	1.00
	323885	AA344308	Hs.128427	Homo sapiens BAC clone RP11-335J18 from	2.31	3.33
50	323911	AL043212	Hs.92550	ESTs	4.38	5.41
	323919	AA862973	Hs.220704	ESTs	5.80	10.20
	323972	AI869964	Hs.182906	ESTs	3.10	6.14
	324005	AA610011	Hs.208021	ESTs	5.34	10.07
	324036	AI472078	Hs.303662	ESTs	1.00	5.03
55	324055	AA528794	Hs.128644	ESTs	0.86	1.00
	324063	AW292740	Hs.272813	dual oxidase 1	0.45	0.91
	324072	AA381829		gb:EST94855 Activated T-cells I Homo sap	2.82	5.12
	324092	AW269931	Hs.202473	Homo sapiens cDNA: FLJ22278 fls, clone H	2.40	2.52
	324095	AW377983	Hs.298140	Homo sapiens cDNA: FLJ22502 fls, clone H	1.32	4.30
60	324129	AI381918	Hs.285833	Homo sapiens cDNA: FLJ22135 fls, clone H	1.40	1.77
	324132	AW504860	Hs.288836	hypothetical protein FLJ12673	4.24	6.21
	324214	AA412395	Hs.225740	ESTs	6.96	10.69
	324227	AA295552	Hs.28631	Homo sapiens cDNA: FLJ22141 fls, clone H	0.81	0.53
	324266	AL047634	Hs.231913	ESTs	2.42	4.05
65	324275	AA429088	Hs.98523	ESTs	3.62	5.38
	324281	AL048026	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	0.14	0.70
	324290	AA432032	Hs.304420	ESTs	3.71	4.34
	324303	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)	0.95	0.91
	324312	AI198841	Hs.128173	ESTs	4.08	5.91
70	324325	AL138153	Hs.300410	ESTs	5.88	8.25
	324338	AL138357	Hs.145078	regulator of differentiation (In S. pomb	0.87	1.25
	324341	AW197734	Hs.99807	ESTs, Weakly similar to unnamed protein	1.28	1.00
	324343	AW452016	Hs.293232	ESTs	2.54	3.46
	324371	AA452305	Hs.270319	ESTs	5.85	8.36
75	324382	AW502749	Hs.24724	MFH-amplified sequences with leucine-ric	0.76	1.64
	324384	AA453395	Hs.127656	KIAA1349 protein	2.88	5.69
	324385	F28212	Hs.284247	KIAA1491 protein	1.81	1.99
	324388	AI924963	Hs.306206	hypothetical protein FLJ11215	1.00	1.00
	324432	AA464510	Hs.152812	ESTs	2.73	2.17
	324497	AW152624	Hs.136340	ESTs, Weakly similar to unnamed protein	0.71	1.90
80	324510	AI148353	Hs.287425	Homo sapiens cDNA FLJ11569 fls, clone HE	1.00	1.00
	324580	AA492588		gb:ng99c08.s1 NCL_CGAP_Thy1 Homo sapiens	2.18	3.50
	324582	AA506935	Hs.132036	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.86	11.36
	324633	AA572994	Hs.325489	ESTs	2.92	4.22
	324640	AW295832	Hs.134798	ESTs, Moderately similar to TTL MOUSE TU	5.48	11.74
85	324675	AW014734	Hs.157969	ESTs	0.39	0.73

	324699	AW504732	Hs.21275	hypothetical protein FLJ11011	0.93	0.93
	324747	AA603532	Hs.130807	ESTs	1.57	1.81
	324748	AA657457	Hs.292385	ESTs	1.55	1.34
5	324801	AI819924	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	6.56
	324804	AI692552		gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	1.00	7.53
	324828	AA843926	Hs.124434	ESTs	2.00	3.25
	324855	AW152305	Hs.122364	ESTs	2.74	3.43
	324866	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.07	0.95
10	324871	AW297755	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	1.68	1.21
	324886	AA808794	Hs.131511	ESTs	2.56	5.61
	324889	D31010		gb:HUML12147 Human fetal lung Homo sapie	2.20	4.65
	324948	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	5.28	7.05
	324953	AI264628	Hs.125428	ESTs	3.37	5.51
15	324958	AA625076	Hs.132892	protocadherin 20	5.12	9.81
	324988	T06997	Hs.121028	hypothetical protein FLJ10549	2.52	1.08
	325024	F13254	Hs.78672	laminin, alpha 4	5.24	10.22
	325105	H97109	Hs.105421	ESTs	1.00	1.00
	325108	AA401863	Hs.22380	ESTs	1.99	2.14
20	325114	D83901	Hs.315562	ESTs	2.73	3.17
	325146	AI084690	Hs.171176	ESTs	1.86	3.41
	325149	D61117	Hs.187646	ESTs	0.42	0.93
	325187	AI653882	Hs.197812	ESTs	6.50	11.31
	325228				6.18	15.76
25	325235				2.64	4.12
	325328				2.87	4.42
	325340				0.29	0.33
	325367				16.56	24.29
	325373				0.63	1.22
30	325389				0.88	1.05
	325436				5.75	14.14
	325471				8.48	17.82
	325498				3.32	6.42
	325557				5.51	8.28
35	325559				7.48	21.40
	325560				4.08	6.25
	325569				4.20	5.24
	325585				1.10	1.13
	325587				1.00	1.00
40	325597				2.98	13.40
	325639				0.78	0.78
	325685				0.46	0.66
	325686				0.95	1.55
	325735				4.48	9.20
45	325739				0.69	0.88
	325740				2.42	6.61
	325792				7.88	9.83
	325819				4.74	7.18
	325883				2.02	2.64
50	325895				7.78	15.98
	325925				2.04	10.60
	325932				4.18	7.36
	325941				3.66	9.03
	325969				0.61	0.80
55	325971				4.88	7.42
	326025				0.55	1.07
	326046				7.21	14.72
	326099				3.60	5.98
	326108				1.27	1.08
60	326163				3.27	5.70
	326165				0.45	1.11
	326189				0.13	0.45
	326204				5.60	9.00
	326230				7.00	12.01
65	326274				1.00	8.09
	326360				9.86	15.35
	326393				0.52	0.77
	326505				1.00	1.42
	326515				1.24	5.84
70	326589				9.20	13.49
	326592				2.77	4.01
	326605				2.01	2.53
	326692				1.00	1.00
	326693				1.00	1.31
75	326720				0.19	0.65
	326742				2.34	7.20
	326770				0.25	0.83
	326818				3.09	4.56
	326936				2.08	3.45
80	326964				0.41	1.70
	326983				2.02	3.80
	326991				1.09	1.20
	327036				1.00	8.04
	327040				3.05	4.22
85	327053				3.55	6.31
	327075				1.59	1.40

	327085	2.50	12.57
	327130	5.38	8.04
	327156	3.74	6.58
5	327220	1.28	1.54
	327224	6.56	12.91
	327288	2.61	5.40
	327321	2.42	3.11
	327332	6.62	10.58
10	327361	2.69	4.41
	327377	2.04	6.72
	327396	2.61	4.50
	327414	1.00	8.01
	327442	5.91	9.85
15	327467	6.58	18.01
	327473	3.79	7.48
	327483	4.08	8.87
	327562	0.68	2.86
	327568	1.00	2.00
20	327608	2.08	3.61
	327611	5.90	14.26
	327642	4.08	8.74
	327654	1.05	2.08
	327734	1.00	1.00
25	327775	1.46	11.79
	327796	3.47	5.65
	327840	3.28	6.64
	327940	6.84	15.58
	327984	0.36	1.50
30	328004	1.87	1.42
	328021	0.42	0.59
	328068	2.83	4.68
	328100	3.04	5.39
	328101	3.54	5.20
35	328113	0.72	0.91
	328157	5.58	5.16
	328196	5.76	11.13
	328197	5.98	10.58
	328264	3.11	4.88
40	328299	2.20	3.06
	328342	1.49	1.94
	328365	1.00	1.00
	328369	4.40	7.36
	328381	1.86	4.93
45	328451	5.51	7.56
	328481	0.13	0.72
	328500	2.71	3.97
	328530	5.41	7.62
	328600	3.14	10.68
50	328608	4.56	8.17
	328616	2.24	11.91
	328623	3.04	5.46
	328632	0.70	1.19
	328664	3.48	6.80
55	328666	10.42	26.47
	328698	9.68	14.56
	328700	2.74	10.22
	328708	0.15	0.57
	328735	6.23	8.91
60	328743	3.62	6.54
	328808	0.22	0.78
	328861	3.68	10.54
	328908	5.42	16.36
	328933	2.02	5.29
65	328934	1.73	4.45
	328949	3.34	5.41
	329005	2.88	7.26
	329011	2.52	3.72
	329033	1.00	1.03
70	329037	5.07	8.16
	329067	1.98	2.41
	329134	2.24	3.25
	329157	2.30	11.04
	329178	2.64	5.02
75	329192	6.41	15.27
	329194	0.31	0.79
	329204	1.60	3.75
	329224	2.99	8.11
	329228	0.83	0.83
80	329288	0.63	1.01
	329337	1.00	1.00
	329541	0.76	1.68
	329560	1.34	2.02
	329588	1.68	2.22
85	329643	4.18	11.77
	329703	1.00	1.00

	329764			5.78	15.50	
	329816			2.09	5.44	
	329860			3.13	10.77	
	329993			7.83	14.21	
5	330020			5.58	13.12	
	330036			3.32	5.57	
	330052			4.31	7.97	
	330085			1.34	1.76	
	330088			4.70	12.46	
10	330093			0.44	1.06	
	330100			3.47	4.83	
	330106			2.14	3.61	
	330107			3.17	6.87	
	330120			5.61	11.89	
15	330123			4.50	12.74	
	330208			1.55	7.62	
	330283			13.10	23.38	
	330300			2.81	4.98	
	330313			3.00	4.41	
20	330366			0.67	0.76	
	330372			4.76	11.82	
	330385	AA449749	Hs.182971	karyopherin alpha 5 (Importin alpha 5)	2.14	2.15
	330397	D14659	Hs.154387	KIAA0103 gene product	0.40	1.15
	330468	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.11	0.94
25	330472	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.67	1.17
	330478	L38486	Hs.295049	microfibrillar-associated protein 4	0.46	1.07
	330493	M27826	Hs.267319	endogenous retroviral protease	1.07	0.95
	330495	M31328	Hs.71642	guanine nucleotide binding protein (G pr	0.97	0.96
	330506	M61906	Hs.6241	phosphoinositide-3-kinase, regulatory su	0.17	3.66
30	330512	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	0.60	1.06
	330537	U19765	Hs.2110	zinc finger protein 9 (a cellular retrov	2.81	2.07
	330547	U32989	Hs.183671	tryptophan 2,3-dioxygenase	3.91	1.49
	330551	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	1.15	1.03
	330568	U56244		(NONE)	2.83	4.79
35	330599	U90437		gb:Human RP1 homolog mRNA, 3'UTR region	2.08	1.54
	330601	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	0.89	1.35
	330605	X02419	Hs.77274	plasminogen activator, urokinase	1.87	1.55
	330609	X04741	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.83	1.30
40	330617	X53587	Hs.85266	integrin, beta 4	1.54	1.15
	330630	X78669	Hs.79088	reticulocalbin 2, EF-hand calcium bindin	1.39	1.19
	330644	Y07755	Hs.38991	S100 calcium-binding protein A2	3.83	1.13
	330650	Z68228	Hs.2340	junction plakoglobin	1.25	0.95
	330660	AA347868	Hs.139293	ESTs, Weakly similar to ALU7_HUMAN ALU S	15.50	29.07
	330692	AA017045	Hs.6702	ESTs	1.00	1.00
45	330707	AA133891	Hs.293690	ESTs	0.20	1.35
	330715	AA233707	Hs.11571	Homo sapiens cDNA FLJ11570 fis, clone HE	0.12	1.40
	330717	AA233926	Hs.52620	Integrin, beta 8	6.62	5.42
	330722	AA243560	Hs.34382	ESTs	1.40	1.65
50	330740	AA297746	Hs.22854	Homo sapiens voltage-gated sodium channe	0.27	2.04
	330742	AA400979	Hs.25691	receptor (calcitonin) activity modifying	0.44	0.90
	330744	AA408142	Hs.12393	dTDP-D-glucose 4,6-dehydratase	0.71	3.23
	330751	AA428286	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.66	1.52
	330760	AA448663	Hs.30469	ESTs	0.52	0.90
55	330763	AA450200	Hs.274337	hypothetical protein FLJ20666	0.37	0.97
	330786	D60374	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	0.78	0.84
	330790	T48536	Hs.105807	ESTs	0.23	3.17
	330814	AA015730	Hs.266398	ESTs, Weakly similar to transformation-r	0.37	2.07
	330827	AA040332	Hs.12744	ESTs	1.60	1.00
60	330844	AA063037	Hs.66803	ESTs	0.93	1.16
	330901	AA157818	Hs.267319	endogenous retroviral protease	1.02	1.03
	330931	F01443	Hs.284256	hypothetical protein FLJ14033 similar to	0.24	0.88
	330952	H02855	Hs.29567	ESTs	0.08	1.31
	330961	H10998	Hs.7164	a disintegrin and metalloproteinase doma	1.29	1.26
65	330968	H16568	Hs.23748	ESTs	0.48	0.96
	331014	H98597	Hs.30340	hypothetical protein KIAA1165	0.29	0.74
	331046	N66563	Hs.191358	ESTs	0.99	8.56
	331060	N75081	Hs.157148	Homo sapiens cDNA FLJ11883 fis, clone HE	1.24	1.00
	331099	R36671	Hs.83937	hypothetical protein	0.76	1.03
70	331108	R41408	Hs.21983	ESTs	1.00	2.75
	331131	R54797		gb:yg87b07.s1 Soares Infant brain 1N1B H	6.04	10.68
	331135	R61398	Hs.4197	ESTs	0.80	0.96
	331170	T23461	Hs.159293	ESTs	2.63	4.29
	331180	T32446	Hs.6640	Human DNA sequence from PAC 75N13 on chr	1.78	2.71
75	331183	T40769	Hs.8469	ESTs	1.00	3.01
	331203	T82310		(NONE)	1.70	3.80
	331271	AA059347	Hs.82226	glycoprotein (transmembrane) nmb	1.20	3.19
	331306	AA252079	Hs.63931	dachshund (Drosophila) homolog	0.31	1.30
	331327	AA281076	Hs.109221	ESTs	2.09	2.41
80	331341	AA303125	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	0.72	2.43
	331359	AA416979	Hs.46901	KIAA1462 protein	0.09	0.91
	331363	AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	1.02	0.87
	331378	AA448881	Hs.49282	hypothetical protein FLJ11088	1.03	1.23
	331384	AA456001	Hs.93847	NADPH oxidase 4	1.40	1.00
85	331402	AA505135	Hs.44037	ESTs	1.80	3.93
	331422	F10802	Hs.163628	ESTs, Moderately similar to ALU7_HUMAN	1.65	1.89

	331490	N32912	Hs.26813	CDA14	2.48	1.73
	331531	N51343		gb:yz15g04.s1 Soares_multiple_sclerosi	0.98	1.68
	331547	N54811		gb:od74f04.s1 NCI_CGAP_Ov2 Homo sapiens	3.80	5.75
5	331578	N67960	Hs.248989	ESTs	0.11	0.67
	331589	N71027	Hs.152618	ESTs	1.09	1.38
	331608	N89861	Hs.112110	PTD007 protein	0.93	0.76
	331614	N92293	Hs.240272	EST	0.17	1.34
	331668	W69707	Hs.58030	EST	2.24	3.82
10	331671	W72033	Hs.194695	ras homolog gene family, member I	1.00	1.24
	331676	W79834	Hs.58559	ESTs, Weakly similar to rhotekin [M.musc	0.08	1.07
	331681	W85712	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	8.72	4.27
	331692	W93592	Hs.152213	wingless-type MMTV Integration site fami	0.94	0.54
	331717	AA190888	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	1.57	1.34
15	331718	AA191404	Hs.104072	ESTs	6.80	11.77
	331811	AA404500	Hs.301570	ESTs	1.10	1.00
	331820	AA405970	Hs.97996	transcription termination factor, mitoc	0.73	0.59
	331831	AA412031	Hs.97901	EST	2.77	4.08
	331852	AA418988	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	0.23	0.93
20	331943	AA453418	Hs.21275	hypothetical protein FLJ11011	0.36	1.88
	331969	AA460702	Hs.82772	collagen, type XI, alpha 1	1.00	1.00
	331990	AA478102	Hs.139631	ESTs	3.04	3.87
	332002	AA482009	Hs.105104	ESTs	1.19	0.78
	332027	AA489671	Hs.65641	hypothetical protein FLJ20073	1.27	1.03
25	332029	AA489697	Hs.145053	ESTs	0.30	1.62
	332033	AA489840	Hs.251014	EST	2.30	3.70
	332048	AA495019	Hs.201591	ESTs	0.17	0.52
	332071	AA598594	Hs.205293	KIAA1211 protein	1.35	1.23
30	332074	AA599012		gb:ae41e11.s1 Gessler Wilms tumor Homo s	0.19	2.00
	332083	AA600200	Hs.155546	KIAA1080 protein; Golgi-associated, gamm	0.31	1.18
	332085	AA600353	Hs.173933	nuclear factor IIA	0.30	1.50
	332125	AA609861	Hs.312447	ESTs	0.22	0.62
	332177	F10812	Hs.101433	ESTs	8.21	18.03
35	332180	H03348	Hs.7327	claudin 1	2.27	1.57
	332185	H10356	Hs.101689	ESTs	0.09	1.18
	332203	H49388	Hs.317769	EST	8.05	5.02
	332232	N48891	Hs.101915	Stargardt disease 3 (autosomal dominant)	0.78	0.85
	332240	N54803	Hs.324267	ESTs, Weakly similar to putative p150 (0.96	1.23
	332261	N70294	Hs.269137	ESTs	2.40	3.74
40	332275	R08838	Hs.26530	serum deprivation response (phosphatidyl	0.27	0.75
	332280	R38100	Hs.148381	RNA binding motif protein, X chromosome	0.39	1.88
	332299	R69250	Hs.21201	nectin 3; DKFZP566B0846 protein	5.24	12.76
	332304	R74041	Hs.101539	ESTs	1.44	3.18
	332314	T25862	Hs.101774	hypothetical protein FLJ23045	0.68	1.32
45	332384	M11433	Hs.101850	retinol-binding protein 1, cellular	1.71	0.88
	332434	N75542	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	0.43	0.86
	332445	T63781	Hs.111112	ESTs	0.68	1.00
	332453	L00205	Hs.111758	keratin 6A	31.54	1.00
	332458	M33493	Hs.250700	trypsin beta 1	0.51	1.00
50	332504	AA053917	Hs.15108	chromosome 14 open reading frame 1	0.79	1.24
	332525	M17252	Hs.278430	cytochrome P450, subfamily XXIA (steroid	0.98	1.70
	332530	M31682	Hs.1735	Inhibin, beta B (activin AB beta polypep	0.88	0.66
	332535	N20284	Hs.19280	cysteine-rich motor neuron 1	0.22	1.46
	332539	AA412528	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	0.93	1.49
55	332559	M13955	Hs.166189	cytokeratin 2	0.35	1.13
	332563	N92924	Hs.274407	protease, serine, 16 (thymus)	1.00	1.00
	332565	AA234896	Hs.25272	E1A binding protein p300	0.36	1.05
	332594	AA279313	Hs.3239	methy1 CpG binding protein 2 (Rett syndr	0.53	0.59
	332634	S38953	Hs.283750	tenascin XA	0.38	1.16
60	332638	AA283034	Hs.50640	JAK binding protein	1.00	1.70
	332640	AA417152	Hs.5101	protein regulator of cytokinesis 1	6.15	1.16
	332654	AA001296	Hs.288217	hypothetical protein MGC2941	1.50	2.73
	332665	AA223335	Hs.63788	propiolyl Coenzyme A carboxylase, beta p	1.20	0.91
	332692	AA496035	Hs.247926	gap junction protein, alpha 5, 40kD (con	0.17	1.12
65	332716	L00058	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.00	1.44
	332736	L13773	Hs.114765	myeloid/lymphoid or mixed-lineage leukem	1.00	1.81
	332758	X93921	Hs.296938	dual specificity phosphatase 7	0.53	0.78
	332781	AA233258	Hs.247112	hypothetical protein FLJ10902	1.44	1.56
	332792				1.70	1.19
70	332816				1.85	2.47
	332858				1.04	1.57
	332906				3.48	8.04
	332911				1.00	1.00
	332912				1.06	4.40
75	332922				1.00	1.00
	332956				0.42	0.88
	332959				1.96	6.34
	332982				0.56	0.99
	332984				0.30	0.78
80	332998				1.47	2.01
	333058				0.47	1.38
	333097				2.14	3.19
	333121				2.76	3.70
	333122				1.92	1.21
85	333123				1.85	1.39
	333138				0.47	0.52

	333139	1.88	0.84
	333140	0.21	0.64
	333221	1.51	1.11
5	333260	0.75	1.01
	333380	6.68	15.75
	333387	4.56	12.61
	333512	5.05	8.01
	333524	2.28	3.98
10	333585	2.31	1.53
	333603	2.23	1.17
	333604	2.51	1.58
	333618	0.52	0.98
	333627	1.44	1.36
	333628	1.90	1.90
15	333650	1.85	2.10
	333678	1.85	2.35
	333750	2.18	5.67
	333763	1.99	2.60
20	333767	1.02	0.98
	333768	1.78	1.65
	333769	2.15	2.13
	333772	1.46	2.53
	333777	1.00	1.42
25	333846	2.99	4.50
	333884	0.47	0.94
	333887	0.50	1.00
	333891	0.43	0.89
	333892	0.51	0.91
30	333904	0.26	1.13
	333906	0.55	0.98
	333948	1.70	2.15
	333954	0.37	1.09
	333966	8.10	14.30
35	333968	0.63	1.38
	334061	4.24	12.30
	334094	1.30	12.03
	334113	4.55	8.63
	334161	0.82	1.59
40	334183	0.47	0.76
	334187	1.36	3.70
	334219	0.69	1.04
	334222	1.88	1.70
	334223	4.72	3.14
45	334239	0.79	0.62
	334255	0.45	1.10
	334333	1.00	3.56
	334378	3.98	5.76
	334382	1.50	1.31
50	334492	3.59	4.75
	334562	5.94	15.40
	334588	8.14	19.53
	334616	1.55	1.56
	334633	5.16	8.07
55	334648	0.59	2.13
	334787	3.70	7.15
	334866	8.13	10.60
	334891	0.32	1.14
	334933	1.00	3.84
60	334934	4.01	7.43
	334945	1.04	2.98
	334967	0.29	1.14
	334990	1.50	1.39
	335015	5.88	18.65
65	335093	0.55	1.75
	335120	4.31	8.01
	335125	0.38	1.97
	335179	1.24	1.98
	335188	0.46	1.47
70	335211	1.61	1.42
	335288	0.73	0.97
	335289	0.20	0.26
	335361	2.18	1.58
	335379	0.50	0.71
75	335414	3.64	14.94
	335416	2.93	3.98
	335496	0.98	0.91
	335497	1.71	1.92
	335548	1.15	2.40
80	335551	3.22	10.54
	335558	3.42	4.89
	335586	5.50	12.75
	335619	2.99	3.07
	335620	3.80	8.29
85	335621	0.28	0.57
	335682	0.46	1.17

	335686	2.55	3.81
	335755	2.24	1.07
	335784	0.20	0.97
5	335814	1.13	1.48
	335815	2.45	3.51
	335823	1.00	4.16
	335835	0.49	1.70
	335851	1.66	1.39
10	335868	2.98	6.43
	335896	0.98	0.99
	335936	12.10	21.93
	335948	1.00	1.64
	335983	1.00	4.21
	335995	0.37	1.17
15	336021	1.04	0.84
	336034	11.40	23.54
	336038	1.19	1.21
	336066	0.54	1.63
20	336107	0.95	0.70
	336205	3.13	6.29
	336275	3.20	10.10
	336292	2.34	3.09
	336331	1.00	1.00
25	336419	0.65	0.79
	336632	2.33	2.16
	336633	2.55	2.23
	336634	2.19	2.03
	336635	2.69	2.48
30	336636	2.13	1.83
	336637	2.43	2.24
	336638	2.31	2.03
	336659	0.60	1.31
	336675	0.31	1.18
35	336684	1.50	1.14
	336694	4.74	7.10
	336716	4.43	6.37
	336721	2.20	0.74
	336798	1.64	2.14
40	336900	6.14	12.73
	336948	1.00	1.00
	337028	1.30	2.09
	337043	4.01	11.53
	337046	1.67	1.84
45	337054	2.78	7.35
	337128	7.20	16.14
	337162	3.45	6.34
	337183	5.72	11.41
	337184	3.72	5.90
50	337192	1.27	1.06
	337194	1.88	1.68
	337229	0.22	1.03
	337268	1.00	3.31
	337299	3.23	5.14
55	337325	2.76	3.72
	337389	5.80	10.42
	337493	2.06	6.30
	337497	7.88	20.29
	337500	3.80	4.48
60	337549	1.66	2.31
	337603	1.27	8.54
	337605	5.76	7.16
	337671	0.73	0.97
	337755	1.54	0.92
65	337786	5.07	9.73
	337809	6.18	12.87
	337862	3.78	12.97
	337871	2.66	8.16
	337958	0.26	1.34
70	338008	1.48	1.12
	338033	2.38	14.59
	338083	0.65	2.16
	338110	1.00	1.61
	338112	5.86	8.25
75	338145	1.70	1.97
	338148	8.07	18.19
	338158	1.30	4.55
	338161	2.58	3.57
	338179	1.00	1.00
80	338182	3.32	4.63
	338189	1.00	3.34
	338197	0.99	1.69
	338199	4.58	7.62
	338215	6.01	15.85
85	338279	0.53	0.95
	338316	20.58	38.66

	338322	3.23	7.39
	338357	4.10	11.39
	338359	10.12	21.59
5	338366	0.69	1.02
	338374	0.40	1.18
	338414	0.47	1.06
	338418	6.12	13.86
	338469	3.09	5.11
10	338501	6.28	10.32
	338506	6.97	12.41
	338523	3.10	5.84
	338549	1.70	2.70
	338561	0.79	0.81
15	338662	1.72	1.46
	338671	0.17	0.91
	338676	2.10	15.86
	338726	1.20	1.09
	338779	0.12	0.57
20	338804	0.99	1.67
	338836	1.00	1.00
	338871	4.30	9.81
	338872	5.02	12.81
	338879	0.23	1.12
25	338937	6.55	12.26
	338966	1.76	5.42
	338993	1.00	2.40
	339047	5.26	10.81
	339100	5.10	6.88
30	339114	1.00	1.70
	339121	1.00	3.75
	339170	10.36	19.67
	339229	4.08	13.48
	339264	2.64	3.83
35	339293	1.73	1.94

TABLE 8B shows the accession numbers for those Pkeys in Table 8A lacking unigenes/D's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
45	Pkey	CAT number	Accessions
	322044	187363_1	AW340926 AA249063 N86075
50	322060	44320_1	AI341937 AW003063 U34725 AA904742
	321430	42705_1	X57414 X57415
	321467	43034_1	X13075 X13076
	322125	46779_1	R93901 AF075073 R93902
	322166	46861_1	H69434 AF085958 H69846
55	322173	46873_1	H52567 H52567 AF085970 H52164
	322178	46882_1	H56535 AF085980 H56712
	322179	46885_1	H92891 AF085982 H92777
	321577	1615102_1	H84849 H84252 H84260 H86664 H85320
	321587	1615333_1	H95531 H95521 H84529
60	313723	111953_1	AA070412 AA102346 AA081885
	320997	627492_1	H22544 H46842 AI204929
	322278	47271_1	W69304 AF086283 W69200
	321687	218439_1	AA625149 AA313030 AA313052 H97463
65	313883	129439_1	AA665089 AA135130 AA484059 AA102419 AW877765
	322320	47422_1	W79150 AF086419
	322339	814584_1	AI668646 AI734214 W17348
	314648	293660_1	AW979268 AA878419 AA431342 AA431628
	300201	682222_1	AI308300 AI308296
	306897	25196_2	AI093967
70	323155	979809_1	AL120701 AL135041 AL121524
	322527	38927_1	AF147359 T58511 T58560
	322585	473768_2	W88919 W89125
	300362	1574395_1	Z42308 H23514
	322635	82296_1	AA005129 AA679084 AA694399
75	322664	85042_1	AA011522 AA702841 AA011691 AA330797
	315454	380580_1	AI239464 AI239473 AA625812 AI208703
	322687	37372_1	AF074666 AI110759 AF090902
	314852	327472_1	AI903735 AA491283 AI694953 AW976903 AA761362
	307783	697809_1	AI347274 AW844024
80	324072	269032_1	AA381722 AA381829 AW983906 AW983902 AA381242
	300627	221345_1	AA488472 W27363 AA317053 BE082689 AW967036 BE079872
	323505	196389_1	AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481
	316791	403558_1	AA678177 AA677034
	324303	233842_1	AL118754 AA333202 H38001
85	316519	442885_1	AA847835 AA768378
	300926	333127_1	AA504860 AA504911

	324580	328264_1	AA492588 AA492498 AA492571
	301882	275087_1	T78054 T79888 AA398185
	324804	398093_1	AI692552 AI393343 AI800510 AI377711 F24263 AA661876
5	324889	1515978_1	D31010 D30991 D31168 D31166 D31465
	302697	43219_1	AJ001409 AJ001410
	302711	45419_1	LD8442 D51348
	302742	458_39	L12081
	318499	364430_1	T25451 AA585295 AA585305
10	310624	34624_4	U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
	302847	458_105	X98941 X98942 X98943 X98953 X98949
	304122	77271_5	H28966
	303598	270283_1	AA382814 AA402411 AA412355
	311409	837264_1	AI698839 AI909260 AI909259
	312094	797889_1	Z78390 T97427
15	319312	1540116_1	Z45481 F12393 T74437
	319407	1688823_1	R05329 R01555 R08276
	319425	1689571_1	T82930 R02424 T85145
	320007	229683_1	AA336314 T82938 AA327744 AW967388 AA639967 T10753
20	320018	1815987_1	T83263 T85731 T85730
	319484	1691553_1	T91772 R07257 R07098
	318865	1535937_1	H10818 F07831 Z43072
	312220	1671607_1	N74613 T98756 T98589
	319546	243305_1	R09692 R09414 AA346353
25	312389	902067_1	AI863140 W80703 R43474
	319611	1566863_1	H14957 R55522 R11908
	312437	291472_1	BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131 AA528743 AA552874 AA564758 AW063245 AI267534 AW070190 AW893483 AA770330 AA906928 AA906582 AA758746 AA551717 AW063311 AA429538
30	311896	579192_1	AW206447 AI248530 AI084433 AI400976 R16653
	319834	112523_1	AA071267 T65940 T64515 AA071334
	321102	80531_1	AA018306 H38925 AA001221
	321158	410938_1	H79670 H47798 AA700289
	321199	212379_1	N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512 AI334966 W32951 H62656 H53902 R88904 AW835732
35	305528	28832_3	AA769156
	321270	1662057_1	N59537 N78278 R83560
	314126	177666_1	AA226431 AA226569 AA488748
	320714	743644_1	R91883 AI445591
40	306442	AA976899	
	306446	AA977348	
	306458	AA978186	
	306510	AA986546	
	306557	AA994530	
45	306572	AA995686	
	306582	AA996248	
	306656	AI004024	
	306686	AI015615	
	306751	AI032589	
50	308011	AI439473	
	306892	AI092465	
	308106	AI476803	
	308154	AI500600	
	306956	AI125111	
55	306958	AI125152	
	308213	AI557041	
	308216	AI557135	
	308219	AI557246	
	308588	AI718299	
60	308599	AI719893	
	308643	AI745040	
	308673	AI760864	
	308697	AI767143	
	308778	AI811109	
65	308808	AI818289	
	308875	AI832332	
	308886	AI833240	
	308898	AI858845	
	308966	AI870704	
70	308979	AI873111	
	303011	41689_1	AF090405 AF090407 AF090406
	303077	44060_1	AF163305 AF163307 AF163303
	305016	AA626876	
	305034	AA630128	
75	305072	AA641012	
	305148	AA654070	
	305190	AA665955	
	303978	AW513315	
	303990	AW515465	
80	303998	AW516449	
	303999	AW516611	
	305235	AA670480	
	305312	AA700201	
	305413	AA724659	
85	305447	AA737856	
	321244	29327_1	AF088654 AF088656 AF088655

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	305614	AA782866	
	305637	AA806124	
	305639	AA806138	
5	305650	AA807709	
	305690	AA813477	
	305728	AA828209	
	305759	AA835353	
	305792	AA845256	
10	307041	AI144243	
	307091	AI167439	
	307181	AI189251	
	305901	AA872968	
	305910	AA875981	
15	307415	AI242118	
	307426	AI243364	
	307517	AI275055	
	307551	AI281556	
	307581	AI282207	
20	307608	AI290295	
	307691	AI318285	
	307730	AI336092	
	307760	AI342387	
	307764	AI342731	
25	307796	AI350556	
	309045	AI910902	
	309051	AI911975	
	307807	AI351799	
	307808	AI351826	
30	307820	AI355761	
	307852	AI365541	
	309122	AI928178	
	309184	AI937761	
	309177	AI951118	
35	307902	AI380462	
	309299	AW003478	
	309303	AW004823	
	309476	AW129368	
	309532	AW151119	
40	309747	AW264889	
	309769	AW272346	
	309799	AW276964	
	309866	AW299916	
	302679	311853_1	H65022 AA186889
45	309923	AW340684	
	309928	AW341418	
	309931	AW341683	
	309933	AW341936	
	302705	31765_1	U09060 U09061
50	302789	34161_1	AJ245067 AJ245070
	304006	AW517947	
	304024	T03036	
	304026	T03160	
	304028	T03266	
55	304046	T54803	
	304061	T61521	
	304063	T62536	
	302802	34487_1	Y08250 Y08245
	304114	R78946	
60	304155	H68696	
	304203	N56929	
	304234	W81609	
	304348	AA179868	
	304430	AA347682	
	304456	AA411240	
65	304521	AA464716	
	304526	AA476427	
	304607	AA513322	
	304735	AA576453	
	304760	AA580401	
70	306015	AA897116	
	306063	AA906316	
	306065	AA906725	
	306104	AA910956	
	306109	AA911881	
75	306242	AA932805	
	306288	AA936900	
	306396	AA970223	
	330568	NOT_FOUND_entrez	U56244
80	330599	15323_-12	U90437
	331131	genbank_R54797	R54797
	331203	NOT_FOUND_entrez	T82310
	331531	genbank_N51343	N51343
	331547	467396_1	AA828597 N54811
85	332074	genbank_AA599012	AA599012

TABLE 8C shows the genomic position for those Pkeys in Table 8A lacking unigene ID's and accession numbers. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

5	Pkey:	Unique number corresponding to an Eos probaset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
10	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	332792	Dunham, I. et al.	Plus	73381-73768
	332816	Dunham, I. et al.	Plus	359844-360030
15	332906	Dunham, I. et al.	Plus	1923101-1923205
	332911	Dunham, I. et al.	Plus	1961767-1961858
	332912	Dunham, I. et al.	Plus	1962120-1962246
	332922	Dunham, I. et al.	Plus	2009620-2009738
20	332956	Dunham, I. et al.	Plus	2510528-2510558
	332959	Dunham, I. et al.	Plus	2518145-2518213
	333138	Dunham, I. et al.	Plus	3369205-3369323
	333139	Dunham, I. et al.	Plus	3369495-3369571
	333221	Dunham, I. et al.	Plus	3978070-3978187
	333380	Dunham, I. et al.	Plus	4904775-4904846
25	333387	Dunham, I. et al.	Plus	4910935-4910997
	333512	Dunham, I. et al.	Plus	5560510-5560564
	333524	Dunham, I. et al.	Plus	5612620-5612780
	333585	Dunham, I. et al.	Plus	6234778-6234894
30	333618	Dunham, I. et al.	Plus	6562391-6562566
	333627	Dunham, I. et al.	Plus	6620584-6620903
	333628	Dunham, I. et al.	Plus	6629004-6629233
	333650	Dunham, I. et al.	Plus	6796852-6797128
	333678	Dunham, I. et al.	Plus	7068223-7068288
35	333750	Dunham, I. et al.	Plus	7608165-7608234
	333763	Dunham, I. et al.	Plus	7692491-7692630
	333767	Dunham, I. et al.	Plus	7694407-7694623
	333768	Dunham, I. et al.	Plus	7695440-7695697
	333769	Dunham, I. et al.	Plus	7696625-7696707
40	333772	Dunham, I. et al.	Plus	7706773-7706902
	333777	Dunham, I. et al.	Plus	7746805-7746916
	333846	Dunham, I. et al.	Plus	8008623-8008757
	333884	Dunham, I. et al.	Plus	8153960-8154161
	333887	Dunham, I. et al.	Plus	8154882-8155025
45	333891	Dunham, I. et al.	Plus	8156437-8156709
	333892	Dunham, I. et al.	Plus	8156825-8157001
	333948	Dunham, I. et al.	Plus	8583497-8583627
	333954	Dunham, I. et al.	Plus	8563186-8563335
	333966	Dunham, I. et al.	Plus	8655643-8655826
50	333968	Dunham, I. et al.	Plus	8681004-8681241
	334061	Dunham, I. et al.	Plus	9686941-9687077
	334094	Dunham, I. et al.	Plus	9889953-9890105
	334113	Dunham, I. et al.	Plus	10282459-10282597
	334161	Dunham, I. et al.	Plus	10599033-10599180
55	334219	Dunham, I. et al.	Plus	12716160-12716384
	334239	Dunham, I. et al.	Plus	13056569-13056693
	334333	Dunham, I. et al.	Plus	13603544-13603657
	334378	Dunham, I. et al.	Plus	13907239-13907370
	334382	Dunham, I. et al.	Plus	13915866-13916036
60	334562	Dunham, I. et al.	Plus	14987847-14987940
	334588	Dunham, I. et al.	Plus	15032740-15032817
	334616	Dunham, I. et al.	Plus	15176123-15176470
	334633	Dunham, I. et al.	Plus	15333206-15333305
	334866	Dunham, I. et al.	Plus	18872214-18872317
65	334891	Dunham, I. et al.	Plus	19299770-19299944
	334934	Dunham, I. et al.	Plus	20103970-20104058
	335015	Dunham, I. et al.	Plus	20682792-20682945
	335120	Dunham, I. et al.	Plus	21436286-21436384
	335125	Dunham, I. et al.	Plus	21441390-21441471
70	335179	Dunham, I. et al.	Plus	21634405-21634526
	335188	Dunham, I. et al.	Plus	21669118-21669328
	335211	Dunham, I. et al.	Plus	21774611-21774680
	335361	Dunham, I. et al.	Plus	22807292-22807445
	335379	Dunham, I. et al.	Plus	22899306-22899420
75	335414	Dunham, I. et al.	Plus	23235546-23235684
	335416	Dunham, I. et al.	Plus	23237354-23237465
	335496	Dunham, I. et al.	Plus	24164386-24164545
	335497	Dunham, I. et al.	Plus	24167666-24167869
	335558	Dunham, I. et al.	Plus	24740167-24740347
80	335588	Dunham, I. et al.	Plus	24990333-24990497
	335686	Dunham, I. et al.	Plus	25439839-25439920
	335784	Dunham, I. et al.	Plus	25942710-25942792
	335823	Dunham, I. et al.	Plus	26365925-26366004
	335983	Dunham, I. et al.	Plus	27938968-27939070
85	335995	Dunham, I. et al.	Plus	28009044-28009184
	336021	Dunham, I. et al.	Plus	28686482-28686559

	336034	Dunham, I. et al.	Plus	29014404-29014590
	336038	Dunham, I. et al.	Plus	29022953-29023165
	336107	Dunham, I. et al.	Plus	29987731-29987869
5	336632	Dunham, I. et al.	Plus	983890-985629
	336633	Dunham, I. et al.	Plus	985591-986221
	336634	Dunham, I. et al.	Plus	986296-986670
	336635	Dunham, I. et al.	Plus	987908-988364
	336636	Dunham, I. et al.	Plus	988418-989185
10	336637	Dunham, I. et al.	Plus	989276-990813
	336638	Dunham, I. et al.	Plus	991906-993240
	336659	Dunham, I. et al.	Plus	1896402-1896478
	336694	Dunham, I. et al.	Plus	2420546-2420616
	336721	Dunham, I. et al.	Plus	3371522-3371586
15	336900	Dunham, I. et al.	Plus	10236423-10236523
	336948	Dunham, I. et al.	Plus	12692290-12692381
	337028	Dunham, I. et al.	Plus	16644817-16644942
	337054	Dunham, I. et al.	Plus	17821742-17821922
	337162	Dunham, I. et al.	Plus	23478943-23479145
20	337183	Dunham, I. et al.	Plus	23943606-23943696
	337184	Dunham, I. et al.	Plus	23973949-23974016
	337268	Dunham, I. et al.	Plus	28011979-28012034
	337299	Dunham, I. et al.	Plus	29022656-29022775
	337389	Dunham, I. et al.	Plus	31401509-31401579
25	337493	Dunham, I. et al.	Plus	33330760-33330981
	337549	Dunham, I. et al.	Plus	34474472-34474531
	337755	Dunham, I. et al.	Plus	3971764-3971900
	337809	Dunham, I. et al.	Plus	4449069-4449193
	337871	Dunham, I. et al.	Plus	5443027-5443101
30	337958	Dunham, I. et al.	Plus	6969162-6969270
	338008	Dunham, I. et al.	Plus	7697068-7697236
	338033	Dunham, I. et al.	Plus	8092128-8092271
	338110	Dunham, I. et al.	Plus	10384481-10384621
	338112	Dunham, I. et al.	Plus	10391398-10391600
35	338145	Dunham, I. et al.	Plus	11386629-11386692
	338148	Dunham, I. et al.	Plus	11448985-11449085
	338179	Dunham, I. et al.	Plus	12808775-12808833
	338197	Dunham, I. et al.	Plus	13638107-13638181
	338279	Dunham, I. et al.	Plus	16168944-16169091
40	338316	Dunham, I. et al.	Plus	17089711-17089988
	338322	Dunham, I. et al.	Plus	17132477-17132547
	338357	Dunham, I. et al.	Plus	18062184-18062402
	338359	Dunham, I. et al.	Plus	18074402-18074501
	338366	Dunham, I. et al.	Plus	18262026-18262189
45	338374	Dunham, I. et al.	Plus	18371200-18371282
	338414	Dunham, I. et al.	Plus	19345573-19345660
	338418	Dunham, I. et al.	Plus	19435506-19435596
	338501	Dunham, I. et al.	Plus	21244713-21244828
	338506	Dunham, I. et al.	Plus	21221871-21221953
50	338523	Dunham, I. et al.	Plus	21509763-21509864
	338662	Dunham, I. et al.	Plus	24404720-24404899
	338804	Dunham, I. et al.	Plus	27236005-27236108
	338836	Dunham, I. et al.	Plus	27792166-27792272
	338879	Dunham, I. et al.	Plus	28410653-28410734
55	338937	Dunham, I. et al.	Plus	29160655-29160725
	338993	Dunham, I. et al.	Plus	30077787-30078184
	339047	Dunham, I. et al.	Plus	30760793-30760968
	339100	Dunham, I. et al.	Plus	31141580-31141765
	339114	Dunham, I. et al.	Plus	31456454-31456519
60	339121	Dunham, I. et al.	Plus	31583467-31583536
	339170	Dunham, I. et al.	Plus	32216399-32216527
	339293	Dunham, I. et al.	Plus	33223671-33223819
	332858	Dunham, I. et al.	Minus	1339607-1339397
	332982	Dunham, I. et al.	Minus	2628296-2628109
65	332984	Dunham, I. et al.	Minus	2632606-2632457
	332998	Dunham, I. et al.	Minus	2711704-2711565
	333058	Dunham, I. et al.	Minus	3028925-3028811
	333097	Dunham, I. et al.	Minus	3204124-3204036
	333121	Dunham, I. et al.	Minus	3308446-3308358
70	333122	Dunham, I. et al.	Minus	3309596-3309531
	333123	Dunham, I. et al.	Minus	3310817-3310749
	333140	Dunham, I. et al.	Minus	3377220-3376309
	333260	Dunham, I. et al.	Minus	4308400-4308304
	333603	Dunham, I. et al.	Minus	6466335-6466727
75	333604	Dunham, I. et al.	Minus	6467090-6466768
	333904	Dunham, I. et al.	Minus	8217374-8217261
	333906	Dunham, I. et al.	Minus	8218238-8218063
	334183	Dunham, I. et al.	Minus	11832582-11832508
	334187	Dunham, I. et al.	Minus	11921456-11921205
80	334222	Dunham, I. et al.	Minus	12732417-12732289
	334223	Dunham, I. et al.	Minus	12734365-12734269
	334255	Dunham, I. et al.	Minus	13200776-13200692
	334492	Dunham, I. et al.	Minus	14478333-14478172
	334648	Dunham, I. et al.	Minus	15363301-15363222
85	334787	Dunham, I. et al.	Minus	16299093-16298937
	334933	Dunham, I. et al.	Minus	20078117-20077991

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	334945	Dunham, I. et.al.	Minus	20138885-20138637
	334967	Dunham, I. et.al.	Minus	20173311-20173218
	334990	Dunham, I. et.al.	Minus	20341159-20341087
5	335093	Dunham, I. et.al.	Minus	21297367-21297214
	335288	Dunham, I. et.al.	Minus	22304275-22303770
	335289	Dunham, I. et.al.	Minus	22305950-22305708
	335548	Dunham, I. et.al.	Minus	24662773-24662673
	335551	Dunham, I. et.al.	Minus	24679828-24678961
10	335619	Dunham, I. et.al.	Minus	25082677-25082498
	335620	Dunham, I. et.al.	Minus	25092561-25092434
	335621	Dunham, I. et.al.	Minus	25098878-25098767
	335682	Dunham, I. et.al.	Minus	25421215-25421093
	335755	Dunham, I. et.al.	Minus	25763806-25763747
15	335814	Dunham, I. et.al.	Minus	26320043-26319845
	335815	Dunham, I. et.al.	Minus	26320518-26320421
	335835	Dunham, I. et.al.	Minus	26393311-26393245
	335851	Dunham, I. et.al.	Minus	26604863-26604742
	335868	Dunham, I. et.al.	Minus	26711437-26711300
20	335896	Dunham, I. et.al.	Minus	26977639-26977558
	335936	Dunham, I. et.al.	Minus	27360474-27360400
	335948	Dunham, I. et.al.	Minus	27555924-27555788
	336066	Dunham, I. et.al.	Minus	29241080-29240842
	336205	Dunham, I. et.al.	Minus	30477456-30477311
25	336275	Dunham, I. et.al.	Minus	32086675-32086536
	336292	Dunham, I. et.al.	Minus	32818035-32817927
	336331	Dunham, I. et.al.	Minus	33594527-33594371
	336419	Dunham, I. et.al.	Minus	34052568-34052445
	336675	Dunham, I. et.al.	Minus	2020758-2020664
30	336684	Dunham, I. et.al.	Minus	2158060-2157993
	336716	Dunham, I. et.al.	Minus	3259952-3259862
	336798	Dunham, I. et.al.	Minus	5888954-5888757
	337043	Dunham, I. et.al.	Minus	17407330-17407251
	337046	Dunham, I. et.al.	Minus	17610892-17610821
35	337128	Dunham, I. et.al.	Minus	22215251-22216034
	337192	Dunham, I. et.al.	Minus	24591853-24591771
	337194	Dunham, I. et.al.	Minus	24610510-24610359
	337229	Dunham, I. et.al.	Minus	26716579-26716481
	337325	Dunham, I. et.al.	Minus	30015948-30015800
40	337497	Dunham, I. et.al.	Minus	33371317-33371258
	337500	Dunham, I. et.al.	Minus	33376212-33376158
	337603	Dunham, I. et.al.	Minus	1299296-1299194
	337605	Dunham, I. et.al.	Minus	1346555-1346397
	337671	Dunham, I. et.al.	Minus	3260634-3260547
45	337786	Dunham, I. et.al.	Minus	4133203-4133081
	337862	Dunham, I. et.al.	Minus	5347658-5347550
	338083	Dunham, I. et.al.	Minus	9318438-9318301
	338158	Dunham, I. et.al.	Minus	11794465-11794343
	338181	Dunham, I. et.al.	Minus	12124716-12124658
50	338182	Dunham, I. et.al.	Minus	12824919-12824827
	338189	Dunham, I. et.al.	Minus	12878594-12878478
	338199	Dunham, I. et.al.	Minus	13760865-13760780
	338215	Dunham, I. et.al.	Minus	14055447-14055355
	338469	Dunham, I. et.al.	Minus	20520387-20520242
55	338549	Dunham, I. et.al.	Minus	22049171-22049081
	338561	Dunham, I. et.al.	Minus	22311966-22311856
	338671	Dunham, I. et.al.	Minus	24508421-24508346
	338676	Dunham, I. et.al.	Minus	24637427-24637369
	338726	Dunham, I. et.al.	Minus	25926206-25925618
50	338779	Dunham, I. et.al.	Minus	27030151-27029795
	338871	Dunham, I. et.al.	Minus	28301708-28301611
	338872	Dunham, I. et.al.	Minus	28300921-28300790
	338968	Dunham, I. et.al.	Minus	29614876-29614749
	339229	Dunham, I. et.al.	Minus	32722330-32722199
55	339264	Dunham, I. et.al.	Minus	32975145-32975053
	325228	6381940 Plus	2630-2694	
	325235	6381943 Minus	162154-162264	
	329588	3962484 Plus	1169-1819	
	329560	3962491 Plus	2095-2990	
70	329541	3983503 Minus	2765-3059	
	325328	5866875 Plus	86780-86854	
	325340	6017033 Minus	166656-166819	
	325373	5866920 Minus	1136686-1136777	
	325367	5866920 Minus	922881-922958	
	325389	5866921 Plus	239672-239759	
75	325436	5866939 Minus	29778-29907	
	325498	5866967 Plus	173372-173930	
	325471	6017034 Minus	289268-289342	
	325557	6056302 Plus	50921-51050	
30	325559	6249595 Minus	118590-119172	
	325560	6249595 Minus	133794-133981	
	325569	6249599 Plus	79927-80217	
	325587	6682462 Plus	126724-126967	
	325585	6682462 Plus	73476-73574	
35	325597	5866992 Plus	1065020-1065089	
	325639	5867002 Plus	253525-253608	

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	325739	5867038	Minus	205138-205269
	325740	5867038	Minus	207533-207690
	325792	6469828	Minus	1018-1176
5	325735	6552447	Minus	269122-269190
	325685	6682468	Plus	117397-117483
	325686	6682468	Plus	118337-118439
	325819	6682490	Minus	130314-130370
	329764	6048195	Minus	109733-109968
10	329703	6065793	Minus	139994-140138
	326643	6448539	Plus	53403-53537
	329816	6624888	Minus	70296-70423
	329860	6687260	Minus	163474-163605
	325883	5867087	Plus	22498-22663
15	325895	5867097	Plus	358317-358476
	325925	5867124	Plus	115749-115962
	325932	5867127	Plus	7369-7441
	325941	5867133	Minus	64228-64402
	325969	5867153	Plus	101911-102081
20	325971	5867153	Plus	105841-106035
	329993	4567166	Minus	101307-101434
	330020	6671887	Plus	172397-172491
	326163	5867168	Minus	7831-8035
	326274	5867171	Minus	410289-410404
25	326025	5867176	Plus	70854-70915
	326046	5867182	Minus	62668-62825
	326099	5867186	Minus	661381-661510
	326108	5867187	Minus	23784-23903
	326165	5867208	Minus	62787-62929
30	326189	5867212	Plus	69288-69413
	326204	5867218	Minus	148088-148200
	326230	5867230	Minus	301868-301972
	330052	4567182	Plus	352560-352963
	330036	6042048	Plus	117120-117216
35	326360	5867293	Plus	13627-13844
	326589	5867320	Plus	22760-22919
	326393	5867341	Plus	41702-41841
	326505	5867435	Minus	8818-8949
	326515	5867439	Plus	36683-36809
40	326592	6138928	Plus	23689-23828
	330107	6015249	Minus	100091-100282
	330106	6015249	Minus	99443-99778
	330100	6015253	Plus	21166-21301
	330093	6015278	Plus	1043-1199
45	330088	6015293	Plus	37517-37638
	330085	6015302	Minus	59613-59770
	330120	6671864	Minus	127553-127656
	330123	6671869	Minus	35311-35406
	326742	5867611	Minus	95187-95248
50	326605	5867637	Plus	24656-24749
	326818	6117831	Minus	15199-15309
	326720	6552456	Plus	84525-84677
	326770	6598307	Minus	513603-513668
	326692	6682502	Plus	117697-117899
55	326693	6682502	Minus	335002-335095
	326983	5867657	Minus	16023-16581
	326991	5867660	Plus	18147-18339
	326936	6004446	Minus	10217-10357
	326964	6469836	Plus	75340-75456
60	327040	6531965	Plus	783670-783817
	327053	6531965	Plus	2247267-2247437
	327075	6531965	Plus	4041318-4041431
	327085	6531965	Plus	4734947-4735069
	327036	6531965	Plus	319951-320040
	327130	6531976	Plus	20247-22343
65	327156	5866841	Minus	2462-2620
	327288	5867481	Plus	48583-48773
	327332	5867516	Minus	56361-56532
	327220	5867525	Minus	65701-65781
70	327224	5867534	Plus	188468-188544
	327321	6249562	Minus	99745-99836
	327361	6552412	Minus	61013-62130
	327396	5867743	Plus	8702-8820
	327414	5867750	Plus	102461-102586
75	327442	5867759	Plus	111483-111618
	327467	5867772	Plus	88030-88151
	327473	5867775	Plus	75101-75181
	327483	5867783	Plus	181573-181662
	327377	5867793	Minus	37610-37676
80	327562	5867804	Minus	343989-344474
	327568	5867811	Minus	46152-46287
	327606	6004463	Plus	200262-200495
	327611	5867868	Minus	175063-175392
	327642	5867891	Minus	2513-2743
85	327654	5867910	Minus	97584-97710
	327734	5867940	Minus	31003-31583

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5	327775	5867964	Minus	130791-130871
	327796	5867982	Plus	85267-85405
	327840	6249578	Minus	73065-73206
	330208	6013599	Plus	66517-66931
	330263	6671884	Minus	101503-101634
10	328004	5867993	Minus	157407-157887
	328101	5868020	Plus	289920-290014
	328100	5868020	Minus	263545-263635
	328113	5868024	Minus	80378-80491
	328157	5868064	Plus	73326-73615
15	328196	5868080	Minus	16551-16729
	328197	5868081	Minus	42133-42438
	327940	5868197	Minus	95240-95428
	327984	5868216	Plus	66611-66677
	328021	5902482	Plus	713478-714590
20	328068	6117819	Plus	253903-254022
	328264	6381912	Plus	55086-55404
	330300	2905862	Minus	3246-3302
	328608	5868222	Minus	87770-87953
	328600	5868229	Minus	38889-40010
25	328616	5868239	Plus	293920-294224
	328623	5868246	Minus	120020-120126
	328632	5868247	Plus	76734-76853
	328666	5868254	Minus	778-901
	328698	5868264	Minus	625555-625633
30	328700	5868264	Plus	764089-764203
	328708	5868271	Minus	68114-68854
	328735	5868289	Plus	89389-89455
	328743	5868289	Plus	274838-274726
	328806	5868324	Plus	29408-29684
35	328299	5868366	Minus	149708-149889
	328342	5868383	Plus	59955-60094
	328365	5868387	Minus	270724-270798
	328369	5868388	Plus	75371-75583
	328381	5868392	Plus	662758-662848
40	328451	5868425	Minus	217275-217336
	328481	5868449	Minus	8987-9180
	328500	5868464	Plus	59098-59481
	328530	5868482	Plus	334973-335408
	328664	6004473	Plus	1193739-1193866
45	328861	6381928	Minus	108317-108403
	328908	5868493	Plus	117002-117059
	328933	5868500	Plus	771765-771889
	328934	5868500	Plus	846342-846448
	328949	6456765	Minus	43552-43619
50	330313	6042030	Minus	33642-33775
	329005	5868542	Plus	85470-85673
	330366	2944106	Plus	151837-151914
	330372	6580495	Minus	317461-317688
	329033	5868561	Minus	5390-5479
55	329037	5868562	Minus	32466-32582
	329067	5868591	Minus	146417-147652
	329134	5868679	Plus	29959-30018
	329157	5868687	Minus	145940-146155
	329178	5868704	Plus	179177-179463
60	329192	5868716	Plus	166936-167020
	329194	5868716	Minus	304450-304559
	329204	5868720	Minus	3050-3190
	329224	5868728	Plus	27422-27664
	329228	5868728	Minus	50118-50287
	329288	5868771	Plus	25554-26299
	329337	5868806	Minus	467155-467222
	329011	6682532	Plus	48658-48741

TABLE 9A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer

Table 9A shows about 1312 genes up-regulated in lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) relative to normal body tissues. These genes were selected from about 59680 probesets on the Eos/Arraymetrix Hu03 Genechip array.

Table 9B show the accession numbers for those Pkey's lacking UnigeneID's for table 9A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 9C show the genomic positioning for those Pkey's lacking UnigeneID's and accession numbers in table 9A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
400195			NM_007057*:Homo sapiens ZW10 interactor	1.00	1.00
400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	15.80	396.00
400220			Eos Control	2.28	2.84
400277			Eos Control	7.68	9.72
400285			Eos Control	1.00	1.00
400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.04	2.24
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.86	74.00
400301	X03835	Hs.1657	estrogen receptor 1	1.00	1.00
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.75	1.65
400328	X87344	Hs.180062	transporter 2, ATP-binding cassette, sub	0.87	1.80
400419	AF084545		Target	155.55	253.00
400512			NM_030878*:Homo sapiens cytochrome P450,	1.00	2.00
400517	AF242388		lengsin	3.67	87.00
400560			NM_030878*:Homo sapiens cytochrome P450,	1.00	1.00
400664			NM_002425:Homo sapiens matrix metallopro	20.26	45.00
400665			NM_002425:Homo sapiens matrix metallopro	1.36	1.07
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
400749			NM_003105*:Homo sapiens sortilin-related	1.00	91.00
400763			Target Exon	7.63	24.00
401027			Target Exon	1.00	1.00
401093			C12000586*:g 6330167 dbj BAA86477.1 (A	1.00	155.00
401203			Target Exon	1.00	86.00
401212			C12000457*:g 7512178 pir T30337 polypr	1.00	400.00
401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	1.00	72.00
401435			C14000397*:g 7499898 pir T33295 hypo	1.00	64.00
401464	AF039241		histone deacetylase 5	3.82	49.00
401714			ENSP00000241802*:CDNA FLJ11007 FIS, CLON	2.02	40.00
401747			Homo sapiens keratin 17 (KRT17)	128.43	68.00
401760			Target Exon	1.74	35.00
401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13	2.70
401797			Target Exon	1.44	2.10
401961			NM_021626:Homo sapiens serine carboxypep	1.41	1.86
401985	AF053004		class I cytokine receptor	1.00	177.00
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
402260			NM_001436*:Homo sapiens fibrillarin (FBL	1.58	1.39
402265			Target Exon	2.09	35.00
402297			Target Exon	1.00	92.00
402408			NM_030920*:Homo sapiens hypothetical pro	28.87	13.00
402420			C1000823*:g 10432400 emb CAC10290.1 (A	1.00	1.44
402674			Target Exon	7.44	243.00
402802			NM_001397:Homo sapiens endothelin conver	1.00	70.00
402994			NM_002463*:Homo sapiens myxovirus (influ	1.37	1.43
403137			NM_005381*:Homo sapiens nucleolin (NCL),	1.00	19.00
403306	NM_006825		transmembrane protein (63kD), endoplasmic	1.00	43.00
403329			Target Exon	1.00	61.00
403381			ENSP00000231844*:Ecotropic virus integra	1.00	119.00
403478			NM_022342:Homo sapiens kinesin protein 9	28.13	136.00
403485			C3001813*:g 12737279 ref XP_012163.1 k	20.23	76.00
403627			Target Exon	6.30	29.33
403715			Target Exon	1.30	35.00
404044			ENSP00000237855*:DJ398G3.2 (NOVEL PROTEI	1.00	54.00
404076			NM_016020*:Homo sapiens CGI-75 protein (14.29	91.00
404101			C8000950*:g 423560 pir A47318 RNA-bind	1.00	1.00
404140			NM_006510:Homo sapiens ret finger protei	1.42	1.44
404165			ENSP00000244562*:NRH dehydrogenase [quino	1.00	54.00
404185			Target Exon	1.00	117.00
404210			NM_005936:Homo sapiens myeloid/lymphoid	5.93	13.77
404253			NM_021058*:Homo sapiens H2B histone fami	1.00	1.00

	404287		C6001909:gi 704441 db BAA18909.1 (D298	29.71	42.00
	404298		C6001238*:gi 121715 sp P26697 GTA3_CHICK	1.30	1.00
	404347		Target Exon	1.00	1.00
5	404440		NM_021048:Homo sapiens melanoma antigen,	1.00	15.00
	404721		NM_005596*:Homo sapiens nuclear factor I	1.00	60.00
	404794	NM_000078	cholesterol ester transfer protein, plas	1.07	1.38
	404854		Target Exon	1.61	2.01
	404877		NM_005365:Homo sapiens melanoma antigen,	1.00	1.00
10	404927		Target Exon	1.00	1.00
	404996		Target Exon	1.00	1.00
	405449		CY000047*:gi 11427234 ref XP_009399.1 z	1.00	1.00
	405568		NM_031413*:Homo sapiens cat eye syndrome	1.00	78.00
	405572		Target Exon	0.76	1.14
15	405646		C12000200:gi 4557225 ref NP_000005.1 al	1.01	1.28
	405676	BE336714	cytochrome c-1	1.13	2.89
	405770		NM_002362:Homo sapiens melanoma antigen,	45.52	37.00
	405932		C15000305:gi 3806122 gb AAC69198.1 (AF0	1.99	1.99
	406137		NM_000179*:Homo sapiens mutS (E. coli) h	2.77	2.38
20	406360		Target Exon	1.00	35.00
	406399		NM_003122*:Homo sapiens serine protease	1.00	39.00
	406467		Target Exon	1.00	1.00
	406621	X57809	Immunoglobulin lambda locus	1.41	1.74
	406642	AJ245210	gb:Homo sapiens mRNA for immunoglobulin	2.16	3.91
25	406663	U24683	Immunoglobulin heavy constant mu	2.07	2.93
	406671	AA129547	met proto-oncogene (hepatocyte growth fa	15.00	51.00
	406673	M34996	major histocompatibility complex, class	0.98	3.09
	406676	X58399	Human L2-9 transcript of unrearranged Im	1.30	1.53
	406678	U77534	gb:Human clone 1A11 immunoglobulin varia	1.33	1.45
30	406685	M18728	gb:Human nonspecific crossreacting antig	1.46	2.85
	406687	M31126	pregnancy specific beta-1-glycoprotein 9	8.61	8.50
	406690	M29540	carcinoembryonic antigen-related cell ad	226.37	350.00
	406698	X03068	major histocompatibility complex, class	1.01	2.52
	406815	AA833930	tRNA isopentenylpyrophosphate transferas	20.25	32.00
35	406851	AA609784	major histocompatibility complex, class	0.76	1.91
	406964	M21305	gb:Human alpha satellite and satellite 3	38.15	1114.00
	406967	M24349	gb:Human parathyroid hormone-like protei	1.00	1.00
	406974	M57293	gb:Human parathyroid hormone-related pep	1.00	1.00
	407103	AA424881	hypothetical protein MGC13170	1.77	1.10
40	407128	R83312	EST	1.00	1.00
	407137	T97307	gb:ye53h05.s1 Soares fetal liver spleen	142.70	135.00
	407168	R45175	ESTs	2.16	18.00
	407239	AA078350	leukocyte immunoglobulin-like receptor,	1.10	1.57
	407242	M18728	gb:Human nonspecific crossreacting antig	1.12	2.85
45	407244	M10014	fibrinogen, gamma polypeptide	3.24	15.38
	407289	AA135159	Homo sapiens cDNA FLJ12149 fis, clone MA	3.53	3.68
	407300	AA102616	gb:zn43e07.s1 Stratagene HeLa cell s3 93	19.74	73.00
	407366	AF026942	gb:Homo sapiens cig33 mRNA, partial sequ	0.06	8.25
	407378	AA299264	ESTs, Moderately similar to I38022 hypot	1.00	26.00
50	407430	AF169351	gb:Homo sapiens protein tyrosine phospho	1.00	25.00
	407453	AJ132087	gb:Homo sapiens mRNA for axonemal dynein	1.00	75.00
	407577	AW131324	hypothetical protein MGC12538	1.00	1.00
	407634	AW016569	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	111.20	228.00
	407710	AW022727	ESTs	1.00	28.00
55	407720	AB037776	KIAA1355 protein	1.89	1.31
	407746	AK001962	hypothetical protein FLJ11100	1.00	1.00
	407756	AA116021	ubiquitin specific protease 18	4.51	5.00
	407758	D50915	KIAA0125 gene product	1.00	28.00
	407782	AA608956	ESTs, Moderately similar to PURKINJE CEL	0.97	1.14
60	407788	BE514982	S100 calcium-binding protein A2	7.88	3.83
	407790	AI027274	Homo sapiens cDNA FLJ14866 fis, clone PL	3.63	42.00
	407811	AW190902	cysteine knot superfamily 1, BMP antagon	89.96	109.00
	407839	AA045144	ESTs	173.91	108.00
	407944	R34008	desmocollin 2	111.30	70.00
65	408000	L11690	bulbos pemphigoid antigen 1 (230/240kD)	151.17	8.00
	408031	AA081395	Homo sapiens cDNA FLJ10366 fis, clone NT	9.91	93.00
	408063	BE086548	calcineurin-binding protein calcisarcin-1	195.78	231.00
	408070	AW148852	gb:xf05d05.x1 NCI_CGAP_Bm35 Homo sapien	1.00	1.00
	408101	AW968504	CDC2-related protein kinase 7	37.84	61.00
70	408122	AI432652	hypothetical protein FLJ10718	0.85	1.71
	408212	AA297567	hypothetical protein	5.88	7.91
	408243	Y00787	interleukin 8	4.27	9.98
	408349	BE546947	homeo box C10	3.79	3.46
	408353	BE439838	mitochondrial ribosomal protein S17	1.88	1.65
75	408354	AI382803	ESTs	1.00	73.00
	408369	R38438	solute carrier family 15 (H777) transport	1.41	16.50
	408380	AF123050	diubiquitin	15.19	37.22
	408482	NM_000676	adenosine A2b receptor	1.65	1.19
	408522	AI541214	Small proline-rich protein SPRK (human,	1.98	1.24
80	408538	AW381532	ESTs	1.55	1.50
	408545	AW235405	ESTs	1.00	1.00
	408572	AA055611	ESTs, Moderately similar to ALU4_HUMAN A	1.00	44.00
	408633	AW963372	PRO2000 protein	107.16	56.00
	408660	AA525775	ESTs, Moderately similar to PC4259 ferri	1.00	1.00
85	408761	AA057264	ESTs, Weakly similar to (define not ava	52.24	141.00
	408771	AW732573	potassium voltage-gated channel, delayed	3.05	109.00

5	408783	AF192522	Hs.47701	NPC1 (Niemann-Pick disease, type C1, gen	1.02	1.07
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	41.19	61.00
	408805	H69912	Hs.48269	vaccinia related kinase 1	24.67	45.00
	408841	AW438865	Hs.256862	ESTs	1.00	58.00
	408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, deli	1.00	89.00
10	408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
	408992	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.00	1.00
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	3.71	5.50
	409015	BE389387	Hs.49767	NM_004553:Homo sapiens NADH dehydrogenas	1.44	1.24
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.28	5.32
15	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	112.42	195.00
	409077	AA401369	Hs.190721	ESTs	1.00	17.00
	409093	BE243834	Hs.50441	CGI-04 protein	2.02	1.93
	409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	14.87	6.00
20	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitocho	1.00	1.00
	409228	AI654298	Hs.271695	ESTs, Weakly similar to 2109260A B cell	1.22	1.00
	409234	AI879419	Hs.27206	ESTs	1.00	1.00
	409268	AA625304	Hs.187579	ESTs	11.90	23.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
25	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	168.91	35.00
	409404	BE220053	Hs.129056	ESTs	1.00	1.00
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	79.74	96.00
	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	1.45	2.10
	409446	AI581173	Hs.67688	ESTs	1.00	4.00
30	409506	NM_006153	Hs.54589	NCK adaptor protein 1	3.97	28.00
	409522	AA075382		gb:zm87b03.s1 Stratagene ovarian cancer	15.98	141.00
	409582	AA401369	Hs.190721	ESTs	1.00	17.00
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibit	292.12	79.00
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	1.00	82.00
35	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	1.00	1.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	0.12	18.12
	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	20.75	51.00
	409757	NM_001898	Hs.123114	cystatin SN	22.46	15.80
	409866	AW502152		gb:UL-HF-BR0p-ajr-f-11-0-UL.r1 NIH_MGC_5	1.00	1.00
40	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.50	1.09
	409902	AI337658	Hs.156351	ESTs	25.92	50.00
	409935	AW511413	Hs.278025	ESTs	2.83	2.11
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.17	4.01
	409958	NM_001523	Hs.57697	hyaluronan synthase 1	0.91	2.07
45	410001	AB041036	Hs.57771	kallikrein 11	1.04	2.28
	410032	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	1.00	58.00
	410037	AB020725	Hs.58009	KIAA0918 protein	1.00	34.00
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	1.00
	410048	W76467	Hs.58218	proline oxidase homolog	1.03	1.44
50	410076	T05387	Hs.7991	ESTs	1.12	1.50
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	1.00	1.00
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	1.00	1.00
	410193	AJ132592	Hs.59757	zinc finger protein 281	42.01	51.00
55	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.72	1.32
	410309	BE043077	Hs.278153	ESTs	1.00	2.00
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	32.08	75.00
	410348	AW182663	Hs.95469	ESTs	1.00	1.00
	410407	X66839	Hs.63287	carbonic anhydrase IX	1.40	1.11
60	410418	D31382	Hs.63325	transmembrane protease, serine 4	4.30	2.03
	410438	AB037756	Hs.45207	hypothetical protein KIAA1335	1.00	18.00
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.34	1.04
	410555	W27235	Hs.64311	a disintegrin and metalloproteinase doma	23.99	1.41
	410561	BES40255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
65	410681	AW246890	Hs.65425	calbindin 1, (28kD)	10.88	18.92
	410781	AI375672	Hs.165028	ESTs	1.00	57.00
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	1.62	3.78
	411074	X60435	Hs.68137	adenylate cyclase activating polypeptide	1.00	1.15
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	1.58	1.58
70	411152	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	1.00	84.00
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.82	1.45
	411252	AB018549	Hs.69328	MD-2 protein	7.32	12.74
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.44	2.55
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	1.35	2.02
75	411402	BE297855	Hs.69855	NRAS-related gene	1.00	46.00
	411573	AB029000	Hs.70823	KIAA1077 protein	11.40	11.35
	411579	AC005258	Hs.70830	U8 snRNA-associated Sm-like protein LSm7	1.08	1.90
	411617	AA247994	Hs.90063	neurocalcin delta	1.74	2.57
	411732	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.02	1.00
80	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	1.34	2.19
	411789	AF245505	Hs.72157	Adlcan	2.19	2.79
	411800	N39342	Hs.103042	microtubule-associated protein 18	23.34	34.00
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	1.00	8.00
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	2.07	1.64
85	412140	AA219691	Hs.73825	RAB6 interacting, kinesin-like (rabkines	118.48	92.00
	412276	BE262621	Hs.73798	macrophage migration inhibitory factor (1.98	1.49
	412464	T78141	Hs.22826	ESTs, Weakly similar to I55214 salivary	1.16	1.34
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	41.52	84.00
	412537	AL031778		nuclear transcription factor Y, alpha	17.90	55.00

	412659	AW753865	Hs.74376	olfactomedin related ER localized protel	14.65	47.00
	412719	AW016610	Hs.816	ESTs	382.46	128.00
	412723	AA648459	Hs.335951	hypothetical protein AF301222	54.90	1.00
5	412811	H06382		ESTs	1.00	11.00
	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	1.63	1.42
	412863	AA121673	Hs.59757	zinc finger protein 281	17.63	56.00
	412924	BE018422	Hs.75258	H2A histone family, member Y	1.00	22.00
	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	2.19	2.05
10	413011	AW068115	Hs.821	biglycan	1.22	1.88
	413048	M93221	Hs.75182	mannose receptor, C type 1	0.30	6.23
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.43	8.71
	413129	AF292100	Hs.104613	RP42 homolog	4.67	4.77
	413142	M81740	Hs.75212	ornithine decarboxylase 1	1.92	2.59
15	413223	AI732182	Hs.191866	ESTs	5.73	27.00
	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	0.99	1.06
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	1.00	18.00
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.10	1.09
	413281	AA861271	Hs.222024	transcription factor BMAL2	95.94	69.00
20	413364	BE536218	Hs.137516	fidgulin-like 1	1.00	1.00
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	0.95	2.09
	413409	AI638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.00	1.00
	413453	AA129640	Hs.128065	ESTs	1.00	31.00
	413527	BE250788	Hs.179882	hypothetical protein FLJ12443	1.08	1.46
25	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	79.15	114.00
	413573	AI733859	Hs.149089	ESTs	1.00	1.00
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	8.80	10.00
	413597	AW302885	Hs.117183	ESTs	1.00	1.00
	413690	BE157489		gb:RC1-HT0375-120200-011-e06 HT0375 Homo	1.00	1.00
30	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	3.16	2.32
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	2.88	9.52
	413753	U17760	Hs.75517	laminin, beta 3 (niclin (125kD), kallirin	144.10	108.00
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	1.00	17.00
	413833	Z15005	Hs.75573	centromere protein E (312kD)	1.00	1.00
35	413882	AA132973	Hs.184492	ESTs	64.24	148.00
	413926	AA133338	Hs.54310	ESTs	1.00	67.00
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	43.42	42.00
	413995	BE048146	Hs.75671	syntaxin 1A (brain)	1.23	1.11
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	2.02	2.51
40	414142	AW368397	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.00	102.00
	414180	AI863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	6.92	77.00
	414245	BE148072	Hs.75850	WAS protein family, member 1	1.00	1.00
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.00	59.00
	414317	BE263280	Hs.75888	phosphogluconate dehydrogenase	1.52	1.73
45	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	1.78	1.72
	414341	D80004	Hs.75909	KIAA0182 protein	33.90	151.00
	414368	W70171	Hs.75939	uridine monophosphate kinase	171.60	97.00
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.32	1.85
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	226.15	66.00
50	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.64	1.98
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	1.87	72.00
	414675	R79015	Hs.296281	interleukin enhancer binding factor 1	1.51	1.39
	414683	S78296	Hs.76888	hypothetical protein MGC12702	43.61	64.00
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	28.63	71.00
55	414711	AI310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	14.86	42.00
	414718	H95348	Hs.107987	ESTs	1.00	5.00
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	1.64	1.44
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	65.01	74.00
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	130.35	121.00
60	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.24	2.19
	414806	D14694	Hs.77329	phosphatidylserine synthase 1	1.63	1.53
	414809	AI434699	Hs.77358	transferrin receptor (p90, CD71)	1.97	2.60
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.48	10.60
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	103.22	143.00
65	414839	X63692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	1.80	1.69
	414883	AA926960		CDC28 protein kinase 1	14.29	10.06
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.95	2.20
	414914	U49844	Hs.77613	ataxia telangiectasia and Rad3 related	3.00	2.90
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.02	1.21
70	414972	BE263782	Hs.77695	KIAA0008 gene product	1.00	1.00
	415014	AW954064	Hs.24951	ESTs	1.42	2.84
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	34.72	107.00
	415227	AW821113	Hs.72402	ESTs	1.87	49.00
75	415238	R37780	Hs.21422	ESTs	1.00	1.00
	415263	AA948033	Hs.130853	ESTs	1.00	1.00
	415295	R41450	Hs.6546	ESTs	1.00	1.00
	415339	NM_015156	Hs.78398	KIAA0071 protein	51.18	166.00
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	30.84	63.00
80	415674	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,	1.48	1.39
	415709	AA649850	Hs.278558	ESTs	1.00	1.00
	415735	AA704162	Hs.120811	ESTs, Weakly similar to I38022 hypotheti	1.00	72.00
	415799	AA653718	Hs.225841	DKFZP434D193 protein	8.23	31.00
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
85	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	32.51	35.00
	415989	AI267700		ESTs	78.89	1.00

	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	1.00	1.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.35	2.32
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (39.03	3.00
5	416177	AA174069	Hs.187607	ESTs	1.00	9.00
	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.83	3.76
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	9.70	1.00
	416239	AL038450	Hs.48948	ESTs	83.87	129.00
10	416250	AA581386	Hs.73452	hypothetical protein MGC10791	1.96	2.12
	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reductase 1	2.08	1.73
	416423	H54375	Hs.268921	ESTs	1.00	89.00
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	1.28	1.54
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	27.29	67.00
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
15	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.96	5.00
	416722	AA354604	Hs.122546	hypothetical protein FLJ23017	3.68	33.00
	416819	U77735	Hs.80205	pim-2 oncogene	1.59	1.84
	416936	N21352	Hs.42987	ESTs, Weakly similar to S21348 probable	1.00	1.00
	417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
20	417061	AI875944	Hs.188691	Homo sapiens cDNA FLJ12033 fs, clone HE	32.95	156.00
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.91	4.93
	417218	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	1.00	51.00
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	3.38	2.05
	417308	H60720	Hs.81892	KIAA0101 gene product	82.94	25.36
25	417315	AI080042	Hs.180450	ribosomal protein S24	106.61	121.00
	417324	AW265494		ESTs	1.20	1.28
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	8.97	3.27
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.59	1.82
30	417428	N87579	Hs.278871	gb:LL2030F Human fetal heart, Lambda ZAP	1.00	52.00
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	304.75	173.00
	417466	AI681547	Hs.59457	hypothetical protein FLJ22127	1.24	1.34
	417512	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.14	5.50
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.66	1.68
35	417542	J04129	Hs.82269	progesterone-associated endometrial prote	1.28	1.35
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	42.76	51.00
	417715	AW969587	Hs.86366	ESTs	6.35	2.75
	417720	AA205625	Hs.208067	ESTs	113.31	58.00
	417791	AW965339	Hs.111471	ESTs	39.98	16.00
40	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	2.61	31.00
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.35	2.44
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.52	1.11
	417933	X02308	Hs.82962	thymidylate synthetase	4.74	2.55
	417944	AU077186	Hs.82985	collagen, type V, alpha 2	3.61	5.21
45	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	12.49	38.00
	417991	AA731452	Hs.190008	ESTs	1.00	26.00
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.02	2.12
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	187.59	1.00
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.85	2.63
50	418057	NM_012151	Hs.83363	coagulation factor VIII-associated (intr	1.54	1.69
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.82	5.22
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	1.26	1.46
	418203	X54942	Hs.83758	CDC28 protein kinase 2	134.19	144.00
	418207	C14685	Hs.34772	ESTs	1.00	1.00
55	418216	AA662240	Hs.283099	AF15q14 protein	64.66	61.00
	418236	AW994005	Hs.337534	ESTs	18.53	147.00
	418249	H89226	Hs.34892	KIAA1323 protein	30.53	106.00
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	1.00	3.00
	418283	S79895	Hs.83942	cathepsin K (pseudosynostosis)	3.96	5.16
60	418300	AI433074	Hs.86582	Homo sapiens cDNA: FLJ21578 fs, clone C	3.18	2.91
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	11.96	6.68
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	9.23	2.22
	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	1.00	1.00
	418379	AA218940	Hs.137516	fidgellin-like 1	21.68	44.00
65	418397	NM_001269	Hs.84746	chromosome condensation 1	1.00	8.00
	418403	D86978	Hs.84790	KIAA0225 protein	16.91	18.98
	418462	BE001596	Hs.85266	integrin, beta 4	1.56	1.16
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.22	2.38
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.66	2.22
70	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.04	2.21
	418538	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor	1.33	37.00
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.04	1.23
	418574	N28754		M-phase phosphoprotein 9	48.60	85.00
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	18.24	26.00
75	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	1.19	1.41
	418661	NM_001949	Hs.1189	E2F transcription factor 3	29.05	43.00
	418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
	418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
	418686	Z36830	Hs.87268	annexin A8	1.54	1.98
80	418689	AI360883	Hs.274448	hypothetical protein FLJ11029	1.19	1.04
	418712	Z42183		gb:HSC0BF041 normalized infant brain cDN	1.00	12.00
	418727	AA227609	Hs.94834	ESTs	1.00	49.00
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	49.85	1.00
	418819	AA228776	Hs.191721	ESTs	1.00	140.00
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	20.97	23.00
85	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	57.09	35.00

	418971	AA360392	Hs.87113	ESTs	1.00	12.00
	418973	AA233056	Hs.191518	ESTs	4.89	28.00
	419078	M93119	Hs.89584	insulinoma-associated 1	1.00	10.00
5	419079	AW014836	Hs.18844	ESTs	1.09	1.98
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	2.06	1.68
	419088	AI538323	Hs.52620	integrin, beta 8	15.60	51.00
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.11	1.83
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
10	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	1.10	1.14
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	3.18	2.43
	419288	AA256108	Hs.87507	ESTs	1.00	34.00
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	1.00	8.00
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	22.63	54.00
15	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.50	1.98
	419423	D26488	Hs.90315	KIAA0007 protein	1.00	7.00
	419443	D62703		gb:HUM316G10B Clontech human aorta polyA	1.00	12.00
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.84	1.84
20	419474	AW968619	Hs.155849	ESTs	13.63	62.00
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4.27	2.26
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	3.66	3.63
	419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
	419539	AF070590	Hs.90869	Homo sapiens clones 24622 and 24623 mRNA	74.60	117.00
25	419558	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.47	4.98
	419569	AI971651	Hs.91143	Jagged 1 (Alagille syndrome)	1.00	4.00
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	94.30	94.00
	419703	AI793257	Hs.128151	ESTs	15.26	50.00
	419721	NM_001650	Hs.288650	aquaporin 4	1.00	191.00
30	419729	AA586442	Hs.21411	gb:nc053a03.s1 NCI_CGAP_SS1 Homo sapiens	1.00	59.00
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.02	1.08
	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	1.00	1.00
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	29.87	77.00
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	50.99	214.00
35	419938	AI792788		gb:cl91d05.y5 NCI_CGAP_Kd5 Homo sapiens	1.00	1.00
	419937	AB040959	Hs.93836	DKFZP434N014 protein	1.64	2.47
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	15.72	94.00
	420005	AW271106	Hs.133294	ESTs	3.15	1.43
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	12.45	39.00
40	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	1.00	117.00
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.43	1.21
	420251	AW374968	Hs.348112	Human DNA sequence from clone RP5-1103G7	2.35	3.23
	420259	AF004884	Hs.96253	calcium channel, voltage-dependent, P/Q	0.77	1.15
	420281	AI623693	Hs.323494	ESTs	45.04	54.00
45	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	49.22	31.00
	420332	NM_001756	Hs.1305	serine (or cysteine) proteinase inhibitor	0.05	2.82
	420380	AA640891	Hs.102406	ESTs	0.99	2.74
	420462	AF050147	Hs.97832	chondromodulin I precursor	1.00	1.00
	420520	AK001978	Hs.98510	similar to rab11-binding protein	49.74	133.00
50	420552	AK000492	Hs.98808	hypothetical protein	94.65	88.00
	420560	AW207748	Hs.59115	ESTs	1.00	17.00
	420610	AI683183	Hs.99348	distal-less homeo box 5	1.00	13.00
	420689	H79979	Hs.88678	ESTs	50.09	95.00
	420721	AA927802	Hs.159471	ZAP3 protein	1.00	31.00
55	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	1.00	48.00
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
	420900	AL045633	Hs.44269	ESTs	2.24	7.00
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
	421002	AF116030	Hs.100932	transcription factor 17	1.00	27.00
60	421027	AA761198	Hs.55254	ESTs	2.87	38.00
	421037	AI684808	Hs.197653	ESTs	1.00	46.00
	421041	N36914	Hs.14691	ESTs, Moderately similar to I38022 hypot	1.00	98.00
	421073	NM_004689	Hs.101448	metastasis associated 1	1.34	1.46
	421110	AJ250717	Hs.1355	cathepsin E	119.47	427.00
65	421133	AA401369	Hs.190721	ESTs	1.10	17.00
	421150	AI913562	Hs.189902	ESTs	1.45	1.63
	421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.37	1.10
	421316	AA287203	Hs.324728	SMA5	1.00	21.00
70	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.92	3.94
	421451	AA291377	Hs.50831	ESTs	5.89	14.00
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.78
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	1.56	1.08
	421508	NM_004833	Hs.105115	absent in melanoma 2	5.11	5.23
75	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	1.00	3.00
	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	2.63	10.58
	421526	AL080121	Hs.105460	DKFZP564O0823 protein	1.46	1.88
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	30.21	50.32
	421574	AJ000152	Hs.105924	defensin, beta 2	1.67	1.74
80	421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
	421633	AF121860	Hs.106260	sorting nexin 10	1.00	116.00
	421659	NM_014459	Hs.106511	protocadherin 17	0.05	6.33
	421677	H64092	Hs.38282	ESTs	1.31	1.42
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	1.41	1.20
85	421773	W69233	Hs.112457	ESTs	1.12	1.14
	421777	BE562088	Hs.108196	HSPC037 protein	1.97	1.29

	421800	AA298151	Hs.222969	ESTs	1.03	1.30
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.88	1.59
	421896	N62293	Hs.45107	ESTs	11.84	22.80
5	421928	AF013758	Hs.109643	polyadenylate binding protein-Interactin	45.89	90.00
	421931	NM_000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	1.13	1.49
	421948	L42583	Hs.334309	keratin 6A	51.83	20.25
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.17	1.15
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
10	422094	AF129535	Hs.272027	F-box only protein 5	67.61	62.00
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
	422109	S73265	Hs.1473	gastrin-releasing peptide	4.18	95.50
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	40.89	71.00
	422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.13	1.38
15	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	41.59	96.00
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.29	1.68
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	4.93	5.73
	422282	AF019225	Hs.114309	apolipoprotein L	1.49	1.71
20	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	25.99	10.91
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	1.54	1.41
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
	422330	D30783	Hs.115263	epiregulin	1.00	112.00
	422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	9.39	60.00
25	422406	AF025441	Hs.116206	Opa-interacting protein 5	18.33	53.00
	422424	AI186431	Hs.296638	prostate differentiation factor	1.71	3.21
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
	422487	AJ010901	Hs.198287	mucin 4, tracheobronchial	73.68	35.54
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	173.97	28.00
30	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.68	2.92
	422655	AI870435	Hs.1569	LIM homeobox protein 2	1.00	1.00
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	3.89	4.55
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	1.05	1.46
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.88	1.53
35	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	99.56	63.00
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	70.46	61.00
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	77.74	3.00
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	5.88	8.55
40	422963	AA401369	Hs.190721	ESTs	171.41	17.00
	422976	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	2.12	1.62
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	10.49	35.00
	422986	AA319777	Hs.221974	ESTs	12.40	32.47
	423034	AL119930		gb:DKFZp761A092_r1 761 (synonym: hamy2)	16.41	60.00
45	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN H	1.00	1.00
	423081	AF262992	Hs.123159	sperm associated antigen 4	1.82	2.96
	423184	NM_004428	Hs.1624	ephrin-A1	1.14	1.53
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.14	1.69
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	7.18	14.00
50	423309	BE006775	Hs.126782	sushi-repeat protein	21.90	64.00
	423361	AW170055	Hs.47628	ESTs	1.00	1.00
	423453	AW450737	Hs.128791	CGI-09 protein	55.52	66.00
	423511	AF036329	Hs.129715	gonadotropin-releasing hormone 2	0.88	1.17
	423516	AB007933	Hs.129729	ligand of neuronal nitric oxide synthase	1.76	5.40
55	423551	AA327598	Hs.233785	ESTs	3.54	4.33
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	38.88	70.00
	423624	AI807408	Hs.166368	ESTs	1.00	67.00
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
60	423642	AW452650	Hs.157148	hypothetical protein MGC13204	19.14	58.00
	423662	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	3.61	13.57
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	240.73	40.00
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	1.00	59.00
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
65	423761	NM_006194	Hs.132576	paired box gene 9	1.00	1.00
	423787	AJ295745	Hs.236204	nuclear pore complex protein	7.18	6.64
	423816	AF151084		hypothetical protein	1.00	44.00
	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	1.00	1.00
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
70	423887	AL080207	Hs.134585	DKFZP434G232 protein	1.00	1.00
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	31.33	31.00
	423954	AW753164	Hs.288604	KIAA1632 protein	5.81	10.87
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	3.55	3.30
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
75	424016	AW163729	Hs.6140	hypothetical protein MGC15730	0.93	1.01
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	21.30	52.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
	424086	AI351010	Hs.102267	lysyl oxidase	21.91	70.00
	424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
80	424120	T80579	Hs.290270	ESTs	1.00	1.00
	424165	AW582904	Hs.142255	islet amyloid polypeptide	1.00	34.00
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	13.06	48.00
	424279	L29306	Hs.171814	tryptophan hydroxylase (tryptophan 5-mon	1.00	1.00
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	164.58	87.00
85	424326	NM_014479	Hs.145296	disintegrin protease	53.72	302.00
	424340	AA339036	Hs.7033	ESTs	0.88	1.15

	424351	BE622117	Hs.145567	hypothetical protein	0.93	1.03
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	7.02	3.24
	424381	AA285249	Hs.146329	protein kinase Chk2	95.55	92.00
5	424411	NM_005209	Hs.146549	crystallin, beta A2	1.63	3.25
	424420	BE614743	Hs.146688	prostaglandin E synthase	1.63	1.33
	424441	X14850	Hs.147097	H2A histone family, member X	1.82	1.29
	424502	AF242388	Hs.149585	lensin	1.00	1.00
	424503	X06256	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	1.02	2.24
10	424513	BE385864	Hs.149894	mitochondrial translational initiation f	1.00	17.00
	424539	L02911	Hs.150402	Activin A receptor, type 1 (ACVR1) (ALK	32.46	108.00
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.40	2.58
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	31.87	25.00
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.58	2.37
15	424645	NM_014682	Hs.151449	KIAA0535 gene product	1.00	1.00
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.12	2.23
	424717	AW992292	Hs.152213	wingless-type MMTV Integration site fami	1.00	1.00
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.65	1.30
	424867	A1024860	Hs.153591	Nol56 (D. melanogaster)-like protein	1.23	1.05
20	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
	424979	D87989	Hs.154073	UDP-galactose transporter related	1.36	1.35
	424999	AW953120		gb:EST365190 MAGE resequences, MAGB Homo	1.24	1.41
	425048	H05468	Hs.164502	ESTs	1.00	11.00
25	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homo	7.46	87.00
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.52	3.82
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.84	4.03
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	3.62	2.73
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	1.00	53.00
30	425234	AW152225	Hs.155909	ESTs, Weakly similar to I38022 hypotheti	100.77	44.00
	425236	AW067800	Hs.155223	stanniocalcin 2	3.30	2.90
	425245	A1751768	Hs.155314	KIAA0095 gene product	1.91	2.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.41	1.49
	425266	J00077	Hs.155421	alpha-fetoprotein	1.00	68.00
35	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	1.97	1.63
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	141.49	123.00
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	1.00	84.00
	425371	D49441	Hs.155981	mesothelin	0.87	1.59
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.90	5.76
40	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00	1.00
	425424	NM_004954	Hs.157199	ELKL motif kinase	10.58	9.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	1.74	1.40
	425568	AW162943	Hs.250618	UL16 binding protein 2	1.49	1.14
	425580	L11144	Hs.1907	galanin	53.29	233.00
45	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	1.00	55.00
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	1.00	10.00
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.00	41.00
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	1.00	48.00
50	425910	A1923627	Hs.31903	ESTs	27.39	98.00
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.99	1.58
	425849	A1077288	Hs.296323	serum/glucocorticoid regulated kinase	71.16	3.42
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.35	1.34
	426067	AA401369	Hs.190721	ESTs	1.01	17.00
55	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	26.26	47.00
	426215	AW067800	Hs.155223	stanniocalcin 2	1.91	2.90
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	22.40	25.00
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	1.00	1.00
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	91.39	229.00
60	426329	AL389951	Hs.271623	nucleoporin 50kD	4.34	4.08
	426427	M85699	Hs.169840	TTK protein kinase	7.02	1.00
	426432	AF001601	Hs.169857	paraoxonase 2	1.16	1.68
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.59	1.71
	426459	AF151812	Hs.169992	hypothetical 43.2 Kd protein	1.56	1.66
65	426471	M22440	Hs.170009	transforming growth factor, alpha	20.60	26.00
	426496	D31765	Hs.170114	KIAA0061 protein	9.81	22.00
	426501	AA401369	Hs.190721	ESTs	19.23	17.00
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	103.74	41.00
	426536	A1949749	Hs.44441	ESTs	4.65	23.00
70	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	1.00	43.00
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	160.08	8.00
	426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	1.51	1.35
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	2.13	1.68
	426752	X69490	Hs.172004	titin	0.02	5.14
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.72	1.71
75	426807	AA385315	Hs.156682	ESTs	1.30	1.64
	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	1.47	1.53
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	1.00	1.00
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrolase	1.51	1.25
80	426897	AA401369	Hs.190721	ESTs	141.56	17.00
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	32.61	38.00
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	2.65	3.16
	426964	AA393739	Hs.287416	Homo sapiens cDNA FLJ11439 fis, clone HE	1.97	3.49
	426966	A1493134		sclerosin	1.00	1.00
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.39	2.28
85	427099	AB032953	Hs.173560	odd Oz1en-m homolog 2 (Drosophila, mous	4.24	17.00

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	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.58	1.05
	427260	AA663848		gb:aa70b06.s1 Stratagene schizo brain S1	1.34	1.60
	427281	AA906147	Hs.102869	ESTs	1.00	66.00
5	427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
	427354	T57896	Hs.191095	ESTs	1.17	1.95
	427356	AW023482	Hs.97849	ESTs	7.31	41.00
	427376	AA401533	Hs.19440	ESTs	1.00	57.00
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.42	1.32
10	427427	AF077345	Hs.177936	lectin, superfamily member 1 (cartilage-	1.00	20.00
	427441	AA412605	Hs.343879	SPANX family, member C	1.00	1.00
	427445	X80818	Hs.178078	glutamate receptor, metabotropic 4	0.97	1.03
	427505	AA361562	Hs.178761	26S proteasome-associated pad1 homolog	4.60	4.04
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	22.00	45.00
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	97.45	92.00
15	427546	AA188763	Hs.36793	hypothetical protein FLJ23188	1.50	3.24
	427562	R56424	Hs.26534	ESTs	6.81	40.00
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	69.91	62.00
	427680	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.70	49.00
	427686	AI791495	Hs.180142	calmodulin-like skin protein	1.37	1.88
20	427688	AA298760	Hs.180191	hypothetical protein FLJ14904	29.55	67.00
	427677	NM_007045	Hs.180296	FGFR1 oncogene partner	3.52	2.63
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.84	70.00
	427719	AI393122	Hs.134726	ESTs	7.03	4.52
25	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.92	1.74
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.76	1.26
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfam	9.63	59.00
	427961	AW293165	Hs.143134	ESTs	41.97	118.00
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	23.82	1.00
30	428023	AL038843		Homo sapiens cDNA: FLJ23602 fis, clone L	1.40	1.33
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	96.28	167.00
	428093	AW594506	Hs.104830	ESTs	1.25	1.29
	428098	AU077258	Hs.182429	protein disulfide isomerase-related prot	1.86	1.60
	428129	AI244311	Hs.26912	ESTs	1.00	42.00
35	428169	AI928984	Hs.182793	golgi phosphoprotein 2	2.76	2.11
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	85.59	181.00
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	8.57	21.64
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.77	15.90
40	428434	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	0.58	1.43
	428450	NM_014791	Hs.184339	KIAA0175 gene product	237.53	204.00
	428471	X57348	Hs.184510	stratifin	6.00	4.60
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	58.54	16.00
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.53	2.15
45	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	1.00	1.00
	428532	AF157326	Hs.184786	TBP-interacting protein	1.00	58.00
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	1.00	1.00
	428698	AA852773	Hs.334838	KIAA1866 protein	187.37	255.00
50	428728	NM_016625	Hs.191381	hypothetical protein	47.24	80.00
	428748	AW593208	Hs.98785	Kap37 protein	1.00	87.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
	428771	AB028992	Hs.193143	KIAA1069 protein	1.98	92.00
	428801	AW277121	Hs.254881	ESTs	1.67	6.15
55	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	1.03	1.27
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	124.17	43.00
	428845	AL157579	Hs.153610	KIAA0751 gene product	1.00	1.00
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	15.16	27.00
	428969	AF120274	Hs.194689	artemin	1.36	1.24
60	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	0.97	3.31
	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	6.82	16.47
	429164	AI688663	Hs.116586	ESTs	19.08	67.00
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
	429183	AB014604	Hs.197955	KIAA0704 protein	79.72	104.00
65	429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.00	1.00
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.33	1.09
	429220	AW207206		ESTs	1.00	7.00
	429228	AI553633	Hs.326447	ESTs	39.47	29.25
	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
70	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
	429278	AF056085	Hs.198612	G protein-coupled receptor 51	3.70	142.00
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.30	1.94
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	94.09	86.00
	429413	NM_014058	Hs.201877	DESC1 protein	41.91	10.00
75	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.19	1.00
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	1.61	1.08
	429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
	429547	AA401369	Hs.190721	ESTs	1.06	17.00
	429551	AW450624	Hs.220931	ESTs	2.89	65.00
80	429563	BE619413	Hs.2437	eukaryotic translation initiation factor	1.49	1.37
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	61.86	100.00
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.78	1.74
	429616	AI982722	Hs.120845	ESTs	1.00	1.00
85	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	1.00	4.00

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	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	69.95	104.00
	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	1.25	1.21
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	1.00	7.00
5	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
	429918	AW873988	Hs.119383	ESTs	1.00	78.00
	429978	AA249027		ribosomal protein S6	1.98	3.09
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	1.00	48.00
	430044	AA464510	Hs.152812	ESTs	69.27	59.00
10	430114	AA847744	Hs.99640	ESTs	1.00	1.00
	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypothe	1.00	51.00
	430147	R60704	Hs.234434	halry/enhancer-of-split related with YRP	1.10	2.22
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	1.00	127.00
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.80	1.47
	430300	U60805	Hs.238648	oncostatin M receptor	1.00	35.00
15	430315	NM_004293	Hs.239147	guanine deaminase	92.31	28.00
	430337	M36707	Hs.239600	calmodulin-like 3	1.18	1.08
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	5.28	66.00
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	16.76	38.00
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.63	1.50
20	430439	AL133561		DKFZP434B061 protein	1.00	1.00
	430451	AA836472	Hs.297939	cathepsin B	1.64	2.12
	430454	AW469011	Hs.105635	ESTs	63.35	44.00
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.47	1.91
	430481	AA479678	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN A	1.00	31.00
25	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
	430508	AI015435	Hs.104637	ESTs	4.75	7.27
	430533	AA480895	Hs.57749	ESTs, Weakly similar to T17288 hypothe	1.00	1.00
	430563	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.00	1.59
	430677	Z26317	Hs.94560	desmoglein 2	1.72	1.30
30	430678	AA401369	Hs.190721	ESTs	0.90	17.00
	430686	NM_001942	Hs.2633	desmoglein 1	1.00	1.00
	430788	AI742925	Hs.7179	ESTs, Weakly similar to 2004399A chromos	1.62	1.84
	430890	X54232	Hs.2699	glypican 1	1.58	1.40
35	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	90.28	132.00
	430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	0.94	1.28
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
	431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
	431092	AI332764	Hs.125757	ESTs	13.48	63.00
40	431124	AF284221	Hs.59506	doublesex and mab-3 related transcriptio	49.43	62.00
	431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	0.44	2.20
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	182.26	101.00
	431221	AW207837	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	4.15	13.97
	431277	AA501806	Hs.345824	ESTs	1.00	86.00
45	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	40.55	200.00
	431342	AW971018	Hs.21659	ESTs	1.00	53.00
	431384	BE158000	Hs.285026	gb:MR2-HT0377-150200-202-e03 HT0377 Homo	0.94	1.14
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.30	1.25
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	3.90	25.00
50	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.41	1.87
	431548	AI834273	Hs.9711	novel protein	5.68	15.00
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	0.99	1.44
	431745	AW972448	Hs.163425	ESTs	0.99	3.51
55	431770	BE221880	Hs.268555	5'-3' exonuclease 2	67.12	91.00
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.36	4.71
	431846	BE019924	Hs.271580	uropod 1B	4.49	2.51
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.20	3.32
	431934	AB031481	Hs.272214	STG protein	1.01	1.04
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	51.17	46.35
60	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	0.94	1.65
	432023	R43020	Hs.236223	EST	0.94	47.00
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	1.10	2.24
	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.42	1.45
	432226	AW182766	Hs.273558	phosphate cytidyltransferase 1, cholin	1.00	1.00
65	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	18.67	1.00
	432265	BE382679	Hs.285753	SCG10-like-protein	1.09	1.21
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	40.98	58.00
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	214.00
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	157.34	37.00
70	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
	432407	AA221036		gb:zr03f12r1 Stratagene NT2 neuronal pr	73.71	75.00
	432441	AW292425	Hs.163484	ESTs	56.35	72.00
	432489	AI804855	Hs.207530	ESTs	1.00	24.00
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	137.72	98.00
75	432552	AI537170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.00	31.00
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	0.27	35.18
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.87	6.22
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	26.63	56.00
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	1.92	5.29
80	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	45.13	31.00
	432753	NM_014076	Hs.336938	Homo sapiens PRO0593 mRNA, complete cds	1.00	68.00
	432788	AA521091	Hs.178499	Homo sapiens cDNA: FLJ23117 fis, clone L	2.69	3.67
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.22	1.34
85	432867	AW016936	Hs.233364	ESTs	1.00	1.00
	432917	NM_014125	Hs.241517	PRO0327 protein	10.25	6.62

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	432920	U37689	Hs.3128	polymerase (RNA) II (DNA directed) polyp	1.44	1.30
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	154.79	85.64
	433023	AW864793	Hs.87409	thrombospondin 1	20.96	100.00
5	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	1.00	10.00
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
	433159	AB035898	Hs.150587	kinesin-like protein 2	13.82	39.00
	433183	AF231338	Hs.222024	transcription factor BMAL2	1.00	69.00
	433258	AA622788	Hs.203613	ESTs, Weakly similar to ALUB_HUMAN IIII	1.00	1.25
10	433409	AI278802	Hs.25661	ESTs	44.81	117.00
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	70.39	105.00
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	11.55	2.00
	433537	AI733692	Hs.112488	ESTs	8.66	55.00
	433547	W04978	Hs.303023	beta tubulin 1, class VI	25.16	83.00
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kn	1.00	19.00
15	433647	AA603367	Hs.222294	ESTs	20.30	49.00
	433658	L03678	Hs.156110	immunoglobulin kappa constant	5.92	10.03
	433800	AI094221	Hs.135150	lung type-I cell membrane-associated gly	2.29	2.22
	433819	AW511097	Hs.112765	ESTs	3.71	8.00
	433862	D86960	Hs.3610	KIAA0205 gene product	62.08	104.00
20	433980	AA137152	Hs.286049	phosphoserine aminotransferase	108.91	47.00
	434088	AF116577	Hs.249270	hypothetical protein PRO1866	1.00	1.00
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	121.27	87.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	1.22	1.23
	434217	AW014795	Hs.23349	ESTs	14.11	57.00
25	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.10	2.56
	434360	AA401369	Hs.190721	ESTs	40.98	17.00
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	1.48	1.56
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
30	434467	BE552368	Hs.231853	Homo sapiens cDNA FLJ13445 fis, clone PL	54.91	85.00
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.46	2.00
	434627	AI221894	Hs.39311	ESTs	1.00	1.00
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.00	23.00
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	7.08	56.00
35	434792	AA649253	Hs.132458	ESTs	8.52	44.00
	434808	AF165108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	11.33	1.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	1.00	1.00
	434876	AF160477	Hs.61460	lg superfamily receptor LNIR	1.25	1.29
	434891	AA814309	Hs.123583	ESTs	1.00	6.00
40	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	1.00	1.00
	435013	H91923	Hs.110024	Target CAT	1.26	1.10
	435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	1.69	1.37
	435087	AW975241	Hs.23557	ESTs	1.00	1.00
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.90	1.93
45	435159	AA668879	Hs.116649	ESTs	1.00	1.00
	435205	X54136	Hs.181125	immunoglobulin lambda locus	1.02	1.46
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	2.04	2.70
	435304	H10709	Hs.269524	ESTs	27.58	139.00
	435313	AI769400	Hs.189729	ESTs	1.00	14.00
50	435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
	435509	AI458679	Hs.181915	ESTs	1.00	1.00
	435525	AI631297	Hs.123310	ESTs	1.00	66.00
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	1.00	2.00
	435550	AI224456	Hs.324507	H.sapiens polyA site DNA	3.42	3.92
55	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	3.95	1.80
	435766	R11673	Hs.186498	ESTs	1.00	28.00
	435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
	436069	AI056879	Hs.263209	ESTs	1.00	58.00
	436170	AW450381	Hs.14529	ESTs	1.00	18.00
60	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.84	22.00
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	1.42	1.27
	436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.51	1.71
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.33	1.64
65	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	108.99	52.00
	436302	AL355841	Hs.99330	hypothetical protein FLJ23589	0.75	2.81
	436396	AW992292	Hs.152213	wingless-type MMTV integration site faml	60.01	1.00
	436414	BE264633	Hs.143638	WD repeat domain 4	2.50	2.19
	436419	AI948626	Hs.171356	ESTs	0.95	1.33
70	436443	AW138211	Hs.128746	ESTs	1.12	9.26
	436474	AJ270693	Hs.199887	ESTs	1.00	1.00
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.28	1.56
	436486	AA742221	Hs.120633	ESTs	1.00	19.00
	436511	AA721252	Hs.291502	ESTs	16.76	14.00
75	436553	X57809	Hs.181125	immunoglobulin lambda locus	1.08	1.74
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	19.20	9.75
	436608	AA628980		down syndrome critical region protein DS	33.92	25.00
	436667	AW025183	Hs.127680	ESTs	0.89	1.19
	436771	AW975687	Hs.292979	ESTs	1.00	10.00
80	436839	AA401369	Hs.190721	ESTs	1.00	17.00
	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	1.06	1.15
	436944	AW268614	Hs.5840	ESTs	1.00	1.00
	436961	AW375974	Hs.156704	ESTs	25.13	25.00
	436972	AA284679	Hs.25640	claudin 3	1.59	1.46
85	437016	AU076916	Hs.5398	guanine monophosphate synthetase	2.35	1.78
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	1.34	1.13

	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	1.00	17.00
	437204	AL110216	Hs.22826	ESTs, Weakly similar to I55214 salivary	40.55	82.00
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	1.00	112.00
5	437259	AI377755	Hs.120695	ESTs	1.00	205.00
	437270	RI8087	Hs.323769	cisplatin resistance related protein CRR	1.56	1.54
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	113.25	125.00
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	1.82	4.57
	437390	AI125859	Hs.112607	ESTs	1.35	1.75
10	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.58	3.20
	437435	AI306152	Hs.27027	hypothetical protein DKFZp762H1311	3.03	1.08
	437444	H46008	Hs.31518	ESTs	1.00	39.00
	437568	AI954795	Hs.156135	ESTs	1.00	19.00
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	1.95	1.57
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00	3.00
15	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.00	45.00
	437840	AA884836	Hs.292014	ESTs	1.07	1.78
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.s	1.68	3.26
	437879	BE262082	Hs.5894	hypothetical protein FLJ10305	1.87	2.52
20	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	74.05	35.00
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	23.15	89.00
	437937	AI917222	Hs.121655	ESTs	1.00	1.00
	437942	AI888266	Hs.307526	ESTs	12.28	31.00
	438091	AW373062		nuclear receptor subfamily 1, group I, m	1.53	10.85
25	438113	AI467908	Hs.8882	ESTs	1.80	2.39
	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	22.67	36.90
	438274	AI918906	Hs.55080	ESTs	1.00	1.00
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	38.92	38.00
	438403	AA806607	Hs.292206	ESTs	1.00	1.00
30	438494	AA908678	Hs.130183	ESTs	2.05	80.00
	438546	AW297204	Hs.125811	ESTs	1.00	131.00
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	1.43	1.45
	438702	AI879064	Hs.54618	ESTs	1.00	34.00
	438724	AW612553	Hs.114670	Human DNA sequence from clone RP11-16L21	1.33	1.10
35	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	2.42	1.59
	438779	NM_003787	Hs.6414	nuclear protein 4	1.00	18.00
	438821	AA826425	Hs.192375	ESTs	2.03	2.57
	438885	AI886558	Hs.184987	ESTs	6.42	88.00
	438898	AA401369	Hs.190721	ESTs	22.41	17.00
40	438916	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-650E9	2.20	1.88
	439000	AW979121		gb:EST391231 MAGE resequences, MAGP Homo	2.78	4.81
	439023	AA745978	Hs.28273	ESTs	1.17	1.31
	439024	R96596	Hs.35598	ESTs	1.00	28.00
45	439128	AI949371	Hs.153089	ESTs	1.00	67.00
	439146	AW138909	Hs.156110	immunoglobulin kappa constant	1.38	1.41
	439223	AW238299	Hs.250618	UL16 binding protein 2	1.93	1.64
	439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	2.00	2.20
50	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	6.10	7.37
	439394	AA401369	Hs.190721	ESTs	3.39	17.00
	439410	AA632012	Hs.188746	ESTs	1.83	3.07
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	18.76	122.00
55	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.78	1.58
	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	1.22	1.44
	439492	AF086310	Hs.103159	ESTs	7.46	39.00
	439523	W72348	Hs.185029	ESTs	1.00	1.19
	439582	AF086413	Hs.58399	ESTs	1.00	1.00
60	439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
	439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
	439702	AW085525	Hs.134182	ESTs	4.30	10.00
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAPI_HUMAN DEATH	86.55	11.00
	439738	BE246502	Hs.9598	sema domain, Immunoglobulin domain (Ig),	2.36	1.88
65	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.02	6.08
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
	439780	AL109688		gb:Homo sapiens mRNA full length insert	7.27	25.00
	439840	AW449211	Hs.105445	GDNF family receptor alpha 1	1.00	1.00
	439926	AW014875	Hs.137007	ESTs	32.68	71.00
70	439953	AW247529	Hs.6793	platelet-activating factor acetylhydrola	21.28	9.55
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	68.83	61.00
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.83	4.02
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	1.42	2.54
	440106	AA864968	Hs.127699	KIAA1603 protein	1.00	54.00
75	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	24.18	52.00
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.21	4.72
	440289	AW450991	Hs.192071	ESTs	38.63	113.00
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	2.35	3.62
80	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	10.84	57.00
	440659	AF134160	Hs.7327	claudin 1	3.18	2.37
	440704	M69241	Hs.162	insulin-like growth factor binding prote	2.89	2.09
	440943	AW082298	Hs.146161	hypothetical protein MGC2408	2.02	1.41
	440994	AI160011	Hs.272068	ESTs	1.29	1.14
85	441020	AA401369	Hs.190721	ESTs	142.99	17.00
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00

	441128	AA570256	ESTs, Weakly similar to T23273 hypothe	4.13	3.50
	441290	W27501	cholinergic receptor, nicotinic, alpha p	1.00	1.00
	441362	BE614410	RAD51 (S. cerevisiae) homolog (E coli Re	130.23	43.00
5	441377	BE218239	ESTs	22.03	1.00
	441390	AI692560	ESTs	3.65	7.70
	441497	R51064	ESTs	1.00	1.00
	441525	AW241867	ESTs	1.53	1.42
	441553	AA281219	ESTs	1.89	1.57
	441607	NM_005010	neuronal cell adhesion molecule	1.47	2.11
10	441633	AW958544	normal mucosa of esophagus specific 1	216.22	363.00
	441636	AA081846	Homo sapiens mRNA; cDNA DKFZp566E183 (fr	2.31	2.05
	441737	X79449	adenosine deaminase, RNA-specific	1.30	1.49
	441790	AA401369	ESTs	44.15	17.00
	441801	AW242799	ESTs	1.00	1.00
15	441919	AI553802	ESTs	1.00	122.00
	441937	R41782	ESTs	0.86	1.37
	441954	AI744935	Fanconi anemia, complementation group G	1.48	1.39
	442025	AW887434	CDA11 protein	1.00	46.00
	442029	AW956698	neural precursor cell expressed, develop	9.92	45.00
20	442072	AI740832	Homo sapiens clone 23570 mRNA sequence	25.05	77.00
	442108	AW452649	ESTs	3.61	3.14
	442117	AW664964	ESTs	3.00	5.49
	442137	AA977235	ESTs, Weakly similar to Z192_HUMAN ZINC	1.00	1.00
	442159	AW163390	heterochromatin-like protein 1	1.92	1.66
25	442179	AA983842	chromosome 2 open reading frame 2	27.22	50.00
	442328	AI952430	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.00	3.42
	442432	BE093589	hypothetical protein FLJ23468	181.59	76.00
	442530	AI580830	Homo sapiens cDNA FLJ14712 fis, clone NT	10.59	144.00
	442547	AA306997	ESTs, Weakly similar to ALU1_HUMAN ALU S	109.23	98.00
30	442556	AL137761	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	1.00	53.00
	442619	AA447492	ESTs, Weakly similar to AF164793 1 prote	29.02	50.00
	442710	AI015631	ESTs	1.00	19.00
	442717	R88362	ESTs, Weakly similar to T23976 hypothe	1.00	5.00
	442875	BE623003	Homo sapiens clone TCCCTA00142 mRNA sequ	22.85	50.00
35	442914	AW188551	hypothetical protein FLJ14007	25.33	82.00
	442932	AA457211	bromodomain adjacent to zinc finger doma	3.18	4.41
	442942	AW167087	ESTs	8.45	64.00
	443068	AI188710	ESTs	1.00	27.00
40	443204	AW205878	Homo sapiens cDNA FLJ13103 fis, clone NT	1.00	24.00
	443211	AI128388	ESTs	12.42	2.00
	443247	BE614387	c-Myc target JPO1	128.84	96.00
	443324	R44013	ESTs	0.02	4.59
	443383	AI792453	ESTs	1.00	47.00
45	443400	R28424	ESTs	18.52	61.00
	443426	AF098158	chromosome 20 open reading frame 1	4.02	1.75
	443572	AA025610	cleavage and polyadenylation specific fa	2.98	2.57
	443575	AI078022	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00	29.00
	443614	AV655386	fibrinogen, B beta polypeptide	1.00	18.00
50	443633	AL031290	similar to pregnancy-associated plasma p	1.00	39.00
	443648	AI085377	ESTs	39.81	70.00
	443715	AI583187	cyclin E1	48.74	7.00
	443723	AI144442	syntaxin 6	1.29	1.30
	443802	AW504924	KIAA1291 protein	1.75	1.61
	443859	NM_013409	folistatin	1.35	1.13
55	443892	AA401369	ESTs	1.00	17.00
	443947	W24187	gb:zb47f09.r1 Soares_fetal_lung_NbHL19W	1.33	1.64
	443991	NM_002250	potassium intermediate/small conductance	5.71	6.87
	444006	BE395085	type I transmembrane protein Fn14	1.47	1.92
60	444009	AI380792	ESTs	1.00	77.00
	444017	U04840	neuro-oncological ventral antigen 1	1.00	1.00
	444127	N63620	ESTs	1.00	29.00
	444129	AW294292	ESTs	1.00	1.00
	444279	U62432	cholinergic receptor, nicotinic, alpha p	0.80	7.80
65	444371	BE540274	forkhead box M1	2.91	1.14
	444378	R41339	ESTs	1.00	1.00
	444381	BE387335	ESTs, Weakly similar to S64054 hypothe	469.00	556.00
	444461	R53734	ESTs, Weakly similar to 2109260A B cell	12.88	105.00
	444471	AB020684	KIAA0877 protein	24.91	90.00
	444489	AI151010	ESTs	1.00	111.00
70	444619	BE538082	ESTs, Moderately similar to A46010 X-in	1.00	70.00
	444665	BE613126	B aggressive lymphoma gene	30.56	139.00
	444707	AI188513	desmocollin 3	1.00	1.00
	444735	BE019923	hypothetical protein FLJ13057 similar to	77.02	90.00
75	444781	NM_014400	GPI-anchored metastasis-associated prote	1.57	1.31
	444783	AK001468	anillin (Drosophila Scraps homolog), act	77.55	2.00
	445236	AK001676	hypothetical protein FLJ10814	1.00	27.00
	445258	AI635931	ESTs	1.00	73.00
	445413	AA151342	CGI-147 protein	28.14	50.00
80	445417	AK001058	Homo sapiens cDNA FLJ10196 fis, clone HE	1.81	2.62
	445443	AV653838	ESTs	1.00	1.00
	445462	AA378776	hypothetical protein MGC3077	2.09	1.70
	445517	AF208855	hypothetical protein	1.87	70.00
	445537	AJ245671	EGF-like domain, multiple 6	1.71	2.72
85	445580	AF167572	skb1 (S. pombe) homolog	1.52	1.34
	445654	X91247	thioredoxin reductase 1	1.51	1.52

	445669	AI570830	Hs.174870	ESTs	10.95	11.45
	445818	BE045321	Hs.136017	ESTs	1.00	1.00
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-1	49.42	64.00
5	445885	AI734009	Hs.127699	KIAA1603 protein	1.00	132.00
	445898	AF070823	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.00	1.00
	445903	AI347487	Hs.132781	class I cytokine receptor	1.00	36.00
	445932	BE046441	Hs.333555	Homo sapiens clone 24859 mRNA sequence	2.41	2.88
	445982	BE410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.60	1.35
10	446078	AI339982	Hs.158061	ESTs	1.00	42.00
	446102	AW168067	Hs.317694	ESTs	1.00	1.00
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	1.70	1.53
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	73.01	48.00
	446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
	446293	AI420213	Hs.149722	ESTs	1.00	2.00
15	446423	AW139655	Hs.150120	ESTs	1.10	4.19
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	0.53	3.26
	446432	AI377320	Hs.150058	ESTs	1.00	5.00
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	1.36	1.31
	446574	AI310135	Hs.335933	ESTs	3.89	72.00
20	446619	AU076643	Hs.313	secreted phosphoprotein 1 (oslopanin,	32.03	20.23
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	4.19	6.07
	446783	AW138343	Hs.141867	ESTs	2.82	9.47
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	110.28	28.00
	446849	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.26	2.94
25	446856	AI814373	Hs.164175	ESTs	6.38	11.30
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	1.98	2.03
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	94.90	113.00
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.67	3.90
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	2.82	3.12
30	447022	AW291223	Hs.157573	ESTs	1.00	170.00
	447033	AI357412	Hs.157601	ESTs	7.15	107.00
	447078	AW885727	Hs.9914	ESTs	47.24	24.00
	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	0.12	17.88
35	447131	NM_004585	Hs.17468	retinoic acid receptor responder (tazaro	0.97	1.48
	447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	1.24	1.26
	447153	AA805202	Hs.315562	ESTs	1.00	54.00
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	1.00	67.00
	447178	AW594641	Hs.192417	ESTs	3.42	50.00
40	447250	AI878909	Hs.17883	protein phosphatase 1G (formerly 2C), ma	1.60	1.52
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00	1.00
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	146.62	51.00
	447350	AI375572	Hs.172634	ESTs	1.00	12.00
45	447377	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.55	63.00
	447415	AW937335	Hs.28149	ESTs, Weakly similar to KF3B_HUMAN KINES	0.91	1.13
	447425	AI963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	1.00	35.00
	447519	U46258	Hs.339665	ESTs	59.89	49.00
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
50	447534	AA401369	Hs.190721	ESTs	1.00	17.00
	447636	Y10043		high-mobility group (nonhistone chromoso	1.41	1.11
	447688	N87079	Hs.19238	Target CAT	1.00	39.00
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.17	1.12
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	6.47	5.95
55	447802	AW593432	Hs.161455	ESTs	0.73	2.34
	447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	86.45	116.00
	447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	1.00	1.00
	447973	AB011169	Hs.20141	similar to S. cerevisiae SSM4	3.50	4.27
	448030	N30714	Hs.326960	membrane-spanning 4-domains, subfamily A	4.13	142.00
60	448105	AI538613	Hs.298241	Transmembrane protease, serine 3	1.15	2.24
	448243	AW369771	Hs.52620	Integrin, beta 8	15.84	1.00
	448278	W07369	Hs.11782	ESTs	0.97	1.90
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	1.00	1.00
	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT	2.42	2.17
65	448357	BE274396	Hs.108923	RAB38, member RAS oncogene family	1.44	1.08
	448390	AL035414	Hs.21068	hypothetical protein	1.00	43.00
	448469	AW504732	Hs.21275	hypothetical protein FLJ11011	2.63	2.49
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.84	2.53
	448663	BE614599	Hs.106823	hypothetical protein MGC14797	3.29	46.00
70	448672	AI955511	Hs.225106	ESTs	1.00	21.00
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.82	1.08
	448741	BE614567	Hs.19574	hypothetical protein MGC5469	2.48	1.92
	448757	AI386784	Hs.48820	TATA box binding protein (TBP)-associa	23.53	20.00
	448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moi	2.34	1.97
75	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	74.07	62.67
	448830	AL031658	Hs.22181	hypothetical protein dJ310013.3	1.37	1.31
	448844	AI581519	Hs.177164	ESTs	1.00	31.00
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.84	1.95
	448993	AI471630		KIAA0144 gene product	1.63	1.49
80	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
	449029	N28989	Hs.22891	solute carrier family 7 (cationic amino	1.97	2.26
	449040	AF040704	Hs.149443	putative tumor suppressor	0.97	1.56
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	27.13	90.00
	449053	AI625777	Hs.344766	ESTs	8.33	44.00
85	449054	AF148848	Hs.22934	myoneurin	73.85	104.00
	449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00

	449167	T05095	Hs.19597	KIAA1694 protein	1.61	2.36
	449207	AL044222	Hs.23255	nucleoporin 155kD	2.36	1.56
	449228	AJ403107	Hs.148590	protein related with psoriasis	1.15	1.15
5	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	206.65	151.00
	449305	AI638293		gb:tt09b07.x1 NCL CGAP_GC6 Homo sapiens	17.28	45.00
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	26.39	35.00
	449448	D60730	Hs.57471	ESTs	1.00	1.00
	449467	AW205006	Hs.197042	ESTs	1.00	1.00
10	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	56.80	216.86
	449722	BE280074	Hs.23860	cyclin B1	150.03	1.00
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	2.16	2.85
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter)	1.17	1.45
	450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.79	2.38
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	1.00	69.00
15	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila)	1.00	1.00
	450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complementation	29.85	34.00
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1.00	1.00
	450372	BE218107	Hs.202436	ESTs	1.00	1.00
20	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain	51.26	93.00
	450447	AF212223	Hs.25010	hypothetical protein P15-2	123.20	181.00
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	19.00
	450589	AI701505	Hs.202526	ESTs	1.00	23.00
	450684	AA872605	Hs.25333	Interleukin 1 receptor, type II	1.00	100.00
25	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.89	1.55
	450705	U90304	Hs.25351	trojan homeobox protein 2A (IRX-2A) (1.00	45.00
	450832	AA401369	Hs.190721	ESTs	25.17	17.00
	450937	R49131	Hs.26267	ATP-dependant interferon response protein	90.92	90.00
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.33	1.70
30	451105	AI761324		gb:wi60b11.x1 NCL CGAP_Co16 Homo sapiens	15.02	124.00
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	143.00
	451253	H48289	Hs.26126	claudin 10	3.02	2.29
	451291	R39288	Hs.6702	ESTs	1.00	1.00
	451320	AW498874		diacylglycerol kinase, zeta (104kD)	2.92	18.00
35	451380	H09280	Hs.13234	ESTs	6.90	6.67
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant)	35.75	72.00
	451437	H24143	Hs.31945	hypothetical protein FLJ11071	1.00	69.00
	451462	AK000367	Hs.26434	hypothetical protein FLJ20360	1.83	2.10
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.13	1.07
40	451541	BE279383	Hs.26557	plakophilin 3	1.88	1.33
	451592	AI805416	Hs.213897	ESTs	1.00	1.00
	451635	AA018899	Hs.127179	cryptic gene	1.52	1.92
	451743	AA401369	Hs.190721	ESTs	4.95	17.00
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	13.55	31.00
45	451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
	451871	AI821005	Hs.118599	ESTs	1.81	2.53
	451952	AL120173	Hs.301663	ESTs	1.00	22.00
	452012	AA307703	Hs.279766	kinasin family member 4A	3.43	2.26
	452046	AB018345	Hs.27657	KIAA0802 protein	56.59	19.00
50	452194	AI694413	Hs.332549	olfactory receptor, family 2, subfamily	1.67	4.09
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	9.31	53.00
	452240	AA401369	Hs.190721	ESTs	13.42	17.00
	452256	AK000933	Hs.28861	Homo sapiens cDNA FLJ10071 fis, clone HE	39.03	94.00
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	153.01	340.00
55	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae)	1.95	23.00
	452295	BE379936	Hs.28866	programmed cell death 10	42.33	61.00
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.17	2.14
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodomain	1.00	13.00
	452349	AB028944	Hs.29189	ATPase, Class VI, type 11A	1.09	1.42
60	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	54.49	53.00
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	1.00	32.00
	452410	AL133619		Homo sapiens mRNA; cDNA DKFZp434E2321 (I	1.26	1.99
	452461	N78223	Hs.108106	transcription factor	24.47	35.00
	452571	W31518	Hs.34685	ESTs	54.61	102.00
65	452613	AA461599	Hs.23459	ESTs	1.39	1.32
	452699	AW295390	Hs.213062	ESTs	1.00	26.00
	452705	H49805	Hs.246005	ESTs	1.00	1.00
	452747	AF160477	Hs.61460	Ig superfamily receptor LNIR	112.87	1.29
	452787	AW294022	Hs.222707	KIAA1718 protein	1.00	1.00
70	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	1.00	1.00
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	7.91	75.00
	452833	BE559681	Hs.30736	KIAA0124 protein	3.16	1.92
	452838	U65011	Hs.30743	preferentially expressed antigen in melanoma	174.35	1.00
	452862	AA401369	Hs.190721	ESTs	98.26	17.00
75	452865	AW173720	Hs.345805	ESTs, Weakly similar to A47582 B-cell granule	1.55	1.00
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.73	1.19
	452946	X95425	Hs.31092	EphA5	1.00	1.00
	452976	R44214	Hs.101189	ESTs	1.58	1.98
	453028	AB006532	Hs.31442	RacQ protein-like 4	1.80	1.60
80	453095	AW295660	Hs.252756	ESTs	0.77	1.50
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1.00	1.00
	453103	AI301052	Hs.153444	ESTs	1.00	1.00
	453120	AA292891	Hs.31773	pregnancy-induced growth inhibitor	1.23	1.20
	453153	N53893	Hs.24360	ESTs	1.00	83.00
	453160	AI263307	Hs.239884	H2B histone family, member L	1.00	30.00
85	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU 5	1.00	134.00

5	453210	AL133161	Hs.32360	hypothetical protein FLJ10867	1.69	1.93		
	453240	AI969564	Hs.166254	hypothetical protein DKFZp5661133	1.00	1.00		
	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	1.19	1.27		
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside tra	4.90	4.11		
	453331	AI240665	Hs.8850	ESTs	199.42	340.00		
	453392	U23752	Hs.32954	SRY (sex determining region Y)-box 11	1.00	18.00		
	453431	AF094754	Hs.32973	glycine receptor, beta	1.00	1.00		
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.44	5.17		
10	453459	BE047032	Hs.257789	ESTs	2.84	5.58		
	453563	AW608906.comp	Hs.181163	hypothetical protein MGC5629	4.58	90.00		
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.74	1.60		
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	19.49	1.00		
	453830	AA534296	Hs.20953	ESTs	24.92	25.00		
15	453857	AL080235	Hs.35861	DKFZP586E1621 protein	167.59	66.00		
	453867	AI929383	Hs.33032	hypothetical protein DKFZp434N185	1.00	39.00		
	453883	AI638516	Hs.347524	cofactor required for Sp1 transcription	1.87	1.58		
	453884	AA355925	Hs.36232	KIAA0186 gene product	63.89	20.00		
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.41	16.00		
20	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	7.09	22.00		
	453941	U39817	Hs.36820	Bloom syndrome	29.75	19.00		
	453964	AI981486	Hs.12744	ESTs	1.00	1.00		
	453988	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	2.06	1.81		
	453976	BE463830	Hs.163714	ESTs	3.02	131.00		
25	454024	AA933527	Hs.293907	hypothetical protein FLJ23403	1.00	131.00		
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.23	1.02		
	454042	T19228	Hs.172572	hypothetical protein FLJ20093	30.63	171.00		
	454059	NM_003154	Hs.37048	stathmin	1.00	1.00		
	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	1.01	1.45		
30	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11		
	454241	BE144686		gb:CM2-HT0176-041099-017-c02 HT0176 Homo	6.33	5.04		
	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	4.30	7.82		
	454439	AW819152	Hs.154320	DKFZP566O1646 protein	1.00	1.00		
	455175	AW993247		gb:RC2-BN0033-180200-014-h09 BN0033 Homo	13.75	103.00		
35	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00		
	456237	AA203682		gb:zx52e07.r1 Soares_fetal_liver_spleen_	1.00	1.00		
	456321	NM_001327	Hs.87225	cancer/testis antigen	1.14	1.10		
	456475	NM_000144	Hs.95998	Friedreich ataxia	1.00	48.00		
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	162.25	189.00		
40	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	2.12	1.80		
	456736	AW248217	Hs.1619	achaete-scute complex (Drosophila) homol	1.15	1.94		
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	1.00	1.00		
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	16.42	84.00		
	457200	U33749	Hs.197764	thyroid transcription factor 1	0.57	1.76		
45	457234	AW968360	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	2.71	4.15		
	457465	AW301344	Hs.122908	DNA replication factor	46.37	47.00		
	457489	AI693815	Hs.127179	cryptic gene	1.12	1.35		
	457646	AA725650	Hs.112948	ESTs	1.55	2.51		
	457733	AW974812	Hs.291971	ESTs	1.00	55.00		
50	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	4.36	3.18		
	458092	BE545684	Hs.343566	KIAA0251 protein	1.00	1.32		
	458098	BE550224		metallothionein 1E (functional)	1.00	22.00		
	458207	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	2.06	1.88		
	458242	BE299588	Hs.29465	Homo sapiens cDNA: FLJ21669 fis, clone H	1.00	1.00		
55	458247	R14439	Hs.209194	ESTs	7.00	9.85		
	458679	AW975460	Hs.142913	ESTs	1.00	3.00		
	458778	AW451034	Hs.326525	arylsulfatase D	1.31	2.01		
	458933	AI638429	Hs.24763	RAN binding protein 1	1.98	1.71		
	459352	AW810383	Hs.206828	ESTs	12.60	63.00		
	459670	F01020	Hs.172004	Ulin	1.00	1.00		
60	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.00	237.00		

TABLE 9B

65	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
70	Pkey	CAT Number	Accession
	407746	10125_1	AK001962 R69415 BE464605 AA418699 AA053293 AA149075 AA058396 AW338226 AW272659 AA454607 AI139535 AW469852 AI275461
			AW271982 AA730033 AA576507 AA991217 AA782067 AI985851 AA805864 AA505598 AW469857 R69546 AA988279 AW001647 N63320
			D82661 T27343 AA306950 AA360989 R58778
	408070	1036688_1	AW148852 BE350895
	408660	107294_1	AA525775 AA056342 AI538978 AW975281 AA664986
75	409522	113735_1	AA075382 AA075431
	409866	1156522_1	AW502152 H41202 H29772
	410032	1170435_1	BE065985 BE065944 BE066008 BE066083 BE066093
	411089	123172_1	AA456454 AA713730 AA091294 AA584921 N86077 AW836781 AA601031 AA579676 AA551106 AA633188 AW905577 AI955808 AI679386
			AI679895 AA514764 AA454562 AI082382 AA595822 AA551351 AA586369 AA666384 AA188934 AA666398 AA551297 AA565188
			BE069199 AW936012 AW877466 AW819782 AW935798 AW835546 AW936042 BE069121 AW835625 AW877536 AW935685 BE069202
80			AW820019 AW935937 BE160180 AW935946 BE069101 BE069125 AW877527 BE160316 BE160398 AW935794 AW835701 AW935784
			AL031778 X59711 NM_002505 M59079 AI870439 AI494259 AW664010 AA405063 AA436132 BE174516 AA412691 AI400314 AA436024
			T29403 BE079412 BE079428 N90322 AI631202 AI141758 AI016793 AI167566 AI862075 AI375230 AI208445 AW235763 AL044113 AA382556
			AW953918 AA927051 AA889823 BE003094 AW390155 AW360805 AW360823 AW360810 AA425472 AI694282 AL044114 AI684577 AI809865

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			AI478773 AI160445 AI674630 N69088 AW665529 N49278 AI129239 AI457890 AI621264 AW297152 AI268215 AA907787 AI286170 AI017982 AI963541 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AW292026 H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689 R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734 BE157489 BE157560 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245 AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T59538 BE279271 AW960304 T29812 AA476873 BE297387 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150 AA872039 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046 AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031 N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045 AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239 AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850 AI494230 AI278887 AA982596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785 AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99531 AW300758 H03431 R76789 AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156 W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086 AW265494 AA455904 AA195677 AW265432 AW991605 AA456370 N28754 N28747 AI568146 AI979339 AA322671 AA322672 AW955043 AI990326 AA776406 AI016250 AA843678 AW451882 N23137 N23129 W70051 AI038748 AA831327 AI225845 AW945895 Z42183 T31621 T97478 D62703 AA242966 D79798 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T76845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T76922 T67736 T68716 T67755 T74765 T73819 T58719 T74766 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R06789 H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656601 AI064470 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40158 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343595 AW470774 AV651266 N54417 AA812862 AW182929 AI11192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T7853 T47778 R95748 H70620 AA701463 AW827166 R98475 C02925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T68906 T71457 T70494 T72956 T70495 T68257 T74407 T65778 AA344726 T72854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 R29500 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341907 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343060 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68261 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29038 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068 AI792788 BE142230 AA252019 AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074058 AW009769 AW050690 AA858276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292 AW881145 AA490718 M85637 AA304575 T06067 AA331991 AL119930 AA320696 AW752565 AL031985 AL137241 AI792368 AI733664 AI857654 AI049911 AA337221 AA335756 AW966196 AW953120 R56325 AA349562 AI483134 AI498691 AW771508 AI498457 AI768408 AI783624 AI383985 AI580267 D79813 AA393768 AK001536 AA191092 AW510354 AI554256 AL353968 AA134266 AA663848 AA400100 AA401424 AL038843 AA161338 BE268213 AA425597 N87306 AA092969 BE566038 AA247451 N47392 AI928802 AW182584 AW027872 AI819831 AI936994 W56258 AI653448 AI278611 AI283557 AI824306 AW338658 AW150899 AA687514 N47393 N29885 AA973469 AI038904 AI292064 AI034339 AW674593 N72156 AI079733 AI038683 AI291616 AA491599 AA93675 AA837380 BE006554 BE006473 AI087090 T33044 AA652043 AI203503 AA583959 W35283 AI129926 Z41844 AW020925 AW575848 AI684603 AA493297 AI140689 AI277175 AA425444 AI932767 W02632 BE396786 R37261 AW207206 AW341473 AA448195 AI951341 AA249027 AL038984 AK001993 AL080066 AV652725 BE566226 AA345557 AA315222 AA090585 AA375688 AA301092 AA298454 W05762 AW607939 H51658 C83880 N84323 BE296821 AW947007 D61461 AW079261 AA329482 AW901780 AI354442 AA772275 R31663 AI354441 AI767525 H92431 AI916735 H93575 AI394255 AW014741 AI573090 C06195 AW612857 AW265195 AI339558 AI377532 AI038821 AI919424 AI589705 AW055215 AI336532 AI338051 AA806547 C75509 C00618 AW071172 AW769904 AA630381 AI678018 AI863985 D79662 BE221049 AW265018 AI589700 AW196655 N76573 AI370908 BE042393 N75017 AI698870 AW960115 AL133561 AL041090 AL117481 AL122069 AW439292 AI968826 AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937 BE041395 AA491828 AA621946 AA715980 AA666102 AW970622 AA503009 AA502989 AA502805 T92188 AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW869639 BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821687 AA055720 AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859 AI798378 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA698929 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570 AA628980 AI126603 BE504035
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438091 44964_1 AW373062 T55662 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616
AA709126 AW898628 AW898644 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522 BE487708 AW243400
AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984 AI922204 N98343 BE174213 AA845571
AI813854 AI214518 AI635262 AI139455 AI707807 AI698085 AW884528 AI024768 AI004723 AW087420 AI565133 N94964 AI268939
AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207
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AI955913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096
AW979121 AA847986 AA829098
AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882
AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
AL109688 R23665 R26578
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AI188710 AI032142 AW078833 N30308 AW675632 AI219028 AI341201 N22181 H95390
W24187 W24194 R17789
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AA369318 AW957081 R05760 AA039903 AI886597 AW630122 AA906264 AA041527 R01145 AI088688 BE463637 AA398795 AI354883
AI768938 AI569996 AI452952 AI168582 AI189869 AI086670 AW262560 AW613854 AA862839 AA435840 AA670197 AI024032 AI990659
AI990089 N81095 AA847919 AW960150 AA211075 AA044704 AA367594 AW582587 AW858854 AW818630 AW818281 AW818433 AW582595
AA096002 N83992
AI471630 BE540637 BE265481 AW07710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 AI656234 AI636283 AI567265
AW340858 BE207794 AA053085 R69173 AA292343 AA454908 AA293504 AI659741 AI927478 AA399460 AI760441 AA345416 BE047245
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AA911497 BE537702
AI638293 AW813561
AI761324 AW880941 AW880937
AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265
AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230
AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612
W52854 AL117600 BE208118 BE208432 BE208239 BE082291 AW963423 AA351619 BE180648 BE140560 W60080 AA865478 N90291
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AI269603 AI665082 AI807095 AI476629 AA505909 AI368449 AI686077 AI582930 AW085038 AA757863 AA730154 AI767072 AA468316
AI734130 AI734138 AA426284 AA433997 AI741241 AW043563 AI732741 AI732734 AA437369 AA425820 AA664048 R74130
BE144656 BE184942 AW238414 BE184946
AW993247 AW861464
AA203682 R11958
BE550224 AA832519 N45402 AW885857 N29245 BE465409 W07677 AW970089 AI299731 AA482971 BE503548 H18151 W79223 AF086393
AA461301 W74510 R34182 AI090689 N46003 BE071550 R28075 AW134982 AI240204 AI138906 AW026179 AI572316 BE466182 AI206395
AI276154 AI273269 AI422817 AI371014 AI421274 AI188525 AA939164 BE549810 AW137865 AI694996 BE503841 AA459718 BE327407
BE467534 BE218421 BE467767 AA899054 BE467063 AI797130 BE327761

TABLE 9C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400512	9796593	Minus	1439-1616
400517	9796686	Minus	49996-50346
400560	9843598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400665	8118496	Plus	16879-17023
400666	8118496	Plus	17982-18115,20297-20456
400749	7331445	Minus	9162-9293
400763	8131616	Minus	35537-35784
401027	7230983	Minus	70407-70554,71060-71160
401093	8516137	Minus	22335-23166
401203	9743387	Minus	172961-173056,173868-173928
401212	9858408	Plus	87839-88028
401411	7799787	Minus	144144-144329
401435	8217934	Minus	54508-55233
401464	6682291	Minus	170688-170834
401714	6715702	Plus	96484-96681
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165996,168189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401797	6730720	Plus	6973-7118
401961	4581193	Minus	124054-124209
401985	2580474	Plus	61542-61750
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125872-126076
402260	3399665	Minus	113765-113910,116653-116765,116808-116940
402285	3287673	Plus	21059-21168
402297	6598824	Plus	35279-35405,35573-35659
402408	9796239	Minus	110326-110491

	402420	9798339	Plus	129750-129919
	402674	8077108	Minus	39290-39502
	402802	3287156	Minus	53242-53432
5	402994	2996643	Minus	4727-4969
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403308	8099945	Plus	127100-127251
	403329	8516120	Plus	96450-96598
	403381	9438267	Minus	26009-26178
10	403478	9958258	Plus	116458-116564
	403485	9966528	Plus	2888-3001,3198-3532,3855-4117
	403627	8569879	Minus	23868-24342
	403715	7239669	Plus	85128-85292
	404044	9558573	Minus	225757-225939
15	404076	9931752	Minus	3848-3967
	404101	8076925	Minus	125742-125997
	404140	9843520	Plus	37761-38147
	404165	9926489	Minus	69025-69128
	404185	4572584	Minus	129171-129327
20	404210	5006246	Plus	169926-170121
	404253	9367202	Minus	55675-56055
	404287	2326514	Plus	53134-53281
	404298	9944263	Minus	73591-73723
	404347	9838195	Plus	74493-74829
25	404440	7528051	Plus	80430-81581
	404721	9856548	Minus	173763-174294
	404794	4826439	Plus	101618-101898
	404854	7143420	Plus	14260-14537
	404877	1519284	Plus	1095-2107
30	404927	7342002	Plus	68690-69563
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405449	7622497	Plus	42236-42570
	405568	6008906	Plus	35912-36065
	405572	3800891	Plus	85230-85938
35	405646	4914350	Plus	741-969
	405676	4557087	Plus	73195-73917
	405770	2735037	Plus	61057-62075
	405932	7767812	Minus	123525-123713
	406137	9166422	Minus	30487-31058
40	406360	9256107	Minus	7513-7673
	406399	9256288	Minus	63448-63554
	406467	9795551	Plus	182212-182958

TABLE 10A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer and Non-malignant Lung Disease

Table 2A shows about 307 genes up-regulated in non-malignant lung disease relative to lung tumors and normal body tissues and/or down-regulated in lung tumors relative to normal lung and non-malignant lung disease. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 10B show the accession numbers for those Pkey's lacking UnigenelD's for table 10A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 10C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 10A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigenel number
 Unigenel Title: Unigenel gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

	Pkey	ExAccn	UnigenelD	Unigenel Title	R1	R2
	404394			ENSP00000241075.TRRAP PROTEIN.	0.79	3.10
	404916			Target Exon	1.00	159.00
	405257			Target Exon	1.00	422.00
70	407228	M25079	Hs.155376	hemoglobin, beta	0.47	2.33
	407568	AA740964	Hs.62699	ESTs	1.00	123.00
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
	409031	AA376836	Hs.76728	ESTs	1.00	128.00
	410434	AF051152	Hs.63668	tol-like receptor 2	39.65	149.00
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	1.00	109.00
75	410808	T40326	Hs.167793	ESTs	1.14	13.14
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	0.37	2.27
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
	413795	AL040178	Hs.142003	ESTs	0.10	11.90
	414154	AW205314	Hs.323060	ESTs	0.62	2.09
80	414214	O49958	Hs.75819	glycoprotein MGA	0.03	4.55
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.64	2.97
	415122	D60708	Hs.22245	ESTs	0.07	8.97
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	0.67	1.65
	415775	H00747	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	0.29	2.64
85	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00

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	416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	15.32	237.00
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	0.64	4.00
	417355	D13168	Hs.82002	endothelin receptor type B	0.01	3.90
5	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	36.30	357.00
	417511	AL049176	Hs.82223	chordin-like	1.00	179.00
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.02	6.00
	418726	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	1.00	113.00
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	0.44	1.90
10	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	0.96	2.04
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	0.62	2.74
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	0.03	6.90
	419235	AW470411	Hs.288433	neurotrophin	1.48	5.13
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	37.55	336.00
15	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.80	3.65
	420656	AA279098	Hs.187636	ESTs	1.65	8.07
	420729	AW964897	Hs.290825	ESTs	2.99	25.82
	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	0.46	1.95
	422080	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
20	422426	W79117	Hs.58559	ESTs	0.03	7.44
	422652	AW967969	Hs.118958	syntaxin 11	0.14	3.62
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	0.01	3.16
	424433	H04607	Hs.9218	ESTs	0.75	141.75
	424585	AA464840	Hs.131987	ESTs	1.00	167.00
25	424711	NM_005795	Hs.152175	calcitonin receptor-like	0.43	3.01
	424973	X92521	Hs.154057	matrix metalloproteinase 19	0.37	19.45
	425023	AW556889	Hs.154210	endothelial differentiation, sphingolipid	0.14	3.35
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	1.00	94.00
	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	0.68	1.42
30	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.03	3.74
	426753	T89832	Hs.170278	ESTs	1.00	141.00
	427558	D49493	Hs.2171	growth differentiation factor 10	1.00	117.00
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	0.75	2.20
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	0.76	2.25
35	428927	AA441837	Hs.90250	ESTs	0.01	3.62
	429496	AA453800	Hs.192793	ESTs	1.00	138.00
	430468	NM_004673	Hs.241519	angiotensin-like 1	1.00	132.00
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
40	431728	NM_007351	Hs.268107	multimerin	1.00	157.00
	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.34	2.24
	432128	AA127221	Hs.117037	ESTs	0.00	1.15
	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	0.01	2.06
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.00	267.00
	433803	AI823593	Hs.27688	ESTs	1.00	105.00
45	434730	AA644669	Hs.193042	ESTs	1.05	3.15
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	0.83	1.94
	436532	AA721522		gbcnv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	1.00	218.00
	437119	AI379921	Hs.177043	ESTs	1.00	133.00
	437140	AA312799	Hs.283689	activator of CREM in testis	0.67	122.67
50	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	1.00	142.00
	437960	AI669586	Hs.222194	ESTs	1.00	147.00
	438202	AW169287	Hs.22588	ESTs	1.00	141.00
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.71	3.66
	438875	AA827640	Hs.189059	ESTs	23.32	370.00
55	441048	AA913488	Hs.192102	ESTs	0.77	8.50
	441188	AW292830	Hs.255609	ESTs	3.43	16.36
	441499	AW298235	Hs.101689	ESTs	1.00	167.00
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	46.47	153.00
60	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	0.01	3.08
	445279	R41900	Hs.22245	ESTs	0.60	141.00
	446017	N98238	Hs.55185	ESTs	0.18	2.39
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	0.10	2.16
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.01	2.53
65	447357	AI375922	Hs.159367	ESTs	0.46	2.64
	448106	AI800470	Hs.171941	ESTs	18.05	296.00
	448253	H25899	Hs.201591	ESTs	1.00	141.00
	449276	AW450848	Hs.205457	perlecan	0.56	1.38
	450400	AI694722	Hs.279744	ESTs	0.88	4.33
70	450698	AI654223	Hs.16026	hypothetical protein FLJ23191	0.52	2.08
	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	0.79	2.01
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	0.35	2.03
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	0.13	2.25
	453636	R67837	Hs.169872	ESTs	1.00	116.00
75	458332	AI000341	Hs.220491	ESTs	1.00	192.00
	459580	AA022888	Hs.176065	ESTs	0.20	2.98
	400269			Eos Control	0.40	2.40
	403421			NM_016369*:Homo sapiens claudin 18 (CLDN	0.53	1.77
	407570	Z19002	Hs.37096	zinc finger protein 145 (Krueppel-like, e	0.01	3.18
80	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.56	1.74
	414517	M24461	Hs.78305	surfactant, pulmonary-associated protein	0.64	1.50
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	0.33	1.16
	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	0.53	1.55
	418935	T28499	Hs.89485	carbonic anhydrase IV	0.20	1.28
85	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	0.78	1.90
	421798	N74880	Hs.29877	N-acylsphingosine amidohydrolase (acid c	0.59	1.54

	423354	AB011130	Hs.127438	calcium channel, voltage-dependent, alph	0.59	1.55
	423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	0.35	1.62
5	425438	T62216	Hs.270840	ESTs	0.23	9.45
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	0.03	1.71
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.01	1.49
	428043	T92248	Hs.2240	ulceroglobulin	0.42	1.26
	430280	AA361258	Hs.237868	interleukin 7 receptor	0.46	2.43
10	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	0.57	1.59
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.29	1.80
	432985	T92363	Hs.178703	ESTs	0.32	2.27
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	0.31	1.51
	442275	AW449467	Hs.54795	ESTs	0.55	1.78
	443709	AI082692	Hs.134662	ESTs	0.00	3.02
15	444325	AW152618	Hs.16757	ESTs	0.32	2.49
	450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	0.46	1.74
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	0.52	1.87
	453310	X70697	Hs.553	solute carrier family 8 (neurotransmitte	0.00	3.30
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	0.01	2.31
20	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	0.66	2.20
	400754			Target Exon	1.00	297.00
	401045			C11001883:g 6753278 ref NP_033938.1 c	1.00	109.00
	401083			NM_016582*:Homo sapiens peptide transp	0.89	1.39
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.45	4.47
25	402808			ENSP00000235229:SEMB.	1.00	1.87
	403021			C21000030:g 5955560 ref NP_063957.1 AT	1.00	149.00
	403438			NM_031419*:Homo sapiens molecule possess	1.06	2.96
	403687			NM_007037*:Homo sapiens a disintegrin-li	0.04	4.89
	403764			NM_005463:Homo sapiens heterogeneous nuc	1.00	225.00
30	404277			NM_019111*:Homo sapiens major histocompa	0.97	1.93
	404288			NM_002944*:Homo sapiens v-ros avlan UR2	1.00	68.00
	404518	AI815601		CD83 antigen (activated B lymphocytes, I	0.02	1.83
	405106			C11001637*:g 5032241 ref NP_005732.1 z	1.00	235.00
	405381			Target Exon	1.00	93.00
35	406387			Target Exon	1.37	6.02
	406646	M33600		major histocompatibility complex, class	0.86	2.46
	406714	AI219304	Hs.266959	hemoglobin, gamma G	0.01	3.19
	406753	AA505665	Hs.217493	annexin A2	1.00	147.00
40	406973	M34996	Hs.198253	major histocompatibility complex, class	1.03	2.04
	407248	U82276	Hs.94498	leukocyte immunoglobulin-like receptor,	1.00	64.00
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	1.00	90.00
	407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	1.00	67.00
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.00	102.00
45	408045	AW138959	Hs.245123	ESTs	1.00	70.00
	408074	R20723		ESTs	1.00	112.00
	408374	AW025430	Hs.155591	forkhead box F1	0.07	10.17
	409064	AA062954	Hs.141883	ESTs	0.39	2.31
	409083	AF050083	Hs.673	interleukin 12A (natural killer cell sti	1.00	95.00
50	409153	W03754	Hs.50813	hypothetical protein FLJ20022	0.01	4.55
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	0.01	3.72
	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.00	79.00
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	0.14	27.35
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	1.00	113.00
55	410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	0.64	2.47
	411020	NM_005770	Hs.67726	macrophage receptor with collagenous str	0.55	2.40
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	1.00	111.00
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	1.00	95.00
	412358	BE047490	Hs.24172	ESTs	1.00	87.00
60	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.43	8.07
	412564	X83703	Hs.31432	cardiac ankyrin repeat protein	0.02	3.07
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	0.93	1.72
	412870	N22788	Hs.82407	CXC chemokine ligand 16	0.97	1.51
	413529	U11874	Hs.846	interleukin 8 receptor, beta	0.02	2.42
65	413533	BE146973		gb:QV4-HT0222-011199-019-e05 HT0222 Homo	0.65	1.50
	413689	BE157286	Hs.20631	zinc finger protein, subfamily 1A, 5 (Pe	20.87	232.00
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	1.00	80.00
	413800	AI129238	Hs.192235	ESTs	1.00	85.00
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65557 alpha-1C-	1.00	213.00
70	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	0.02	3.93
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [1.00	115.00
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	0.49	1.94
	414700	H63202	Hs.38163	ESTs	0.03	3.75
	415078	AA311223	Hs.283091	found in inflammatory zone 3	0.86	1.95
75	415120	N84464	Hs.34950	ESTs	1.00	120.00
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	0.60	2.48
	415335	AA847758	Hs.111030	ESTs	1.00	95.00
	415582	W92445	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT	1.00	136.00
	416030	H15261	Hs.21948	ESTs	0.02	8.07
80	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	1.00	73.00
	416464	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co	0.70	3.36
	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	0.06	6.66
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.70	3.68
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	1.00	114.00
85	417370	T28651	Hs.82030	typhlophanyl-tRNA synthetase	0.85	1.30
	417673	T87281	Hs.16355	ESTs	0.16	15.54

	418067	AI127958	Hs.83393	cystatin E/M	0.81	1.74
	418296	C01566	Hs.86671	ESTs	1.00	99.00
	418643	J03798	Hs.86948	small nuclear ribonucleoprotein D1 polyp	1.00	60.00
5	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	2.40	14.74
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.67	3.16
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	1.00	73.00
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	1.00	192.00
	419574	AK001989	Hs.91165	hypothetical protein	1.00	94.00
10	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	61.16	500.00
	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	0.52	1.70
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	1.00	172.00
	420577	AA278436	Hs.186649	ESTs	1.00	97.00
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	1.00	64.00
15	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	0.88	1.61
	421470	R27496	Hs.1378	annaxin A3	0.05	11.26
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.00	73.00
	421563	NM_006433	Hs.105806	granulysin	0.82	2.42
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	5.50	31.57
20	421855	F06504	Hs.27384	ESTs, Moderately similar to ALLJ4_HUMAN A	1.00	129.00
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	1.00	101.00
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 H	0.60	63.60
	422232	D43945	Hs.113274	transcription factor EC	1.00	148.00
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	1.40	3.98
25	423168	R34385	Hs.124940	GTP-binding protein	0.34	3.59
	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	0.55	2.00
	423387	AJ012074		vasoactive intestinal peptide receptor 1	0.09	2.13
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	1.00	141.00
	423456	AL110151	Hs.128797	DKFZP586D0824 protein	1.00	66.00
30	423698	Z92546		Sushi domain (SCR repeat) containing	0.73	1.27
	424027	AW337575	Hs.201591	ESTs	0.54	2.58
	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	0.77	2.47
	425087	R62424	Hs.126059	ESTs	1.00	74.00
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	0.85	1.98
35	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.18	2.56
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	1.00	76.00
	427507	AF240467	Hs.179152	toll-like receptor 7	1.00	63.00
	427618	NM_000760	Hs.2175	colony stimulating factor 3 receptor (gr	0.60	2.19
	427732	NM_002980	Hs.2199	secretin receptor	0.97	1.42
40	427952	AA765368	Hs.293941	ESTs, Moderately similar to A53959 throm	1.00	105.00
	428709	BE268717	Hs.104916	hypothetical protein FLJ21940	1.00	80.00
	428769	AW207175	Hs.106771	ESTs	0.09	2.65
	428780	AI478578	Hs.50636	ESTs	1.00	98.00
	428833	AI928355	Hs.185805	ESTs	1.00	113.00
45	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	1.00	52.00
	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	1.00	132.00
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	0.11	15.60
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	1.00	103.00
50	430414	AW365665	Hs.120388	ESTs	0.50	6.96
	430656	AA482900	Hs.162080	ESTs	1.00	70.00
	430843	AI734149	Hs.119514	ESTs	1.00	90.00
	430998	AF126847	Hs.204038	indolethylamine N-methyltransferase	0.29	1.84
	431217	NM_013427	Hs.260830	Rho GTPase activating protein 6	1.00	79.00
	431921	N46466	Hs.58879	ESTs	0.91	1.67
55	432176	AW090386	Hs.112278	arrestin, beta 1	0.66	2.63
	432203	AA305745	Hs.49	macrophage scavenger receptor 1	1.00	76.00
	432231	AA339977	Hs.274127	CLST 11240 protein	0.46	1.46
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	0.79	2.25
	432522	D11466	Hs.51	phosphatidylinositol glycan, class A (pa	1.93	4.83
60	432596	AJ224741	Hs.278461	matrilin 3	0.04	5.79
	432850	X87723	Hs.3110	angiotensin receptor 2	1.00	167.00
	433138	AB029496	Hs.59729	semaphorin sem2	0.04	9.16
	433563	AI732637	Hs.277901	ESTs	1.00	91.00
	433588	AI056872	Hs.133386	ESTs	120.16	315.00
65	434445	AI349306	Hs.11782	ESTs	0.60	1.84
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	128.00
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	108.00
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	1.00	91.00
	437157	BE048860	Hs.120655	ESTs	1.00	87.00
70	437207	T27503	Hs.15929	hypothetical protein FLJ12910	1.00	105.00
	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	1.00	71.00
	437439	H29796	Hs.269622	ESTs	1.00	115.00
	438199	AW016531	Hs.122147	ESTs	1.00	80.00
	439551	W72062	Hs.11112	ESTs	0.30	3.10
75	440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	1.00	77.00
	440887	AI799488	Hs.135905	ESTs	1.00	85.00
	441025	AA913880	Hs.176379	ESTs	1.00	82.00
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	0.79	1.89
	441735	AI738675	Hs.127346	ESTs	1.00	75.00
80	442200	AW590572	Hs.235768	ESTs	0.78	6.83
	442832	AW206560	Hs.253569	ESTs	0.03	10.88
	442957	AI949952	Hs.49397	ESTs	1.00	70.00
	443282	T47764	Hs.132917	ESTs	1.00	197.00
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	1.00	253.00
85	443951	F13272	Hs.111334	femlin, light polypeptide	0.55	2.09
	444330	AI597655	Hs.49265	ESTs	1.00	90.00

	444515	AW204908	Hs.169979	ESTs	1.00	84.00
	445769	AI741471	Hs.23666	ESTs	0.02	4.38
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	1.00	97.00
	446291	BE397753	Hs.14623	Interferon, gamma-inducible protein 30	0.93	1.69
5	446917	AI347863	Hs.156672	ESTs	1.00	106.00
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.40	47.20
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked mol	1.00	100.00
	447482	AB033059	Hs.18705	KIAA1233 protein	0.05	8.21
10	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheli	0.02	5.42
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	1.00	79.00
	448782	AL050295	Hs.22039	KIAA0758 protein	0.42	1.56
	450575	NM_005859	Hs.29117	purine-rich element binding protein A	0.17	11.33
	450584	AA040403	Hs.60371	ESTs	1.00	94.00
15	450693	AW450461	Hs.203965	ESTs	1.00	91.00
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	1.00	152.00
	451103	R52804	Hs.25956	DKFZP564D206 protein	1.00	86.00
	451220	AF124251	Hs.26054	novel SH2-containing protein 3	0.60	1.30
	451668	Z43948	Hs.326444	cartilage acidic protein 1	0.54	1.91
20	452197	AW023595	Hs.232048	ESTs	1.00	67.00
	452331	AA598509	Hs.29117	purine-rich element binding protein A	4.53	11.07
	452353	C18825	Hs.29191	epithelial membrane protein 2	0.72	2.24
	453049	BE537217	Hs.30343	ESTs	1.00	68.00
	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	0.83	1.70
25	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	1.00	132.00
	453390	AA862496	Hs.28482	ESTs	1.00	72.00
	453531	AA417940		ESTs, Weakly similar to JC5795 CDEP prot	1.00	68.00
	454741	BE154396		gb:CM2-HT0342-091299-050-b05 HT0342 Homo	0.57	2.89
	456579	AA287827	Hs.284205	up-regulated by BCG-CWS	1.00	82.00
30	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	0.79	1.96
	457400	AF032906	Hs.252549	cathepsin Z	1.03	3.25
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	113.00
	459696	F03027		gb:HSC1KA072 normalized infant brain cDN	1.00	544.00

TABLE 10B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT Number	Accession
40	408074	103684_1	R20723 AA263003 AA333976 AA334725 AA334151 AW965490 AA310513 AI810530 D31302 AW134897 AA830127 AA046953 AI668930 C06094 AW104534
	411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
45	413533	1375344_1	BE146973 BE146972 BE147042 BE147018 BE146783 BE147020 BE146781 BE147019 BE146766 BE147021 BE146952 BE146767 BE147044 BE146797 BE146776 BE146985 BE146793 BE146768 BE146771 BE146954 BE146760 BE147048 BE147025 BE147030
	423387	22779_1	AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 AI872991 R72136 AW449839 T81622 T79697 T29519 R94105 T83923 R73300 AI797007 R73380 AA981010 H74168 AI689932 BE045543 AI808418 AI608912 AI806573 AW884084 AW872978 AW872985 AA565655 AI022915 R50647 R73210 H45098 R46451 AW166269 T71132 AI264547 R52146 AI304920 R73391 AW884059 AW884085 H73241 T60038 T79612 R73145 R50549 AI094557 AI668793 R72302 AI564366 W01956 AA418962 W32571 R72840 H45409 R72085 R46356 R46758
50	423698	23112_1	AA508805 AA418798 T83751 R94072 T16182 AA928785 AA903896 Z92546 AA330586 AI570568 AW341487 AI827050 AW298668 AI792189 AI015693 AI733599 AI572251 AI672488 AW193262 AI244716 AI864375 AI206100 AA912444 AI269365 AI640254 AW772466 AI867336 AA627604 H16914 AA358477 AA338009
	430212	314437_1	AA469153 AI718503 AA469225
55	436532	421802_1	AA721522 AW975443 T93070
	453531	97026_1	AA417940 AA036735 T07025
	454741	1232559_1	BE154396 AW817959 BE154393

TABLE 10C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NT_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NT_position
	400754	7331445	Plus	144559-144684
70	401045	8117619	Plus	90044-90184,91111-91345
	401083	3242744	Plus	33192-33360
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	402808	6456148	Minus	114964-115136,115461-115585,115931-116047,117666-117771,118004-118102
	403021	7547270	Plus	120799-120965
75	403421	9665041	Minus	126609-126773,139988-140205
	403438	9719679	Plus	90792-90938
	403687	7387384	Plus	9009-9534
	403764	7717105	Minus	118692-118853
	404277	1834458	Minus	91665-91946
80	404288	2769644	Plus	3512-3691
	404394	3135305	Minus	37121-37205,37491-37762,41053-41140,41322-41593,41773-41919
	404518	8151988	Plus	84494-84603
	404916	7341826	Plus	91057-91188
	405106	8079395	Minus	80877-81418
85	405257	7329310	Plus	73121-73273
	405381	6006920	Minus	7636-8054

WO 02/086443
406387 9256180 Plus

116229-116371,117512-117651

PCT/US02/12476

TABLE 11A: Genes Distinguishing Adenocarcinoma from Other Lung Diseases and Normal Lung

Table 11A shows about 84 genes upregulated in lung adenocarcinomas relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 11B show the accession numbers for those Pkey's lacking UnigenelD's for table 11A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 11C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 11A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset Identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
403329			Target Exon	1.00	61.00
406399			NM_003122*:Homo sapiens serine protease	1.00	39.00
406690	M29540	Hs.220529	cardioembryonic antigen-related cell ad	226.37	350.00
407869	A1827976	Hs.24391	hypothetical protein FLJ13612	0.77	1.18
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	1.00	10.00
408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
409187	AF154830	Hs.50968	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
410076	T05387	Hs.7991	ESTs	1.12	1.50
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
410399	BE068889		synuclein, gamma (breast cancer-specific	0.92	1.06
411908	L27943	Hs.72924	cytidine deaminase	1.00	1.00
412612	NM_000047	Hs.74131	arylsulfatase E (chondrodysplasia puncta	1.02	1.03
414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	0.84	1.07
416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
417542	J04129	Hs.82269	progesterone-associated endometrial prote	1.28	1.35
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
419631	AW188117	Hs.303154	popeye protein 3	1.00	13.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
421190	U85031	Hs.102482	mucin 5, subtype B, tracheobronchial	1.17	1.55
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.78
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, l	1.00	3.00
421582	A1910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
422095	A1868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.16	1.78
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	48.13	72.00
423554	M90518	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
424502	AF242388	Hs.149585	lengsin	1.00	1.00
424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.00	59.00
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
424960	BE245380	Hs.153952	5' nucleotidase (CD73)	1.00	1.00
425523	AB007948	Hs.158244	KIAA0479 protein	1.00	35.00
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.00	83.00
427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
428585	AB007863	Hs.185140	KIAA0403 protein	1.00	6.00
428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
430508	A1015435	Hs.104637	ESTs	4.75	7.27
430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	0.94	1.28
431548	A1834273	Hs.9711	novel protein	5.66	15.00
431566	AF176012	Hs.260720	J domain containing protein 1	49.76	37.00
431986	AA536130	Hs.149018	Novel human gene mapping to chromosome 20	1.19	1.47
432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
433558	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
433819	AW511097	Hs.112765	ESTs	3.71	8.00
434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	29.31	72.00
434424	A1811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
434792	AA649253	Hs.132458	ESTs	8.52	44.00
436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.10	1.41
436972	AA284679	Hs.25640	claudin 3	1.59	1.46
437866	AA156781		metallothionein 1E (functional)	3.62	101.00
437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	1.60	1.39
438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
439451	AF096270	Hs.278554	heterochromatin-like protein 1	23.28	52.00

439769	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00
441377	BE218239	Hs.202656	ESTs	22.03	1.00
443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	16.00
443813	AA876372	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr	1.20	1.99
443991	NM_002250	Hs.10082	potassium intermediate/small conductance	5.71	6.87
444670	H58373	Hs.332938	hypothetical protein MGC5370	1.98	38.00
444931	AV652066	Hs.75113	general transcription factor IIIA	1.00	54.00
446102	AW168067	Hs.317694	ESTs	1.00	1.00
446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1.00	36.00
446469	BE094848	Hs.15113	homogenisate 1,2-dioxygenase (homogenit	1.00	11.00
447388	AW630534	Hs.76277	Homo sapiens, clone MGC:9381, mRNA, comp	1.24	1.16
447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
448243	AW369771	Hs.52620	integrin, beta 8	15.84	1.00
448844	AI591519	Hs.177164	ESTs	1.00	31.00
449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	1.00	83.00
451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
452689	F33868	Hs.284176	transferrin	1.54	1.44
453392	U23762	Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00
453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	1.55	2.45
453735	AI066629	Hs.125073	ESTs	1.01	1.30

TABLE 11B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

410399	11995_1	BE068889 BE068882 AF044311 AF017256 NM_003087 AF037207 AF010126 AA633976 AA872836 BE298825 BE299889 AI016464 AI684600 AI936527 AA804675 AA394097 AI139933 AA946606 BE171313 AA722407 AA293803 AI468480 AA056035 AA055968 AW796957 AI637713 AA410737 H49348 AA486472 AA411094 AA235594 AA402624 AA443638 AW452137 AA421708 AW265211 AI493266 AA365132 AW966044 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T68786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60830 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M54982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T81109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R05796 H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI064740 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R85521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596 AW470774 AV651256 N54417 AA812862 AW182929 AI111192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778 AA344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 R29500 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343080 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62138 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64784 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068 AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA505678 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA588276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI471883 W84421 AA156850 W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291 AW450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827628 AA904788 AA380381 AA886045 AA774409 BE003229 Z41758
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TABLE 11C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403329	8516120	Plus	96450-96598
406399	9256288	Minus	63448-63554

TABLE 12A: Genes Distinguishing Squamous Cell Carcinoma from Other Lung Diseases and Normal Lung

Table 12A shows about 72 genes upregulated in squamous cell carcinomas of the lung relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Atfytmatrix Hu03 Genechip array.

Table 12B show the accession numbers for those Pkey's lacking UnigenelD's for table 12A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 12C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 12A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset Identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigena number
 Unigena Title: Unigena gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigena Title	R1	R2
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
401780			NM_005557:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275:Homo sapiens keratin 15 (KRT1	4.13	2.70
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
404996			Target Exon	1.00	1.00
407839	AA045144	Hs.161566	ESTs	173.91	108.00
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.98	1.24
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	8.97	3.27
418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
421773	W69233	Hs.112457	ESTs	1.12	1.14
421948	L42583	Hs.334309	keratin 6A	51.83	20.25
421978	AJ243662	Hs.110196	NICE-1 protein	1.01	0.91
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00
427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
430890	X54232	Hs.2699	glypican 1	1.58	1.40
431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
434360	AW015415	Hs.127780	ESTs	40.98	27.00
434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.00	1.00
435505	AF200492	Hs.211238	Interleukin-1 homolog 1	1.00	38.00
435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
436511	AA721252	Hs.291502	ESTs	16.76	14.00
438403	AA806607	Hs.292206	ESTs	1.00	1.00
439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
441525	AW241867	Hs.127728	ESTs	1.53	1.42
443162	T49951	Hs.9029	DKFZP434G032 protein	31.11	38.00
444378	R41339	Hs.12569	ESTs	1.00	1.00

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446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
447078	AW885727	Hs.9914	ESTs	47.24	24.00
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00
450832	AW970602	Hs.105421	ESTs	25.17	36.00
452240	AI591147	Hs.61232	ESTs	13.42	1.00
453317	NM_002277	Hs.41698	keratin, hair, acidic, 1	1.19	1.27
453830	AA534296	Hs.20953	ESTs	24.92	25.00
454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11
455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	208.11	1.00

TABLE 12B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077

TABLE 12C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400666	8118496	Plus	17982-18115,20297-20456
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450

TABLE 13A: Genes Distinguishing Non-Malignant Lung Disease from Lung Tumors and Normal lung

Table 13A shows about 23 genes upregulated in non-malignant lung disease relative to lung tumors and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 13B show the accession numbers for those Pkey's lacking UnigeneID's for table 13A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 13C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 13A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
409031	AA376836	Hs.76728	ESTs	1.00	128.00
412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00
417511	AL049176	Hs.82223	chordin-like	1.00	179.00
418819	AA228776	Hs.191721	ESTs	1.00	140.00
422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
424585	AA464840	Hs.131987	ESTs	1.00	167.00
426753	T89832	Hs.170278	ESTs	1.00	141.00
429496	AA453800	Hs.192793	ESTs	1.00	138.00
430719	AA488988	Hs.293798	ESTs	1.00	133.00
431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
431728	NM_007351	Hs.268107	multimerin	1.00	157.00
436532	AA721522		gb:mv54h12.r1 NCL_CGAP_Ew1 Homo sapiens	1.00	218.00
437960	AI669586	Hs.222194	ESTs	1.00	147.00
438202	AW169287	Hs.22588	ESTs	1.00	141.00
441499	AW298235	Hs.101689	ESTs	1.00	167.00
444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
448253	H25899	Hs.201591	ESTs	1.00	141.00
453636	R67837	Hs.169872	ESTs	1.00	116.00
458332	AI000341	Hs.220491	ESTs	1.00	192.00
459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	1.00	154.00

TABLE 13B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
431089	327825_1	BE041395 AA491826 AA621946 AA715980 AA666102
436532	421802_1	AA721522 AW975443 T93070

TABLE 13C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

TABLE 14A: Preferred Utility and Subcellular Localization for Potential Lung Disease Targets

Table 14A shows the subcellular localization and preferred utility for the genes appearing in Tables 9A and 10A. mAb symbolizes monoclonal antibody, diag symbolizes diagnostic, s.m. symbolizes small molecule, and CTL symbolizes cytotoxic lymphocytic ligand. These genes were selected from 59680 probesets on the Eos/Affymatrix Hu03 Genechip array.

Table 14B show the accession numbers for those Pkey's lacking UnigenelD's for table 14A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 14C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 14A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigenel number

Unigenel Title: Unigenel gene title

Pref.Utility: Preferred Utility

Pred.Loc: Predicted subcellular localization

Pkey	ExAccn	UnigenelD	Unigenel Title	Pref Utility	Pred. Loc
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin)	mAb & diag & s.m.	extracellular
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	mAb	plasma membrane
402075			ENSP00000251056*:Plasma membrane calcium	mAb & diag	secreted
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	diag	secreted
408243	Y00787	Hs.624	interleukin 8	diag	secreted
408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	mAb & s.m.	plasma membrane
408908	BE296227	Hs.250822	serine/threonine kinase 15	s.m.	cytoplasm
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	CTL & diag	secreted
409103	AF251237	Hs.112208	XAGE-1 protein	CTL	nuclear
409420	Z16008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalni	diag	secreted
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	diag	secreted
409757	NM_001898	Hs.123114	cystatin SN	diag	extracellular
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	CTL	nuclear
409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	diag	extracellular
410001	AB041036	Hs.57771	kallikrein 11	diag	extracellular
410407	X66839	Hs.63287	carbonic anhydrase IX	mAb & s.m.	plasma membrane
410418	D31382	Hs.63325	transmembrane protease, serine 4	mAb & diag & s.m.	plasma membrane
412140	AA219591	Hs.73625	RAB6 interacting, kinesin-like (rabkines	s.m.	
412719	AW018610	Hs.816	ESTs	s.m.	nuclear
414774	X02419	Hs.77274	plasminogen activator, urokinase	diag	extracellular
414883	AA926960		CDC28 protein kinase 1	s.m.	
415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	CTL & diag	extracellular
415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor	mAb & diag & s.m.	secreted
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	mAb & s.m.	plasma membrane
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	diag	extracellular
417034	NM_008183	Hs.80962	neurotensin	diag	extracellular
417079	U65590	Hs.81134	Interleukin 1 receptor antagonist	diag	extracellular
417308	H60720	Hs.81892	KIAA0101 gene product	s.m.	mitochondrial
417389	BE260984	Hs.82045	midkine (neurite growth-promoting factor	mAb & diag	secreted
417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	mAb	plasma membrane
417933	X02308	Hs.82962	thymidylate synthetase	s.m.	endoplasmic reticulum
418478	U89945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	s.m.	cytoplasm
418506	AA084248	Hs.85339	G protein-coupled receptor 39	mAb & s.m.	plasma membrane
418678	NM_001327	Hs.187379	cancer/testis antigen (NY-ESO-1)	CTL	cytoplasmic
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	diag	secreted
419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	mAb & s.m.	plasma membrane
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	CTL & s.m.	mitochondrial
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	diag	secreted
419235	AW470411	Hs.288433	neurotrophin	mAb & diag	plasma membrane
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	mAb & s.m.	plasma membrane
419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	mAb & diag	extracellular*
420610	AI683183	Hs.99348	distal-less homeo box 5	CTL	nuclear
421110	AJ250717	Hs.1355	calthepsin E	sm & diag	extracellular
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	diag	secreted
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	mAb & s.m.	plasma membrane
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	diag	secreted
421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	mAb & s.m.	plasma membrane
421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	mAb & s.m.	plasma membrane
422109	S73265	Hs.1473	gastrin-releasing peptide	diag	secreted
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	diag	secreted
422282	AF019225	Hs.114309	apolipoprotein L	diag	secreted
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	s.m.	nuclear
422424	AI186431	Hs.296638	prostate differentiation factor	diag	extracellular
422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	s.m.	cytoplasm
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	s.m.	nuclear
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	diag	extracellular
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	CTL & s.m.	
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	diag	
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	mAb & diag & s.m.	secreted
423961	D13666	Hs.136348	perforin (OSF-2os)	mAb & diag	extracellular
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor	diag	secreted
424381	AA285249	Hs.146329	protein kinase Chk2	s.m.	nuclear

	424502	AF242388	Hs.149585	lensin	s.m.	cytoplasmic
	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	mAb & s.m.	plasma membrane
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	diag	extracellular
5	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	mAb & diag & s.m.	secreted
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	s.m.	cytoplasmic
	425550	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	mAb	plasma membrane
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	s.m.	
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	mAb & diag	plasma membrane
10	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	mAb & s.m.	plasma membrane
	426215	AW963419	Hs.155223	stanniocalcin 2	mAb & diag	secreted
	426427	M86699	Hs.169840	TTK protein kinase	CTL & s.m.	nuclear
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	mAb & diag	secreted
	427335	AA448542	Hs.251877	G antigen 7B	CTL	cytoplasmic
	427747	AW411425	Hs.180655	serine/threonine kinase 12	s.m.	cytoplasmic
15	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	diag	
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	mAb & diag & s.m.	extracellular
	428450	NM_014791	Hs.184339	KIAA0175 gene product	s.m.	nuclear
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	s.m.	nuclear
20	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	mAb & s.m.	plasma membrane
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	CTL & s.m.	nuclear
	428698	AA852773	Hs.334838	KIAA1866 protein	mAb	
	428748	AW593206	Hs.98785	Ksp37 protein	diag	extracellular
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	diag	mitochondria*
	428969	AF120274	Hs.194689	artemin	diag	extracellular
25	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	mAb & s.m.	plasma membrane
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	mAb & s.m.	plasma membrane
	429547	AW009166	Hs.99376	ESTs	diag	secreted
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	mAb & diag	secreted
30	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	s.m.	
	430488	BE062109	Hs.241551	chloride channel, calcium activated, fam	mAb & s.m.	plasma membrane
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	diag	extracellular
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	mAb & s.m.	plasma membrane
	431846	BE019924	Hs.271580	uroplakin 1B	mAb & diag	plasma membrane
35	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	mAb & diag	plasma membrane
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	mAb & diag & s.m.	plasma membrane
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	s.m.	nuclear
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	diag	secreted
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	s.m.	
40	437016	AU076916	Hs.5398	guanine monophosphate synthetase	s.m.	cytoplasm
	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	CTL	ER
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	CTL	nuclear
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.sa	mAb & s.m.	plasma membrane
	439223	AW238299	Hs.250618	UL16 binding protein 2	mAb	plasma membrane
45	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN	mAb & s.m.	
	439606	W79123	Hs.58561	G protein-coupled receptor 87	mAb & s.m.	plasma membrane
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	mAb & s.m.	plasma membrane
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-II	s.m.	nuclear
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	s.m.	
50	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	mAb & s.m.	plasma membrane
	443247	BE614387	Hs.333893	c-Myc target JPO1	CTL	extracellular*
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	CTL	
	443859	NM_013409	Hs.9914	folliculin	diag	extracellular
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	mAb	plasma membrane
55	444371	BE540274	Hs.239	forkhead box M1	s.m.	nuclear
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	diag	secreted
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	mAb & diag	plasma membrane
	445537	AJ245871	Hs.12844	EGF-like-domain, multiple 6	mAb & diag	secreted
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	diag	secreted
60	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	diag	extracellular
	447033	AI357412	Hs.157601	ESTs	CTL & diag	secreted
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	CTL	
	448243	AW369771	Hs.52620	Integrin, beta 8	mAb & s.m.	plasma membrane
	448844	AI581519	Hs.177164	ESTs	mAb & s.m.	
65	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	mAb	plasma membrane
	449722	BE280074	Hs.23960	cyclin B1	s.m.	cytoplasm
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	mAb & s.m.	plasma membrane
	450376	AA009647		a disintegrin and metalloproteinase doma	mAb & diag & s.m.	plasma membrane
	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	mAb & diag	plasma membrane
70	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	diag	secreted
	451668	Z43948	Hs.326444	cartilage acidic protein 1	mAb & diag	plasma membrane
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	diag	
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	diag	extracellular
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	mAb	plasma membrane
75	452838	U65011	Hs.30743	preferentially expressed antigen in mela	CTL	nuclear
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	CTL & s.m.	nuclear
	457489	AI693815	Hs.127179	cryptic gene	diag	secreted

TABLE 14B

80 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession

WO 02/086443

PCT/US02/12476

414883 15024_1 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245
AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387
AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA869955 AI204630 W25243 AI935150
AA872039 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667
R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046
AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031
N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045
AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239
AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850
AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785
AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789
AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923
H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156
W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672
15 450375 83327_1 AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

TABLE 14C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
25 NT_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NT_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

TABLE 15A: Information for all sequences in Table 16

Table 15A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigene Title for all of the sequences in Table 16.

5 Table 15B show the accession numbers for those Pkey's lacking UnigenelD's for table 15A. For each probaset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10 Table 15C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 15A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

15 Seq ID No: Sequence ID number
 Pkey: Unique Eos probaset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title

20	Seq ID No:	Pkey	ExAccn	UnigenelD	Unigene Title
	Seq ID No: 1 & 2	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 3 & 4	412719	AW016610	Hs.816	ESTs
	Seq ID No: 5 & 6	417034	NM_006183	Hs.80862	neurotensin
25	Seq ID No: 7 & 8	430486	BE082109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 9 & 10	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 11 & 12	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 13 & 14	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 15 & 16	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
30	Seq ID No: 17 & 18	439285	AL133916		hypothetical protein FLJ20093
	Seq ID No: 19 & 20	413753	U17760	Hs.75517	laminin, beta 3 (niclin (125kD), kalinin
	Seq ID No: 21 & 22	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog
	Seq ID No: 23 & 24	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 25 & 26	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines
35	Seq ID No: 27 & 28	423573	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
	Seq ID No: 29 & 30	452838	U65011	Hs.30743	preferentially expressed antigen in mela
	Seq ID No: 31 & 32	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 33 & 34	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 35 & 36	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor
40	Seq ID No: 37 & 38	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
	Seq ID No: 39 & 40	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 41 & 42	431846	BE019924	Hs.271580	uroplakin 1B
	Seq ID No: 43 & 44	418830	BE513731	Hs.88959	hypothetical protein MGC4816
	Seq ID No: 45 & 46	424098	AF077374	Hs.139322	small proline-rich protein 3
45	Seq ID No: 47 & 48	443648	AJ085377	Hs.143610	ESTs
	Seq ID No: 49	311034	BE567130	Hs.311389	ESTs, Highly similar to NKGD_HUMAN NKG2-
	Seq ID No: 50 & 51	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,
	Seq ID No: 52 & 53	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
	Seq ID No: 54 & 55	435505	AF200492	Hs.211238	interleukin-1 homolog 1
50	Seq ID No: 56 & 57	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)
	Seq ID No: 58 & 59	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
	Seq ID No: 60 & 61	441020	W79283	Hs.35962	ESTs
	Seq ID No: 62 & 63	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys
	Seq ID No: 64 & 65	429538	BE182592	Hs.11261	small proline-rich protein 2A
55	Seq ID No: 66 & 67	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte
	Seq ID No: 68 & 69	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 70 & 71	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 72 & 73	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 74 & 75	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
60	Seq ID No: 76 & 77	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
	Seq ID No: 78 & 79	429259	AA420450	Hs.292911	Plakophilin
	Seq ID No: 80 & 81	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu
	Seq ID No: 82 & 83	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
	Seq ID No: 84 & 85	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro
65	Seq ID No: 86 & 87	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
	Seq ID No: 88 & 89	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq ID No: 90 & 91	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
	Seq ID No: 92 & 93	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr
	Seq ID No: 94 & 95	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated
70	Seq ID No: 96 & 97	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re
	Seq ID No: 98 & 99	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
	Seq ID No: 100 & 101	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o
	Seq ID No: 102 & 103	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
	Seq ID No: 104 & 105	409103	AF251237	Hs.112208	XAGE-1 protein
75	Seq ID No: 106 & 107	417542	J04129	Hs.82269	progesterone-associated endometrial prote
	Seq ID No: 108 & 109	428471	X57348	Hs.184510	stratifer
	Seq ID No: 110 & 111	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member
	Seq ID No: 112 & 113	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2
	Seq ID No: 114 & 115	418203	X54942	Hs.83758	CDC28 protein kinase 2
80	Seq ID No: 116	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m
	Seq ID No: 117 & 118	437018	AU076916	Hs.5398	guanine monophosphate synthetase
	Seq ID No: 119 & 120	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 121 & 122	446989	AK001898	Hs.16740	hypothetical protein FLJ11036
	Seq ID No: 123 & 124	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein
85	Seq ID No: 125 & 126	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B

5	Seq ID No: 127 & 128	414430	AI348201	Hs.76118	ubiquitin carboxyl-terminal esterase L1
	Seq ID No: 129 & 130	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 131 & 132	100868	L05424	Hs.169610	CD44 antigen (homing function and Indian
	Seq ID No: 133 & 134	458933	AI638429	Hs.24763	RAN binding protein 1
	Seq ID No: 135 & 136	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
10	Seq ID No: 137 & 138	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 139 & 140	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 141 & 142	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 143 & 144	446269	AW263155	Hs.14559	hypothetical protein FLJ10540
	Seq ID No: 145 & 146	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur
15	Seq ID No: 147 & 148	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con
	Seq ID No: 149 & 150	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma
	Seq ID No: 151 & 152	439606	W79123	Hs.58561	G protein-coupled receptor 87
	Seq ID No: 153 & 154	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 155 & 156	453884	AA355925	Hs.36232	KIAA0186 gene product
20	Seq ID No: 157 & 158	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 159 & 160	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 161 & 162	404877			NM_005365:Homo sapiens melanoma antigen,
	Seq ID No: 163 & 164	413129	AF292100	Hs.104613	RP42 homolog
	Seq ID No: 165 & 166	413281	AA861271	Hs.222024	transcription factor BMAL2
25	Seq ID No: 167 & 168	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 169 & 170	416819	U77735	Hs.80205	pim-2 oncogene
	Seq ID No: 171 & 172	451320	AW118072		diacylglycerol kinase, zeta (104kD)
	Seq ID No: 173 & 174	418543	NM_005329	Hs.85952	hyaluronan synthase 3
	Seq ID No: 175 & 176	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member
30	Seq ID No: 177 & 178	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)
	Seq ID No: 179 & 180	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 181 & 182	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 183 & 184	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 185 & 186	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
35	Seq ID No: 187 & 188	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 189 & 190	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 191 & 192	448993	AI471630	Hs.8127	KIAA0144 gene product
	Seq ID No: 193 & 194	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 195 & 196	430393	BE185030	Hs.241305	estrogen-responsive B box protein
40	Seq ID No: 197 & 198	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol
	Seq ID No: 199 & 200	420462	AF050147	Hs.97932	chondromodulin 1 precursor
	Seq ID No: 201 & 202	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta
	Seq ID No: 203 & 204	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid
	Seq ID No: 205 & 206	101175	U82671	Hs.36980	melanoma antigen, family A, 2
45	Seq ID No: 207 & 208	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like
	Seq ID No: 209 & 210	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 211 & 212	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 213 & 214	131927	AJ003112	Hs.34780	doublecortin, lissencephaly, X-linked (d
	Seq ID No: 215 & 216	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT
50	Seq ID No: 217 & 218	427335	AA448542	Hs.251677	G antigen 78
	Seq ID No: 219 & 220	409420	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini
	Seq ID No: 221 & 222	114346	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II
	Seq ID No: 223 & 224	438956	W00847	Hs.135055	Human DNA sequence from clone RP5-850E9
	Seq ID No: 225 & 226	404440			NM_021048:Homo sapiens melanoma antigen,
55	Seq ID No: 227 & 228	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor
	Seq ID No: 229 & 230	103312	Y12642	Hs.3185	lysosomal
	Seq ID No: 231 & 232	320843	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr
	Seq ID No: 233	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fls, clone NT
	Seq ID No: 234 & 235	446102	AW168067	Hs.317694	ESTs
60	Seq ID No: 236 & 237	330495	U47924	Hs.71642	guanine nucleotide binding protein (G pr
	Seq ID No: 238	413573	AI733859	Hs.149089	ESTs
	Seq ID No: 239 & 240	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
	Seq ID No: 241 & 242	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
	Seq ID No: 243 & 244	332180	AF134160	Hs.7327	claudin 1
65	Seq ID No: 245	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca
	Seq ID No: 246 & 247	441553	AA281219	Hs.121296	ESTs
	Seq ID No: 248 & 249	331692	AI683487	Hs.152213	wingless-type MMTV integration site fami
	Seq ID No: 250 & 251	429413	NM_014058	Hs.201877	DESC1 protein
	Seq ID No: 252 & 253	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis
70	Seq ID No: 254 & 255	448357	N20169	Hs.108923	RAB38, member RAS oncogene family
	Seq ID No: 256 & 257	446292	AF081497	Hs.279682	Rh type C glycoprotein
	Seq ID No: 258 & 259	416209	AA235776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h
	Seq ID No: 260 & 261	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1
	Seq ID No: 262 & 263	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor
75	Seq ID No: 264 & 265	439223	AW238299	Hs.250618	UL16 binding protein 2
	Seq ID No: 266 & 267	429228	AI553633	Hs.326447	ESTs
	Seq ID No: 268 & 269	409757	NM_001898	Hs.123114	cystatin SN
	Seq ID No: 270 & 271	411089	AA456454	Hs.214291	cell division cycle 2-like 1 (PITSLRE pr
	Seq ID No: 272 & 273	436511	AA721252	Hs.291502	ESTs
80	Seq ID No: 274 & 275	428969	AF120274	Hs.194689	artemin
	Seq ID No: 276 & 277	428969	AF120274	Hs.194689	artemin
	Seq ID No: 278 & 279	428969	AF120274	Hs.194689	artemin
	Seq ID No: 280 & 281	428969	AF120274	Hs.194689	artemin
	Seq ID No: 282	407137	T97307		gbye53h05.s1 Soares fetal liver spleen
85	Seq ID No: 283 & 284	412723	AA648459	Hs.335951	hypothetical protein AF301222
	Seq ID No: 285 & 286	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 287 & 288	405770			NM_002362:Homo sapiens melanoma antigen,
	Seq ID No: 289 & 290	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13
	Seq ID No: 291 & 292	414774	X02419	Hs.77274	plasminogen activator, urokinase

5	Seq ID No: 293 & 294	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub
	Seq ID No: 295 & 296	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 297 & 298	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 299 & 300	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 301 & 302	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
10	Seq ID No: 303 & 304	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 305 & 306	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso
	Seq ID No: 307 & 308	403478			NM_022342:Homo sapiens kinesin protein 9
	Seq ID No: 309	441525	AW241867	Hs.127728	ESTs
	Seq ID No: 310 & 311	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro
15	Seq ID No: 312 & 313	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep
	Seq ID No: 314 & 315	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B
	Seq ID No: 316 & 317	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f
	Seq ID No: 318 & 319	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell
	Seq ID No: 320 & 321	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg
20	Seq ID No: 322 & 323	413582	AW295647	Hs.71331	hypothetical protein MGC5350
	Seq ID No: 324 & 325	438403	AA806607	Hs.292206	ESTs
	Seq ID No: 326 & 327	403329			unnamed protein product (Homo sapiens)
	Seq ID No: 328 & 329	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.
	Seq ID No: 330 & 331	119073	BE245360	Hs.279477	v-ets erythroblastosis virus E26 oncogen
25	Seq ID No: 332 & 333	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
	Seq ID No: 334 & 335	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11
	Seq ID No: 336 & 337	101345	NM_005795	Hs.152175	calcitonin receptor-like
	Seq ID No: 338 & 339	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
	Seq ID No: 340 & 341	102012	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
30	Seq ID No: 342 & 343	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds
	Seq ID No: 344 & 345	134299	AW580939	Hs.97199	complement component C1q receptor
	Seq ID No: 346 & 347	412719	AW016610	Hs.816	ESTs
	Seq ID No: 348 & 349	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
	Seq ID No: 350 & 351	128924	BE279383	Hs.26557	plakophilin 3
35	Seq ID No: 352 & 353	100486	T19006	Hs.10842	RAN, member RAS oncogene family
	Seq ID No: 354 & 355	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 356 & 357	409459	D86407	Hs.54481	low density lipoprotein receptor-related
	Seq ID No: 358 & 359	330493	M27826		endogenous retroviral protease
	Seq ID No: 360 & 361	417866	AW067903	Hs.82772	collagen, type XI, alpha 1
40	Seq ID No: 362 & 363	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4
	Seq ID No: 364 & 365	437016	AU076916	Hs.5398	guanine monophosphate synthetase
	Seq ID No: 366 & 367	429612	AF062649	Hs.252587	pituitary tumor-transforming 1
	Seq ID No: 368 & 369	440704	M69241	Hs.162	insulin-like growth factor binding prote
	Seq ID No: 370 & 371	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye
45	Seq ID No: 372 & 373	431565	AF161470	Hs.260622	butyrate-induced transcript 1
	Seq ID No: 374 & 375	431565	AF161470	Hs.260622	butyrate-induced transcript 1
	Seq ID No: 376 & 377	132354	BE185289	Hs.1076	small proline-rich protein 1B (comifin)
	Seq ID No: 378 & 379	424441	X14850	Hs.147097	H2A histone family, member X
	Seq ID No: 380 & 381	103768	AF086009	Hs.296398	gb:Homo sapiens full length insert cDNA
50	Seq ID No: 382 & 383	417512	X76534	Hs.82226	glycoprotein (transmembrane) numb
	Seq ID No: 384 & 385	425266	J00077	Hs.155421	alpha-fetoprotein
	Seq ID No: 386 & 387	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,
	Seq ID No: 388 & 389	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
	Seq ID No: 390 & 391	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
55	Seq ID No: 392 & 393	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 394 & 395	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino
	Seq ID No: 396 & 397	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2
	Seq ID No: 398 & 399	418506	AA084248	Hs.85339	G protein-coupled receptor 39
	Seq ID No: 400 & 401	423961	D13666	Hs.136348	perostin (OSF-2os)
60	Seq ID No: 402 & 403	414812	X72755	Hs.77367	monokine induced by gamma interferon
	Seq ID No: 404 & 405	417433	BE270268	Hs.82128	ST4 oncofetal trophoblast glycoprotein
	Seq ID No: 406 & 407	417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein
	Seq ID No: 408 & 409	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
	Seq ID No: 410 & 411	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy
65	Seq ID No: 412 & 413	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe
	Seq ID No: 414 & 415	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated
	Seq ID No: 416 & 417	411789	AF245505	Hs.72167	Adlcan
	Seq ID No: 418 & 419	428698	AA852773	Hs.334838	KIAA1866 protein
	Seq ID No: 420 & 421	450098	W27249	Hs.8109	hypothetical protein FLJ21080
70	Seq ID No: 422 & 423	421552	AF026692	Hs.105700	secreted frizzled-related protein 4
	Seq ID No: 424 & 425	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR
	Seq ID No: 426 & 427	450376	AA009647		a disintegrin and metalloproteinase doma
	Seq ID No: 428 & 429	426215	AW963419	Hs.155223	stanniocalcin 2
	Seq ID No: 430 & 431	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin
75	Seq ID No: 432 & 433	432201	AI538613	Hs.298241	Transmembrane protease, serine 3
	Seq ID No: 434 & 435	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph
	Seq ID No: 436 & 437	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447
	Seq ID No: 438 & 439	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn
	Seq ID No: 440 & 441	447033	AI357412	Hs.157601	ESTs
80	Seq ID No: 442 & 443	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 444 & 445	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 446 & 447	115522	BE614387	Hs.333893	c-Myc target JPO1
	Seq ID No: 448 & 449	410418	D31382	Hs.63325	transmembrane protease, serine 4
	Seq ID No: 450 & 451	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
85	Seq ID No: 452 & 453	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 454 & 455	452461	N78223	Hs.108106	transcription factor
	Seq ID No: 456 & 457	412420	AL035668	Hs.73853	bone morphogenetic protein 2
	Seq ID No: 458 & 459	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara
	Seq ID No: 460 & 461	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon

	Seq ID No: 462 & 463	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [Hsa
	Seq ID No: 464 & 465	402075			ENSP00000251056*:Plasma membrane calcium
	Seq ID No: 466 & 467	421110	AJ260717	Hs.1355	cathepsin E
5	Seq ID No: 468 & 469	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 470 & 471	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 472 & 473	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 474 & 475	422282	AF019225	Hs.114309	apolipoprotein L
	Seq ID No: 476 & 477	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member
10	Seq ID No: 478 & 479	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),
	Seq ID No: 480 & 481	427747	AW411425	Hs.180655	serine/threonine kinase 12
	Seq ID No: 482 & 483	420281	AI623693	Hs.323494	Predicted cation efflux pump
	Seq ID No: 484 & 485	405932			C15000305:gi 3806122 gb AAC69198.1 (AF0
	Seq ID No: 486 & 487	405932			C15000305:gi 3806122 gb AAC69198.1 (AF0
15	Seq ID No: 488 & 489	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane
	Seq ID No: 490 & 491	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy
	Seq ID No: 492 & 493	417079	U65590	Hs.81134	Interleukin 1 receptor antagonist
	Seq ID No: 494 & 495	430890	X54232	Hs.2699	glypican 1
	Seq ID No: 496 & 497	419721	NM_001650	Hs.288650	aquaporin 4
20	Seq ID No: 498 & 499	444471	AB020684	Hs.11217	KIAA0877 protein
	Seq ID No: 500 & 501	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
	Seq ID No: 502 & 503	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly
	Seq ID No: 504 & 505	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 506 & 507	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
25	Seq ID No: 508 & 509	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte
	Seq ID No: 510 & 511	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 512 & 513	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s
	Seq ID No: 514 & 515	412719	AW016610	Hs.816	ESTs
	Seq ID No: 516 & 517	417034	NM_006183	Hs.80962	neurotensin
30	Seq ID No: 518 & 519	430488	BE062109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 520 & 521	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
	Seq ID No: 522 & 523	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 524 & 525	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
	Seq ID No: 526 & 527	418663	AK001100	Hs.41690	desmocollin 3
35	Seq ID No: 528 & 529	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 530 & 531	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
	Seq ID No: 532 & 533	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 534 & 535	431846	BE019924	Hs.271580	uroplakin 1B
	Seq ID No: 536 & 537	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
40	Seq ID No: 538 & 539	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
	Seq ID No: 540 & 541	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
	Seq ID No: 542 & 543	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
	Seq ID No: 544 & 545	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq ID No: 546 & 547	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
45	Seq ID No: 548 & 549	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
	Seq ID No: 550 & 551	417542	J04129	Hs.82269	progestagen-associated endometrial prote
	Seq ID No: 552 & 553	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 554 & 555	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 556 & 557	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
50	Seq ID No: 558 & 559	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B
	Seq ID No: 560 & 561	418462	BE001596	Hs.85266	Integrin, beta 4
	Seq ID No: 562 & 563	410274	AA381807	Hs.61762	hypoxia-inducible protein 2
	Seq ID No: 564 & 565	439606	W79123	Hs.58561	G protein-coupled receptor 87
	Seq ID No: 566 & 567	404877			NM_005365:Homo sapiens melanoma antigen,
55	Seq ID No: 568 & 569	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 570 & 571	418543	NM_005329	Hs.85962	hyaluronan synthase 3
	Seq ID No: 572 & 573	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 574 & 575	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 576 & 577	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
60	Seq ID No: 578 & 579	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 580 & 581	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 582 & 583	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 584 & 585	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 586 & 587	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
65	Seq ID No: 588 & 589	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 590 & 591	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
	Seq ID No: 592 & 593	332180	AF134160	Hs.7327	claudin 1
	Seq ID No: 594 & 595	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
	Seq ID No: 596 & 597	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
70	Seq ID No: 598 & 599	439223	AW238299	Hs.250618	UL16 binding protein 2
	Seq ID No: 600 & 601	409757	NM_001898	Hs.123114	cystatin SN
	Seq ID No: 602 & 603	428969	AF120274	Hs.194689	artemin
	Seq ID No: 604 & 605	428969	AF120274	Hs.194689	artemin
	Seq ID No: 606 & 607	428969	AF120274	Hs.194689	artemin
75	Seq ID No: 608 & 609	428969	AF120274	Hs.194689	artemin
	Seq ID No: 610 & 611	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 612 & 613	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 614 & 615	414774	X02419	Hs.77274	plasminogen activator, urokinase
	Seq ID No: 616 & 617	407944	R34008	Hs.239727	desmocollin 2
	Seq ID No: 618 & 619	407944	R34008	Hs.239727	desmocollin 2
80	Seq ID No: 620 & 621	457489	AI693815	Hs.127179	cryptic gene
	Seq ID No: 622 & 623	429547	AW009166	Hs.99376	ESTs
	Seq ID No: 624 & 625	407242	M18728		gb:Human nonspecific crossreacting anti
	Seq ID No: 626 & 627	407242	M18728		gb:Human nonspecific crossreacting anti
	Seq ID No: 628 & 629	407242	M18728		gb:Human nonspecific crossreacting anti
85	Seq ID No: 630 & 631	444006	BE395085	Hs.10086	type 1 transmembrane protein Fn14

Seq ID No: 632 & 633	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain
Seq ID No: 634 & 635	422109	S73265	Hs.1473	gastrin-releasing peptide
Seq ID No: 636 & 637	419235	AW470411	Hs.288433	neurotrophin
Seq ID No: 638 & 639	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced
Seq ID No: 640 & 641	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cyt)
Seq ID No: 642 & 643	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precursor
Seq ID No: 644 & 645	448243	AW369771	Hs.52620	integrin, beta 8
Seq ID No: 646 & 647	426427	M86699	Hs.169840	TTK protein kinase
Seq ID No: 648 & 649	445537	AJ245871	Hs.12844	EGF-like domain, multiple 6
Seq ID No: 650 & 651	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6
Seq ID No: 652 & 653	428450	NM_014791	Hs.184339	KIAA0175 gene product
Seq ID No: 654 & 655	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,
Seq ID No: 656 & 657	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11
Seq ID No: 658 & 659	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic)
Seq ID No: 660 & 661	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 662 & 663	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 664 & 665	431515	NM_012152	Hs.258583	endothelial differentiation, lysophosphatidyl
Seq ID No: 666 & 667	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7
Seq ID No: 668 & 669	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 670 & 671	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 672 & 673	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 674 & 675	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 676 & 677	410001	AB041036	Hs.57771	kallikrein 11
Seq ID No: 678 & 679	426501	AW043782	Hs.293616	ESTs
Seq ID No: 680 & 681	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport
Seq ID No: 682 & 683	445413	AA151342	Hs.12677	CGI-147 protein
Seq ID No: 684 & 685	422424	AI186431	Hs.296638	prostate differentiation factor
Seq ID No: 686 & 687	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,
Seq ID No: 688 & 689	420610	AI683183	Hs.99348	distal-less homeo box 5

TABLE 15B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
309931	AW341683	
330493	33264_5	M27826 R78416 AA307645 AW957879 AW957800 AA633529 H03662
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI348341 AI887454 N54784 AI655270 AI421279 AW014882
		AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151186 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
		AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067
451320	86576_1	AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265
		AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230
		AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612

TABLE 15C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402075	8117407	Plus	121907-122035, 122804-122921, 124019-124161, 124455-124610, 126672-126076
403329	8518120	Plus	96450-96598
403478	9958258	Plus	116458-116564
404440	7528051	Plus	80430-81581
404877	1519284	Plus	1095-2107
405770	2735037	Plus	61057-62075
405932	7767812	Minus	123525-123713

Table 16

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: NM_001216
Coding sequence: 43..1422

5	1	11	21	31	41	51	
10	GCCCGTACAC	ACCGTGTGCT	GGGACACCCC	ACAGTCAGCC	GCATGGCTCC	CCTGTGCCCC	60
	AGCCCTGGC	TCCCTCTGTT	GATCCCGGCC	CCTGCTCCAG	GCCTCACTGT	GCAACTGCTG	120
	CTGTCACTGC	TGCTTCTGAT	GCCTGTCCAT	CCCCAGAGGT	TGCCCCGGAT	GCAGGAGGAT	180
	TCCCCCTTGG	GAGGAGGCTC	TTCTGGGGAA	GATGACCCAC	TGGGCGAGGA	GGATCTGCCC	240
	AGTGAAGAGG	ATTACACCCAG	AGAGGAGGAT	CCACCCGGAG	AGGAGGATCT	ACCTGGAGAG	300
15	GAGGATCTAC	CTGGAGAGGA	GGATCTACCT	GAAGTTAAGC	CTAAATCAGA	AGAAGAGGGC	360
	TCCCTGAAGT	TAGAGGATCT	ACCTACTGTT	GAGGCTCCTG	GAGATCTCTA	AGAACCCAG	420
	AATAATGCCC	ACAGGGACAA	AGAAGGGGAT	GACCAGAGTC	ATTGGCGCTA	TGGAGGCGAC	480
	CGCCCTGGC	CCGGGTGTC	CCCAGCCTGC	CGCGGCCCTG	TCCAGTCCCC	GGTGGATATC	540
	CGCCCCAGC	TCCCGGCTT	CTGCCCGGCC	CTGCCGCCCC	TGGAATCCTT	GGGCTTCCAG	600
20	CTCCGCGCGC	TCCCGGCTT	GGCCCTGCGC	AACAATGGCC	ACAGTGTGCA	ACTGACCTCG	660
	CCTCTGCGG	TAGAGATGGC	TCCTGGTCCC	GGGCGGGAGT	ACCGGCTCT	GCAGCTGCAT	720
	CTGCACTGGG	GGGCTCGAGG	TCGTCGCGGC	TCGAGACACA	CTGTGGAAGG	CCACCGTTTC	780
	CCTGCCGAGA	TCCACGTGGT	TCACCTCAGC	ACCGCCTTTG	CCAGAGTTGA	CGAGGCCCTT	840
	GGGCGCCCGG	GAGGCTGGC	CGTGTGCGC	GCCTTTCTGG	AGGAGGGCCC	GGAGAGAAAC	900
25	AGTGCTATG	AGCAGTGTCT	GTCTCGCTTG	GAAGAAATCG	CTGAGGAAGG	CTCAGAGACT	960
	CAGGTCCAG	GACTGGACAT	ATCTGCACTC	CTGCCCTCTG	ACTTCAGCCG	CTACTTCCAA	1020
	TATGAGGGGT	CTCTGACTAC	ACCGCCCTGT	GCCCAGGGTG	TCATCTGGAC	TGTGTTTAA	1080
	CAGACAGTGA	TGCTGAGTGC	TAAAGCAGTC	CACACCTCT	CTGACACCTT	GTGGGACCT	1140
	GGTGAATCTC	GGCTACAGCT	GAACTTCCGA	CGCAGCGAGC	CTTTGAATGG	GCGAGTGATT	1200
30	GAGGCTCTCT	TCCCTGCTAG	AGTGGACAGC	AGTCTCTGGG	CTGCTGAGCC	AGTCCAGCTG	1260
	AATTCCTGCC	TGGCTGCTGG	TGACATCTTA	GCCCTGTTT	TTGGCTCTCT	TTTGTCTGTC	1320
	ACCAGCGTCG	CGTTCCTTGT	CGAGATGAGA	AGGCAGCACA	GAAGGGGAAC	CAAAGGGGGT	1380
	GTGAGCTACC	GCCCAGCAGA	GGTAGCCGAG	ACTGGAGCCT	AGAGGCTGGA	TCTTGAGAAA	1440
	TGTGAGAAGC	CAGCCAGAGG	CATCTGAGGG	GGAGCCGGTA	ACTGTCTCTG	CCTGCTCATT	1500
35	ATGCCACTTC	CTTTAACTG	CCAAGAAATT	TTTTAAATA	AATATTATATA	AT	

Seq ID NO: 2 Protein sequence:
Protein Accession #: NP_001207

40	1	11	21	31	41	51	
	MAPLCPSFWL	PLLIPAPAPG	LTVQLLSLL	LLMPVHPQRL	PRMOEDSPLG	GGSSGEDDPL	60
	GEEDLPSEED	SPREDPPGE	EDLPGEEDLP	GEEDLPVKP	KSEEGSLKL	EDLPVTRAPG	120
	DPQEPQNNAH	RDKEGDDQSH	WRYGGDFPWF	RVSPACAGRF	QSPVDIRPQL	AAFCPALRPL	180
45	ELLGLQPLPL	PELRLRNNGH	SVQLTLPPGL	EMALGPGREY	RALQLHLHWG	AAGRPGSEHT	240
	VEGHRFPPEI	HVHLSTAFSA	RVDEALGRPG	GLAVLAAPLE	EGPEENSAYE	QLLSRLIEIA	300
	EEGSETQVPG	LDISALPSD	PSRYFQYEGS	LTPPCAQGV	IWTVFNQTVM	LSAKQLHTLS	360
	DTLWPGDSR	LQLNFRATQP	LNGRVIEASF	PAGVDSPPRA	AEFVQLNSCL	AAGDILALVF	420
	GLLPAVTSVA	FLVQMRQRH	RGTGKGVSYR	PAEVAETGA			

Seq ID NO: 3 DNA sequence
Nucleic Acid Accession #: BC013923
Coding sequence: 438-1391

55	1	11	21	31	41	51	
	AGCGGGGTG	TCTATTAAC	TGTTCAAAA	GTATCAGGAG	TTGTCAAGGC	AGAGAAGAGA	60
	GTGTTTGCA	AAGGGGAAA	GTAAGTTGCT	GCCTCTTAA	GACTAGGACT	GAGAGAAAGA	120
	AGAGGAGAGA	GAAAGAAAG	GAGAGAAGTT	TGAGCCCCAG	GCTTAAGCCT	TTCCAAAAAA	180
60	TAATAATAAC	AATCATCGGC	GGCGGCAGGA	TCGGCCAGAG	GAGGAGGGAA	GCGCTTTTTT	240
	TGATCCTGAT	TCCAGTTTGC	CTCTCTCTTT	TTTTCCCCCA	AATTATTTCT	CGCCTGATTT	300
	TCCTCGCGGA	GCCCTGCGCT	CCCGACACCC	CGGCCCGCCT	CCCTCTCTCC	TCTCCCCCG	360
	CCCGCGGGCC	CCCCAAAGTC	CCGCGCGGGC	CGAGGGTCGG	CGGCCGCGG	CGGGCCGGGC	420
	CCGCGCACAG	CGCCCGCATG	TACAACATGA	TGGAGACGGA	GCTGAAGCCG	CGGGCCCGGC	480
65	AGCAAACTTC	GGGGGGCGGC	GGCGGCAACT	CCACCGCGGC	GGCGGCGCGC	GGCAACCAGA	540
	AAAACAGCCC	GGACCGCGTC	AAGCGGCCCA	TGAATGCCTT	CATGTGTGG	TCCGCGGGC	600
	AGCGGCGCAA	GATGGCCAG	GAGAAACCCA	AGATGCACAA	CTCGGAGATC	AGCAAGCGCC	660
	TGGGCGCGGA	GTGAAACTT	TTGTGCGAGA	CGGAGAAAGC	GCCGTTTATC	GACGAGGCTA	720
	AGCGGCTGCG	AGCGCTGCAC	ATGAAGGAGC	ACCGGATTA	TAAATACCGG	CCCGGGCGGA	780
70	AAACCAAGAC	GCTCATGAAG	AAGGATAAGT	ACACGCTGCC	CGCGCGGCTG	CTGGCCCCCG	840
	GCGGCAATAG	CATGGCGAGC	GGGGTCGGGG	TGGGCGCGGG	CCTGGGCGCG	GGCGTGAACC	900
	AGCGCATGGA	CAGTTACGCG	CACATGAACG	GCTGGAGCAA	CGGCAGCTAC	AGCATGATGC	960
	AGGACAGACT	GGGCTACCGG	CAGCACCCGG	GCCTCAATGC	GCACGCGCGA	GCGCAGATGC	1020
75	AGCCCATGCA	CCGCTACGAC	GTGAGCGCCC	TGCAGTACAA	CTCCATGACC	AGCTCGCAGA	1080
	CCTACATGAA	CGGCTCGCCC	ACCTACAGCA	TGTCTTACTC	GCAGCAGGGC	ACCCCTGGCA	1140
	TGGCTCTTGG	CTCCATGGGT	TCGGTGGTCA	AGTCCGAGGC	CAGCTCCAGC	CCCCCTGTGG	1200
	TTACTCTTTC	CTCCCATCTC	AGGGCGCCCT	GCCAGGCGGG	GGACCTCCGG	GACATGATCA	1260
	GCATGTATCT	CCCGGGCGCC	GAGGTGCCGG	AACCGCGCGC	CCCCAGCAGA	CTTCACATGT	1320
	CCAGCACTA	CCGAGAGCGC	CCGCTGCCCG	GCACGGCCAT	TAAAGGCGCA	CTGCCCTCT	1380
80	CACACATGTG	AGGGCCGGAC	AGCGAACTGG	AGGGGGGAGA	AATTTTCAAA	GAAAAACGAG	1440
	GGAAATGGGA	GGGGTGCAAA	AGAGGAGAGT	AAGAAACAGC	ATGGAGAAAA	CCCGGTACGC	1500
	TCAAAAAAAA	AAAAAATCCAT	CACCCACAGC	AAATGACAGC	AAATGACAGC	TGCAAAAGAG	1560
	AACACCAATC	CCATCCACAC	TCACGCAAAA	ACCGCGATGC	CGACAAGAAA	ACTTTTATGA	1620
	GAGAGATCCT	GGACTTCTTT	TTGGGGGACT	ATTTTGTGAC	AGAGAAAAAC	TGGGGAGGGT	1680
85	GGGGAGGGCG	GGGGAATGGA	CCTTGTATAG	ATCTGGAGGA	AAGAAAGCTA	CGAAAAACTT	1740
	TTTAAAGATT	CTAGTGGTAC	GGTAGGAGCT	TTGCAGGAAG	TTTGCAGGAAG	TCTTTACCAA	1800
	TAATATTAG	AGTAGTCTC	CAAGCGACGA	AAAAAATGTT	TTAATATTG	CAAGCAACTT	1860
	TGTACAGTA	TTTATCGAGA	TAAACATGTC	AATCAAAATG	TCCATTGTTT	ATAAGCTGAG	1920

AATTGGCCAA TATTTTTCAA GGAGAGGCTT CTTGCTGAAT TTTGATTCTG CAGCTGAAAT 1980
 TTAGGACAGT TGCAACCGTG AAAAGAAGAA AATTATTCAT ATTTGGACAT TTTAATTGTT 2040
 TAAAAATGT ACAAAGGAA AAAATTAGAA TAAGTACTGG CGAACCATCT CTGTGGTCTT 2100
 GTTTAAAAAG GGCAAAAGTT TTAGACTGTA CTAAATTTTA TAACCTACTG TTTAAAGCAA 2160
 AAATGGCCAT GCAGGTTGAC ACCGTTGGTA ATTTATAATA GCTTTTGTTC GATCCCAACT 2220
 TTCCATTTTG TTCAGATAAA AAAAACCATG AAATTACTGT GTTTGAAATA TTTTCTTATG 2280
 GTTTGTAATA TTTCTGTAAA TTTATGTGTA TATTTTAAGG TTTTCCCCC TTTATTTTCC 2340
 GTAGTTGTAT TTTAAAGAT TCGGCTCTGT ATTATTTGAA TCAGTCTGCC GAGAATCCAT 2400
 GTATATATTT GAATAATAT CATCCTTATA ACAGGTACAT TTTCAACTTA AGTTTCTTACT 2460
 CCATTATGCA CAGTTTGAGA TAAATAAAT TTTGAAATAT GGACACTGAA AAAAAAAGAA 2520
 AAAAAACAA AACAAAAAA CAAAAACAA AACACAGAAA AACAAAAAA AAAACAAAC 2580
 CACAACACA AACAAAAAA AAAAAAAGA AACAAACACA CAACACAACA CAACACAACA 2640
 CCACAACACA AACACAACA CACAGAGGG

Seq ID NO: 4 Protein sequence:
Protein Accession #: CAA83435.1

1 11 21 31 41 51
 MYNMMETELK PPGPQQTSGG GGNSTAAAA GGNQKNSPDR VKRPMNAPMV WSRGQRRKMA 60
 QENPKMHNSE ISKRLGAEWK LLSETEKRPF IDEAKRLRAL HMKEHPDYKY RPRRKTKTLM 120
 KKDKYTLPGG LLAPGGNSMA SGVGVGAGLG AGVNQRMDSY AHMNGWSNGS YSMMQDQLGY 180
 PQHPGLNARG AAQMPPMRY DVSALQYNMS TSSQTYMNGS PTYSMSYSQQ GTPGMALGSM 240
 GSVVKSEASS SPVVVTSSSH SRAPCQAGDL RDMISMYLPG AEPVEPAAPS RLHMSQHYQS 300
 GPVPGTAING TLPLSHM

Seq ID NO: 5 DNA sequence
Nucleic Acid Accession #: U91618
Coding sequence: 29-541

1 11 21 31 41 51
 CGGACTTGCG TTGTTAGAAG GCTGAAAGAT GATGGCAGGA ATGAAAAATCC AGCTTGATATG 60
 CATGCTACTC CTGGCTTTCA GCTCCTGGAG TCTGTGCTCA GATTCAGAAG AGGAAATGAA 120
 AGCATTAGAA GCAGATTTCT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180
 TCCCTCTGGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC 240
 AGCTGAGGAA ACAGGAGAAG TTCATGAAGA GGAGCTTGTT GCAAGAAGGA AACTTCCTAC 300
 TGCTTTAGAT GGCTTTAGCT TGGAAAGCAAT GTTGACAATA TACCAGCTCC ACAAAATCTG 360
 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA 420
 TGACAAAAAT GGAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAAACGGCA 480
 GCTGTATGAG AATAAACCCA GAAGACCCCTA CATACTCAA AGAGATTCTT ACTATTACTG 540
 AGAGAATAAA TCATTATTTT ACATGTGATT GTGATTATC ATCCCTTAAT TAAATATCAA 600
 ATTATATTTG TGTGAAATG TGACAAACAC ACTTATCTGT CTCCTTACA ATTGTGGTTT 660
 ATTGAATGTG TTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCAA TAAATCTAAA 720
 TCTTCAAAAA AAAAAAATA AAATGGGGCC GCAATT

Seq ID NO: 6 Protein sequence:
Protein Accession #: AAB50564

1 11 21 31 41 51
 MMAGMKIQLV CMLLLAPSSW SLCSDSSEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN 60
 VCSLVNNLNS PAETGSEVHE BELVARRKLP TALDGFSLAE MLTIYQLHKI CHSRAFAQHE 120
 LIQEDILDTG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSYY

Seq ID NO: 7 DNA sequence
Nucleic Acid Accession #: NM_006536.2
Coding sequence: 109-2940

1 11 21 31 41 51
 ACCTAAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA 60
 ATGTATGCAG CAGGCTCAGT GTGAGTGAA C TGAGGCGTTC TCTACAACAT GACCCAAAGG 120
 AGCATTTGAG GTCCTATTTG CAACCTGAAG TTTGTGACTC TCTTGGTTGC CTTAAGTTCA 180
 GAACCTCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240
 ATTGCAATTA ATCTCAGGT ACCTGAGAA CAGAACCCTA TCTCAAACAT TAAGGAAATG 300
 ATAAGTGAAG CTTCAATTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTGAGAAAT 360
 ATAAAGATTT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA 420
 TCATATGAAA AGGCAAAATG CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA 480
 TACACCTTAC AATACAGAGG GTGTGGAAAA GAGGAAAAAT ACATTCAATT CACACCTAAT 540
 TTCCTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTTGTCCAT 600
 GAATGGGCCC ACCTCGGTTG GGGTGTGTTG GATGAGTATA ACAATGACAA ACCTTCTTAC 660
 ATAAATGGGC AAAATCAAAT TAAAGTGACA AGGTGTTTCA CTGACATCAC AGGCATTTTT 720
 GTGTGTGAAA AAGGTCTCTG CCCCCAAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780
 GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840
 AGTTTATCTT CTGTGGTGA ATTTTGTAA GCAAGTACCC ACAACCAAGA AGCAACCAAC 900
 CTACAGAAC AGATGTGCAG CCTCAGAAAT GCATGGGATG TAATCACAGA CTCTGCTGAC 960
 TTTCAACACA GCTTCTCCAT GAATGGGACT GAGCTTCCAC CTCCTCCAC ATTCTGCTT 1020
 GTACAGGCTG GTGACAAAGT GGTCTGTTTA GTGCTGGATG TGTCCAGCAA GATGGCAGAG 1080
 GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGAAATTT ATTGTATGCA GATTGTTGAA 1140
 ATTCATACCT TCGTGGGCTT TGCCAGTTTC GACAGCAAA GAGAGATCAG AGCCCACTA 1200
 CACCAATTA ACAGCAATGA TGATCGAAAG TTGCTGGTTT CATATCTGCC CACCACTGTA 1260
 TCAGCTAAAA CAGACATCAG CATTGTGTTA GGGCTTAAGA AAGGATTGGA GGTGGTTGAA 1320
 AAACGTAATG GAAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAGCGG AGATGATAAG 1380
 CTTCTTGCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCATTGGC 1440

	CTGGGTTTCAT	CTGCAGCCCC	AAATCTGGAG	GAATTATCAC	GTCTTACAGG	AGGTTTAAAG	1500
	TTCTTTGTTC	CAGATATATC	AAACTCCAAT	AGCATGATTG	ATGCTTTCAG	TAGAAATTTCC	1560
	TCTGGAACTG	GAGACATTTT	CCAGCAACAT	ATTCAGCTTG	AAAGTACAGG	TGAAAAATGTC	1620
5	AAACCTCACC	ATCAATTGAA	AAACACAGTG	ACTGTGGATA	ATACTGTGGG	CAACGACACT	1680
	ATGTTTCTAG	TTACGTGGCA	GGCCAGTGGT	CCTCCTGAGA	TTATATTATT	TGATCCTGTAT	1740
	GGACGAAAT	ACTACACAAA	TAATTTTATC	ACCAATCTAA	CTTTTCGGAC	AGCTAGTCTT	1800
	TGGATTCCAG	GAACAGCTAA	GCCTGGGCAC	TGGACTTACA	CCCTGAACAA	TACCCATCAT	1860
	TCTCTGCAAG	CCCTGAAAGT	GACAGTGACC	TCTCGCGCCT	CCAACTCAGC	TGTGCCCCCA	1920
10	GCCACTGTGG	AAGCCTTTGT	GGAAAGAGAC	AGCCTCCATT	TTCTCATCC	TGTGATGATT	1980
	TATGCCAATG	TGAACAGGG	ATTTTATCCC	ATTCCTAATG	CCACTGTCAC	TGCCACAGTT	2040
	GAGCCAGAGA	CTGGAGATCC	TGTTACGCTG	AGACTCCTTG	ATGATGGAGC	AGGTGCTGAT	2100
	GTTATAAAAA	ATGATGGAAT	TTACTCGAGG	TATTTTTTCT	CCTTTGCTGC	AAATGGTAGA	2160
	TATAGCTTGA	AAGTGATGT	CAATCACTCT	CCCAGCATAA	GCACCCCAAC	CCACTCTATT	2220
	CCAGGGAGTC	TGTATCTGTA	TGTACCAGGT	TACACAGCAA	ACGTAATAT	TCAGATGAAT	2280
15	GCTCCAAGGA	ATCAGTAGG	CAGAAATGAG	GAGGAGCGAA	AGTGGGGCTT	TAGCCGAGTC	2340
	AGCTCAGGAG	GCTCCTTTTC	AGTGCTGGGA	GTTCCAGCTG	GCCCCCACC	TGATGTGTTT	2400
	CCACCATGCA	AAATATTGTA	CCTGGAAGCT	GTAAGAGTAG	AAGAGGAATT	GACCTTATCT	2460
	TGGACAGCAC	CTGGAGAAGA	CTTTGATCAG	GGCCAGGCTA	CAGCTATGA	AATAAGAAATG	2520
	AGTAAAGTCA	TACGATATAT	CAAGATGAC	TTTAAACATG	CTATTTTAGT	AAATACATCA	2580
20	AAGCGAAATC	CTCAGCAAGC	TGGCATCAGG	GAGATATTTA	CGTTCCTACC	CCAGATTFTCC	2640
	ACGAATGGAC	CTGAACATCA	GCCAAATGGA	GAAACACATG	AAAGCCACAG	AATTTATGTT	2700
	GCAATACGAG	CAATGGATAG	GAACTCCTTA	CAGTCTGCTG	TATCTAACAT	TGCCCAGGCG	2760
	CCTCTGTTTA	TTCCCCCAA	TTCTGATCCT	GTACCTGCCA	GAGATTATCT	TATATTGAAA	2820
	GGAGTTTAA	CAGCAATGGA	TTTGATAGGA	ATCATTGGCC	TTATTATAGT	TGTGACACAT	2880
25	CATACCTTAA	GCAGGAAAAA	GAGAGCAGAC	AAGAAAGAGA	ATGGAACAAA	ATTATTATAA	2940
	ATAAATATCC	AAAGTGTCTT	CCTTCTTAGA	TATAAGACCC	ATGGCCTTCG	ACTACAAAAA	3000
	CATACTAACA	AAGTCAAAT	AACATCAAAA	CTGTATTAAA	ATGCATTGAG	TTTTTGTACA	3060
	ATACAGATAA	GATTTTACAA	TGGTAGATCA	ACAATTCCTT	TTGGGGGTAG	ATTAGAAAAAC	3120
	CCTTACACTT	TGCTATGATA	CAATAAATAA	AAATTATCT	TTAAAGTAAT	GTCTTTAAAG	3180
30	GCAAAGGGAA	GGGTAAAGTG	GGACCAAGTG	CAAGGAAAGT	TTGTTTTATT	GAGGTGGAAA	3240
	AATAGCCCCA	AGCAGAGAAA	AGGAGGGTAG	GTCTGCATTA	TAACTGTCTG	TGTGAAGCAA	3300
	TCATTAGATT	ACTTTGATTA	ATTTTTCTTT	TCTCCTTATC	TGTGCAGTAC	AGGTGTCTTG	3360
	TTTACATGAA	GATCATGCTA	TATTTTATAT	ATGTAGCCCC	TAATGCAAGG	CTCTTACCTT	3420
	CTTGCTATTT	TGTTATATAT	ATTTACAGATG	ACATCTCCCT	GCTAATGCTC	AGAGATCTTT	3480
35	TTTCACTGTA	AGAGGTAAAC	TTTAAACAATA	TGGGTATTAC	CTTTGTCTCT	TCATACCGGT	3540
	TTTATGACAA	AGGTCTATTG	AATTTATTTG	TNTGTAAAGT	TCTACTCCCA	TCAAAGCAGC	3600
	TTTCTAAGTT	TATTGCCTTG	GGTTATTATG	GAATGATAGT	TATAGCCCN	TATAATGCCT	3660
	TACCTAGGAA	A					

Seq ID NO: 8 Protein sequence:
Protein Accession #: NP_006527.1

	1	11	21	31	41	51	
45	MTQRSIAGPI	CNLKFVTLV	ALSSSELPFLG	AGVQLQDNGY	NGLLIAINPQ	VPENQNLISN	60
	IKEMITEASF	YLFNATKRRV	FFRNKILIP	ATWKANNNSK	IKQESYEKAN	VIVTDWYGAH	120
	GDDPYTLQYR	CGCKEGKYIH	FTPNFLINDN	LTAGYGSRRG	VFVHEWAHLR	WGVFDEYNND	180
	KPFYINGQNG	IKVTRCSSDI	TGIFVCEKGP	CPQENCIIISK	LFKEGCTFIY	NSTQWATASI	240
50	MEMQSLSSVV	EFCNASTHNQ	EAPNLQNQMC	SLRSANDVIT	DSADFHHSFP	MNGTELPPPP	300
	TFSLVQAGDK	VVCLVLVDVSS	KMAEADRLLO	LQQAEEFYLM	QIVRIHTFVG	IASFDSKGEI	360
	RAQLHQINSN	DDRKLVLVSYL	PTTVSAKTDI	SICSLKKKGF	EVVEKLNGKA	YGSVMILVTS	420
	GDDKLLGNCL	PTVLSGSSTI	HSIALGSSAA	PNLEELSRIT	GGLKFPVPDI	SNSNSMIDAF	480
	SRISSGTGD	FQHQHILEST	GENVKPHEQL	KNTVTVDNVT	GNDTMFLVTW	QASGPPEIIL	540
55	FDPDRKYYT	NNPITNLTFR	TASLWIPGTA	KPGHWTYTLN	NTHHSLQALK	VTVTSRASNS	600
	AVPPATVEAF	VERDLSHFPH	PVMYIANVKQ	GFYPILNATV	TATVEPETGD	PVTLRLLDDG	660
	AGADVINKNF	IYGRYLFHFA	ANGRYSLKVH	VNRSPSISTP	AHSIPGSHAM	VVPGYTANGN	720
	IQMNAPRKSV	GRNEEERKWG	FSRVSSGGSF	SVLGVPAGPH	PDVFPCKII	DLEAVKVBBE	780
	LTLSTWAPGE	DFDQGGQATSY	EIRMSKSLQN	IQDDFNAIL	VNTSKRNPPQ	AGIREIFTFS	840
60	PQISTNGPEH	QPNGETHESH	RIYVAIRAMD	RNSLQSAVSN	IAQAPLFIPP	NSDPVPARDY	900
	LILKCVLTAM	GLTGICLII	VVTHHTLSRK	KRADKENG	KLL		

Seq ID NO: 9 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 336-632

	1	11	21	31	41	51	
70	CTCCCTCAC	CCCGGTCCAG	GATGCCAGT	CCCCACGACA	CCTCCCACTT	CCCACTGTGG	60
	CCTGGGTGGG	CTCAGGGGCT	GCCCTTGACC	TGGCCTAGAG	CCCTCCCCCA	GCTGGTGGTG	120
	GAGCTGGCAC	TCTCTGGGAG	GGAGGGGGCT	GGGAGGGAAT	GAGTGGGAAT	GGCAAGAGGC	180
	CAGGGTTTGG	TGGGATCAGG	TTGAGGCAGG	TTTGGTTTCC	TTAAATGCC	AAGTTGGGGG	240
	CCAGTGGGCG	CCACATATAA	ATCCTCACCC	TGGGAGCCTG	GCTGCCTTGC	TCTCCTTCT	300
75	GGGTCTGTCT	CTGCCACCTG	GTCTGCCACA	GATCCATGAT	GTGCAGTTCT	CTGGAGCAGG	360
	CGCTGGCTGT	GCTGGTCACT	ACCTTCCACA	AGTACTCCTG	CCAAGAGGGC	GACAAGTTCA	420
	AGCTGAGTAA	GGGGGAAATG	AAGGAACCTC	TGCACAAGGA	GCTGCCACGC	TTTGTGGGGG	480
	AGAAAGTGGG	TGAGGAGGGG	CTGAAGAAGC	TGATGGGCAG	CCTGGATGAG	AACAGTGACC	540
	AGCAGGTGGA	CTTCCAGGAG	TATGCTGTTT	TCTTGGCACT	CATCACTGTC	ATGTGCAATG	600
80	ACTTCTTCCA	GGGCTGCCCA	GACCGACCTT	GAAGCAGAAC	TCTTGACTTC	CTGCCATGGA	660
	TCTCTTGGGC	CCAGGACTGT	TGATGCCTTT	GAGTTTGTGA	TTCAATAAAC	TTTTTTTGTG	720
	TGTTGATAAT	ATTTTAATTG	CTCAGTGATG	TTCCATAACC	CGGCTGGCTC	AGCTGGAGTG	780
	CTGGGAGATG	AGGGCTCTCT	GATCCTGCT	CCCTTCTGGG	CTCTGACTCT	CCTGGAATC	840
	TCTCCAAGGC	CAGAGCTATG	CTTAGGTCT	CAATTTTGA	ATTTCACAAA	CCAGCAAAAA	900
85	ATTGGAATC	GAGATAGGTT	GCTGACTTTT	ATTTTGTCAA	ATAAGATAT	TAAAAAAGGC	960
	AAATACCA						

Seq ID NO: 10 Protein sequence:

Protein Accession #: NP_005969.1

1 11 21 31 41 51
5 | | | | |
MMCSLSLEQAL AVLVTTFPHKY SCQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM 60
GSLDENSDQQ VDFQYAVFL ALITVMCNDF FQGCPRDP

Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 336-626

1 11 21 31 41 51
15 | | | | |
CTCCCTCAC CCCGGTCCAG GATGCCAGT CCCCACGACA CCTCCCACTT CCACTGTGG 60
CCTGGGTGGG CTCAGGGGCT GCCCTTGACC TGGCCTAGAG CCCTCCCCCA GCTGGTGGTG 120
GAGCTGGCAC TCTCTGGGAG GGAGGGGGCT GGGAGGGAAT GAGTGGGAAT GGCAAGAGGC 180
CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTTGGTTTCC TTAATATGCC AAGTTGGGGG 240
CCAGTGGGGC CCACATATAA ATCCTCACCC TGGGAGCCTG GCTGCCTTGC TCTCCTTCTT 300
20 GGGTCTGTCT CTGCCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG 360
CGCTGGCTGT GCTGTCTCAGT ACCTTCCACA AGTACTCCTG CCAAGAGGGC GACAAGTTCA 420
AGCTGAGTAA GGGGAAATG AAGGAACTTC TGCACAAGGA GCTGCCACGC TTTGTGGGGC 480
ATTCCAGAGA ACCATGTGCT GTGAGGGCCT TCCGAGTCCA TCTGTTTAACT CCTGTCAATG 540
GAGACTTGAG AAACCAAGAGC CCAGAAGGGA AAAGTGATTG TCCCAAGATC ACACAGCACT 600
25 GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC AGCCTGGATG AGAACAGTGA 660
CCAGCAGGTG GCTTTCAGG AGTATGCTGT TTTCTGGCA CTCACTCACTG TCATGTGCAA 720
TGACTTCTTC CAGGGCTGCC CAGACCGACC CTGAAGCAGA ACTCTTGACT TCCTGCCATG 780
GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTGG TATTCAATAA ACTTTTTTTG 840
TCTGTTGATA ATATTTTAAAT TGCTCAGTGA TGTTCCATAA CCGGCTGGC TCAGCTGGAG 900
30 TGCTGGGAGA TGAGGGCCTC CTGGATCCTG CTCCCTTCTG GGTCTGACT CTCCTGGAAA 960
TCTCTCCAAG GCCAGAGCTA TGCTTTAGGT CTCATTTTGA GAATTTTCAA CACCAGCAAA 1020
AAATTTGAAA TCGAGATAGG TTGCTGACTT TTATTTTGTG AAATAAGAT ATTAATAAAG 1080
GCAATATCCA

Seq ID NO: 12 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
40 | | | | |
MMCSLSLEQAL AVLVTTFPHKY SCQEGDKFKL SKGEMKELLH KELPSFVGHS REPCAVRAFR 60
VHLFNPVIGD LRNQSPEGKS DCPKITQHWK KWMRRG

Seq ID NO: 13 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 58-354

1 11 21 31 41 51
50 | | | | |
GTGAGCTCAC CATGTGGGGG TGAGGCTGAG AGAAAACAAG TACACAGCCA CAGATCCATG 60
ATGTGCAGTT CTCTGGAGCA GCGCGTGCTG GTGCTGGTCA CTACCTTCCA CAAGTACTCC 120
TGCCAAAGAG GCGACAAGTT CAAGCTGAGT AAGGGGGAAG TGAAGGAAGT TCTGCACAAG 180
GAGCTGGCCA GCTTTGTGGG GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC 240
55 AGCCTGGATG AGAACAGTGA CCAGCAGGTG GACTTCCAGG AGTATGCTGT TTTCTGGCA 300
CTCATCACTG TCATGTGCAA TGACTTCTTC CAGGGCTGCC CAGACCGACC CTGAAGCAGA 360
ACTCTTGACT TCCTGCCATG GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTGG 420
TATTCAATAA ACTTTTTTTG TCTGTTGATA ATATTTTAAAT TGCTCAGTGA TGTTCCATAA 480
CCCGCTGGC TCAGCTGGAG TGCTGGGAGA TGAGGGCCTC CTGGATCCTG CTCCTTCTG 540
60 GGCTCTGACT CTCCTGGAAA TCTCTCCAAG GCCAGAGCTA TGCTTTAGGT CTCATTTTGG 600
GAATTTCAA CACCAGCAAA AAATTTGAAA TCGAGATAGG TTGCTGACTT TTATTTTGTG 660
AAATAAGAT ATTAATAAAG GCAATATCCA

Seq ID NO: 14 Protein sequence:
Protein Accession #: NP_005969.1

1 11 21 31 41 51
65 | | | | |
MMCSLSLEQAL AVLVTTFPHKY SCQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM 60
GSLDENSDQQ VDFQYAVFL ALITVMCNDF FQGCPRDP

Seq ID NO: 15 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 62-358

1 11 21 31 41 51
75 | | | | |
GGAGGGTGTG CCGCTGAGTC ACTGCCTGGG CATCTGGGCC TGGAACTCG GCCACAGATC 60
CATGATGTGC AGTCTCTCTG AGCAGGCGCT GGCTGTGCTG GTCACTACCT TCCACAAGTA 120
80 CTCCTGCCAA GAGGGGCGCA AGTTCAGCT GAGTAAGGGG GAAATGAAGG AACTTCTGCA 180
CAAGGAGCTG CCCAGCTTTG TGGGGAGAA AGTGGATGAG GAGGGGCTGA AGAAGCTGAT 240
GGGAGCCTG GATGAGAACCA GTGACCAGCA GGTGGACTTC CAGGAGTATG CTGTTTCTCT 300
GGCAGCTCAT ACTGTCATGT GCAATGACTT CTTCAGGGC TGCCAGAGCC GACCTGAAG 360
CAGAACTCTT GACTTCTCTG CATGGATCTC TTGGGCCAG GACTGTGAT GCCTTTGAGT 420
85 TTTGATTTCA ATAACTTTT TTTGTCTGTT GATAATATT TAATTGCTCA GTGATGTTCC 480
ATAACCCGGC TGGCTCAGT GAAATCTCTC CAAGGCCAGA GCTATGCTTT AGGTCTCAAT 600
TCTGGGCTCT GACTCTCTG GAAATCTCTC CAAGGCCAGA GCTATGCTTT AGGTCTCAAT 660
TTTGAATTT CAACACCCAG CAAAAAATTG GAAATCGAGA TAGGTGCTG ACTTTTATTT

Seq ID NO: 16 Protein sequence:
Protein Accession #: NP_005969.1

1 11 21 31 41 51 60
MMCSSLEQAL AVLVTTFFHKY SQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKILM
GSLDENSQQ VDFQEYAVFL ALITVMCNDF FQGCPRDP

Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 939-2372

1 11 21 31 41 51 60
AAGACGGATT CTCAGACAAG GCTTGCAAAAT GCCCGCAGC CATCATTTAA CTGACCCGCG 60
AGAATAGTTA CGGTTTGTC CCGACCCCTC CCGATCGCC TAATTGTGTC CTAGTGAGAC 120
CCGAGGGCTC TCGCCGGCGCC TGGCTTCTTC GTAGCTGGAT GCATATCGTG CTCGGGGCAG 180
CGCGGGCGCA GGGCAGCGGT TCGCGCACAC CCTAGCACAC ATGAACACGC GCAAGAGCTG 240
AACCAGCAC GGTTCATT TCAAAAAGGG AGACAGCCTC TACCGCGATT GTAGAAGAGA 300
CTGTGGTGTG AATTAGGGAC CGGAGGCGGT CGAACGGAGG AACGGTTCAT CTAGAGACT 360
AATTTCTGG AGTTTCTGCC CCGCTCTGTC GTCAGCCCTC ACCTCACTTC GCCAGCAGTA 420
GCAGAGGGCG CGCGGGCGGC TCCCGGAATT GGGTTGGAGC AGGAGCCTCG CTGGCTGCTT 480
CGCTCGCGCT CTACGCGCTC AGTCCCGGCG GGTAGCAGGA GCCTGGACCC AGGCGCGGCC 540
GGCGGGCGTG AGGCGCGGGA GCCCGCCTC GAGGTGCATA CCGGACCCCT ATTCTCATCT 600
AACAAGGAAT CTGCGCCCCA GAGAGTCCCG GGAGCGCGCG CGGTCTGCTC CCGCGCGGCC 660
GGGCCATGCA GCGACGGCGG CCGCGGAGCT CCGAGCAGCG GTAGCGCCCC CCTGTAAAGC 720
GGTTCTGCTAT CGCGGGGCGA CTGTGAACCC TGCCGCGCTG CGGAACACTC TTCGCTCGGG 780
ACGAGCTCAG CCTCTGATAA GCTGGAAGCT GCACGCGCGC AACAAACACC GAGGAGTTAA 840
GAGAGCCGCA AGGCGAGGGA AGGCTCTCCC GCACGGGTGG GGGAAAGCGG CCGGTGCAGC 900
CGCGGGACAG GCACCTCGGGC TGGCACTGGC TGCTAGGGAT GTGCTCTGCG ATAAGGTGGC 960
ATGGAACCGC CATGGCGCGG CTCTGGGGCT TCTGCTGGCT GGTGTGGGCG TTCGAGGGG 1020
CCGCTTTTGG CTGTCCACAG TCCTGCAAAAT GCAGTGCCTC TCGGATCTGG TGCAGCGACC 1080
CTTCTCCTGG CATCGTGGCA TTTCCGAGAT TGGAGCCTAA CAGTGTAGAT CCTGAGAAC 1140
TCACGGAAT TTTTATCGCA AACGAGAAA GGTAGAAAT CATCAACGAA GATGATGTTG 1200
AAGCTTATGT GGGACTGAGA AATCTGACAA TTGTGGATTG TGGATTAAAA TTTGTGGCTC 1260
ATAAAGCATT TCTGAAAAAC AGCAACCTGC AGCACATCAA TTTTACCGA AACAACTGA 1320
CGAGTTTGTG TAGGAAACAT TTCCGTCACC TTGACTTGTC TGAACCTGAT CTGGTGGGCA 1380
ATCCATTAC ATGCTCTCTGT GACATTATGT GGATCAAGAG TCTCCAAAGG GCTAAATCCA 1440
GTCCAGACAG TCAAGATTGT TACTGCTGTA ATGAAGCAG CAAGAATATT CCCCTGGCAA 1500
ACCTGCAGAT ACCCAATTGT GGTTCGCCAT CTGCAAACTC GGCAGCACT AACCTCACTG 1560
TGGAGGAAGG AAGTCTATC ACATTATCCT GTAGTGTGGC AGGTGATCCG GTTCTTAATA 1620
TGTATTGGGA TGTGGTAAAC CTGGTTTCCA AACATATGAA TGAACAAGC CACACACAGG 1680
GCTCCTTAAG GATAACTAAC ATTTTATCCG ATGACAGTGG GAAGCAGATC TCTTGTGTGG 1740
CGGAAATCTG TGTAGGAGAA GATCAAGATT CTGTCAACCT CACTGTGCAT TTTGCACCAA 1800
CTATCACATT TCTGGAATCT CCAACCTCAG ACCACCACTG GTGCATTCCA TTTACTGTGA 1860
AAGGCAACCC CAACACAGCG CTTCAGTGGT TCTATAACGG GGCAATATTG AATGAGTCCA 1920
AATACATCTG TACTAAAAATA CATGTTACCA ATCACACGGA GTACCACGGC TGCCTCCAGC 1980
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GGAAGGATGA GAAACAGATT TCTGCTCACT TCATGGGCTG GCCTGGAATT GACGATGGTG 2100
CAAAACCAAA TTAATCTGAT GTAATTTATG AAGATTATGG AACTGCAGCG AATGACATCG 2160
GGGACACAC GAAAGTGTGC ATGAAATCC CTTCACAGA CGTCACTGAT AAAACCGGTC 2220
GGGAACATCT CTCGGTCTAT GCTGTGGTGG TGATTGGCTC TGTGGTGGGA TTTTGCTTTT 2280
TGGTAATGCT GTTTCCTGCT AAGTTGGCAA GACACTCCAA GTTTGGCATG AAAGGTTTTG 2340
TTTTGTTTCA TAAGATCCCA CTGGATGGGT AGCTGAAATA AAGGAAAAGA CAGAGAAAGG 2400
GGCTGTGGTG CTGTTGGTGT GATGCTGCCA TGTAAGCTGG ACTCCTGGGA CTGCTGTTGG 2460
CTTATCCCGG GAAGTGTCTG TTATCTGGGG TTTTCTGGTA GATGTGGGCG GTGTTGGAG 2520
GCTGTACTAT ATGAAGCCTG CATATACTGT GAGCTGTGAT TGGGGAACAC CAATGCAGAG 2580
GTAACCTCA GGCAGCTAAG CAGCACCTCA AGAAAACATG TTAATTAAT GCTTCTCTTC 2640
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AAAGTGTGCT TTTTGACCTT ACTGGACATT TATTGACTTA ATTGCTTCTG TTTATTAATA 2760
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GTCTAATCTA CATGTAACAC ATATTTTAGT GTGATTTTCT ATACTCTAAT CAGCACTGAA 2880
TTAGAGGGT TTGACTTTTT CATCTATAAC ACAGTACTA AAAGAGTTAA GGGTATATAT 2940
ACCATCACTT TGGGACTTGG TAGTATTATT AAAAGGTTAT TTCCTTCACT GTCATAAAAA 3000
GTCCAAATGT TTAGCTTAGG TCTGAGAGTC AAACAATGTT AAGGATTGTC TTAAGTTTCC 3060
TTAGCCAGCA AAACAAAACA AAACAAAACA AACAAATGAA AACCGTTTAA AAAGAAGAAG 3120
AAGAAAAAAA ACAAGAACAA GCAGCAACAG CTGTTTGTGT GGGGCTATAG ATTTAAGTTA 3180
GGCATAGTCA ATTTGAGAAT AACTAAGAGT GGAATATATG CATATGGTGA AATTATAACC 3240
TTGCCCTTTT TTATTTGCCC TCTGCGATCC ACCTGCTTTT TAGAAGTCTG CCGAGTGAGA 3300
AGGCCACAGT ATCTCATGCT GTTTGCATTA CAGAACTGCA GCTTTTCTAC TCTGAAAAGG 3360
CCTGGGAGCA GAATGGCTGG CCGTCTGTGA GCAGGAGAGG AGATTCTAAG AAGGATAGTC 3420
CCCCCTACAA CATACTGTCA TACTGCTGGG TTTTCATGGG TAGGAAAGCT TGTCTGACC 3480
CCAGCAGCAA AGAGSTGGCA GGTGCTAAT GAATATATGC TTTATAATGT CCTTCTCAT 3540
TGCTGAGAGG CGAGCCTTAG AGCTGGGAT TTCTGCATCC CCCCTGAGTC TGACCCATGG 3600
ACACCTGTTT CATTCACCTT AGCATCACAG TGACCTTTGT ATGCTCTGTT CAGTCTGTGT 3660
CAGGCAGTAT GCTTCTCTG AGAGAGGTT TGGCTATCCC CACCCCAACC CACCCCAACC 3720
TGTTCCTTTT TTATCAGGAG GACTTCAGAG CCAGCCCTGC AGCATTTTGT TTGAAAACAC 3780
AATCAGCTCT GACAGTTAGA CATGCACACA GACGCCATAG CTGGATTGGA AACATTGATG 3840
TTTTAAAAAT TTTATTTTTT TGGAAATAGT TGCACAAATG CTGCAATTTA GCTTTAAGGT 3900
TCTATAGATT TTTAACTAGT CCAACACAGT CAGAAACATT GTTTTGAATC CTCTGTAAC 3960
CAAGGCATTA ATCTTAATAA ACCAGGATCC ATTTAGGTAC CACTTGATAT AAAAAGGATA 4020
TCCATAATGA ATATTTTATA CTGCATCCTT TACATTAGCC ACTAAATACG TTATTGCTTG 4080
ATGAAGACCT TTCACAGAAT CCTATGGATT GCAGCATTTT ACTTGCTTAC TTCATACCCA 4140

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TGCCTTAAAG	AGGGGCAGTT	TCTCAAAAGC	AGAAACATGC	CGCCAGTTCT	CAAGTTTTCC	4200
TCCTAACTCC	ATTGGAATGT	AAGGGCAGCT	GGCCCCCAAT	GTGGGGAGGT	CCGAACATTT	4260
TCTGAATCCC	CATTTTCTTG	TTCGCGGCTA	AATGACAGTT	TCTGTCTATTA	CTTAGATTCC	4320
GATCTTTCCC	AAAGGTGTTG	ATTACAAAG	AGGCCAGCTA	ATAGCAGAAA	TCATGACCCT	4380
GAAAGAGAGA	TGAAATTCAA	GCTGTGAGCC	AGGCAGGAGC	TCAGTATGGC	AAAGGTTCTT	4440
GAGAATCAGC	CATTTGGTAC	AAAAAAGATT	TTTAAAGCTT	TTATGTTATA	CCATGGAGCC	4500
ATAGAAAGGC	TATGGATTGT	TTAAGAACTA	TTTTAAAGTG	TTCCAGACCC	AAAAAGGAAA	4560
AATAAAAAAA	AAGGAATATT	TGTACCCCAAC	AGCTAGAAGG	ATTGCAAGGT	AGATTTTTGT	4620
TTTAAATGG	AGAGAAGTGG	ACAGATAAGG	CCATTTAATA	TATCAAAGAT	CAGTTGACAT	4680
CTCCTAGGGA	ATGATGAAAA	CAGCAGGCTA	T			

Seq ID NO: 18 Protein sequence:
Protein Accession #: CAA53571

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NSVDPENITE	IFIANQKRLE	IINEDDVEAY	VGLRNLITVD	SLGLKFVAHKA	FLKNSNLQHI	120
NFTRNKLTSL	SRKHFRHLDL	SELILVGNFF	TCSCDIMWIK	TLQEAKESSPD	TQDLYCLNES	180
SKNIPLANLQ	IPNCGLPFSAN	LAAPNLTVEE	GKSITLSCSV	AGDPVFNMYW	DVGNLVSXHM	240
NETSHTQSSL	RITNISSDDS	GKQISCVAEN	LVGEDQDSVN	LTVHFAPTIT	FLESPTSDDH	300
WCIPFTVKGN	PKPALQWFYN	GAILNESKYI	CTKIHTVNTHT	EYHGCLQLDN	PTHMNGDYT	360
LIANKNEYKGD	EKQISAHFMG	WPGIDDGANP	NYPDVIYEDY	GTAANDIGDT	TNRNSNEIPST	420
DVTDKGTREH	LSVYAVVVIA	SVVGFCLLVM	LFLLKLARHS	KFGMKGFVLF	HKIPLDG	

Seq ID NO: 19 DNA sequence
Nucleic Acid Accession #: NM_000228
Coding sequence: 82-3600

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CTTGTGGGGA	GGACCCGGTT	TCTCCGAGCT	TCATCTACCT	GTGGACTGAC	CAAGCCTGAG	240
ACCTACTGCA	CCAGATGTTG	CGAGTGGCAG	ATGAAATGCT	GCAAGTGTGA	CTCCAGGCAG	300
CCTCACAACT	ACTACAGTCA	CCGAGTAGAG	AATGTGGCTT	CATCCTCCGG	CCCCATGCGC	360
TGGTGGCAGT	CCGAGAATGA	TGTGAACCTT	GTCTCTCTGC	AGCTGGACCT	GGACAGGAGA	420
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GAGCGCTCCT	CAGACTTCGG	TAAGACCTGG	CGAGTGTACC	AGTACCTGGC	TGCCGACTGC	540
ACCTCCACCT	TCCCTCGGGT	CGGCCAGGGT	CGGCCTCAGA	GCTGGCAGGA	TGTTGGGTGC	600
CAGTCCCTGC	CTCAGAGGCC	TAATGCACGC	CTAAATGGGG	GGAGGTCCA	ACTTAACTCT	660
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CCTCCACAGC	CCTACTATGC	TGTGTCCAG	CTCCGTCTGC	AGGGGAGCTG	CTTCTGTAC	840
GGCCATGCTG	ATCCCTGGGC	ACCCAGCCT	GGGGCCTCTG	CAGGCCCTCT	CACCGCTGTG	900
CAGGTCCACG	ATGCTCTGTG	CTGCCAGCAC	AACACTGCCG	GCCCAAATTG	TGAGCGCTGT	960
GCACCCCTCT	ACAACAAACG	GGCCTGGAGA	CCGGCGGAGG	GCCAGGACGC	CCATGAATGC	1020
CAAGAGTGCG	ACTGCAATGG	GCACTCAGAG	ACATGTCACT	TGACCCCTCG	TGTGTTTGCC	1080
GCCAGCCAGG	GGGCATATGG	AGGTGTGTGT	GACAATTGCC	GGGACCAAC	CGAAGGCAG	1140
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AACATCCTGG	GGTCCCGGAG	GGACATGCCG	TGTGACGAGG	AGAGTGGGCG	CTGCCTTTGT	1440
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GCAGCCATCC	CCAGTGTGCC	AGACCGGACC	TATGGAGACG	TGGCCACAGG	ATGCCGAGCC	1680
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CAGGTGGCTG	AGCAGCTGCG	GGGCTTCAAT	GCCAGCTTCC	AGCGGACCGG	GCAGATGATT	2640
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GAGAGCGGCA	GCGCTCCCA	GATGGAGGAA	GATGTGACAG	GACACCGGCT	CCTAATCCAG	2760
CAGGTCCGGG	ACTTCTTAAC	AGACCCGAC	ACTGATGCAG	CCACTATCCA	GGAGGTGAGC	2820
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GAGATCCAGG	CCATTGTCAG	CAGGCTCCCC	AACGTGGACT	TGGTGTCTGT	CCAGACCAAG	2940
CAGGACATTG	CGCGTGCCTG	CGGTTGTCAG	GCTGAGGCTG	AGGAAGCCAG	GAGCCGAGCC	3000
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AAGCAGCTGG	GTGACTTCTG	GACACGGATG	GAGGAGCTCC	GCCACCAAGC	CCGGCAGCAG	3240
GGGGCAGAGC	CAGTCCAGGC	CCAGCAGCTT	GCGGAAGGTG	CCAGCGAGCA	GGCATTGAGT	3300
GCCCCAGAGG	GATTGAGAG	AATAAAACAA	AAGTATGCTG	AGTTGAAGGA	CCGGTTGGGT	3360

CAGAGTTCCA TGCTGGGTGA GCAGGGTGCC CGGATCCAGA GTGTGAAGAC AGAGGCAGAG 3420
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Seq ID NO: 20 Protein sequence:
 Protein Accession #: NP_000219

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 NARLNGGKVG LNLMDLVSGI PATQSQKIQE VGEITNLRVN FTRLAPVPQR GYHPPSAYYA 240
 VSQRLRQGSF FCHGHADRC A PKPGASAGPS TAVQVHDCV CQHNTAGPNC ERCAPFYNNR 300
 PWRPAEGQDA HECQRCDCNG HSETCHFDPA VFAASQGA YG GVCNDCRDHT EGKNCERCQL 360
 HYFRNRRPGA SIQETCLSC E CDPDGA VPGA PCDPVTGQCV CKEHVQGERC DLCKPGFTGL 420
 TYANPQGGHR CDNCLGSRR DMPDEESGR CLCLPNVVG P KCDQCAPYHW KLASGQGCPE 480
 CACDPHNSFP PTVPQVRRV PCREGFGGLM CSAAAIROCP DRTYGDVATG CRACDCDFRG 540
 TEGPGCDKAS GRCLCRPGLT GPRCDQCQRG YCNRYFVCVA CHPCFQTYDA DLREQALRFG 600
 RLNRNATSLW SGPGLDRLG ASRILDASK IEQIRAVLSS PAVTEQEVQA VASAILSLRR 660
 TLQGLQLDLP LEEETLSLPR DLESLLDRSFN GLLTMYQRKR EQFEKISSAD PSGAFRMLST 720
 AYEQSAQAQ QVSDSSRLLD QLRRDSRREAE RLVRQAGGGG GTGSPKLVAL RLEMSSSLPDL 780
 TPTFNKLKCN SRQMACTPIS CPGELCPQDN GTACGSRCRG VLPRAAGGAF MAGQVAEQLR 840
 GFNAQLQRT R QMIRAAEESA SIQSSAQRL ETQVSASRSQ MEEDVRTRL LIQQVRDLFT 900
 DPDTDAATIQ EVSEAVLALW LPTDSATVLQ KMNEIQAI A RLPNVDLVLS QTKQDIARAR 960
 RLQAEAEER SRAHAVEGV EDVVGNLRRQ TVALQEAQDT MQGTSRSLRL IQDRVAEVQQ 1020
 VLRPAEKLV T SMTQQLGDFW TRMEELRHQA RQQGAEAQVA QQLAEGASEQ ALSAQEGFER 1080
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Seq ID NO: 21 DNA sequence
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 Coding sequence: 145-1491

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 ATTGACTTGA ACTTGTGGA TGAACCATCA GAAGATGGTG CGACAAACAA GATTGAGATT 300
 AGCATGGACT GTATCCGACT GCAGGACTCG GACCTGAGTG ACCCCATGTG GCCACAGTAC 360
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 AGTCCCTATA ACACAGACCA CGCGCAGAAC AGCGTCACGG CGCCCTCGCC CTACGCACAG 480
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Seq ID NO: 22 Protein sequence:
 Protein Accession #: NP_003713

1 11 21 31 41 51
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 SPSPAIPSNIT DYPGPHSFDV SFQSSSTAKS ATWTYSTELEK KLYCQIAKTC PIQIKVMTFP 180
 PQGAIVIRAMP VYKKAHVTE VVRCPCNHEL SREFNEGQIA PPSHLIRVEG NSHAQYVEDP 240
 ITGRQSVLVP YEPQVQTEF TTVLYNFMEN SSCVGMNRR PILIIVTLET RDGQVLGRRC 300
 FEARICACFG RDRKADDSI RKQVSDSTK NGDGTKRPFQ QNTHGIQMTS IKRRSPDDE 360
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Seq ID NO: 23 DNA sequence
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Seq ID NO: 24 Protein sequence:
 Protein Accession #: NP_001935.1

1 11 21 31 41 51

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	ATDADEPNHL	NSKIAFKIVS	QEPAGTFMFL	LSRNTGVEVRT	LITNSLDREQA	SSYRLVVSGA	240
	DKDGEGLSTQ	CECNIVKVDV	NDNPPMFRDS	QYSARIEENI	LSSELLRFQV	TDLDEEYTDN	300
	WLAVYFPTSG	NEGNWPEIQT	DPRINEGILK	VVKALDYDQL	QSVKLSIAVK	NKAEFHQSVI	360
	SRYRVQSTPV	TIQVINVREG	IAFRPASKTF	TVQKGISSEK	LVDYILGTQY	AIDEDTNKAA	420
10	SNVKYVMGRN	DGGYLMIDSK	TAEIKFVKIM	NRDSTFIVNK	TITAEVLAI	EXTGKTSTGT	480
	VYVRVPDFND	NCPTAVLEKD	AVCSSSPSVV	VSARTLNTRY	TGPTYFALED	QPVKLEPAVNS	540
	ITTLNATSAL	LRAQEQIPPG	VYHISLVLT	SQNNRCMPR	SLTLEVCCQD	NRGICGTSYP	600
	TTSPGTRYGR	PHSGRLGPAA	IGLLLLGLLL	LLAPLLLLT	CDGAGSTGG	VTGGFIPVFD	660
	GSEGTIHQWG	IEGAHPEDKE	ITNICVFPVT	ANGADFMESS	EVCTNTYARG	TAVEGTSGME	720
15	MTTKLGAATE	SGGAAGPATG	TVSGAASGFG	AATGVGICSS	GQSGTMRTRH	STGGTNKDYA	780
	DGAISMNPLD	SYFSQKAFAC	AEEDDGQEAN	DCLLIYDNEG	ADATGSPVGS	VGCCSFIADD	840
	LDSPLDSLQ	LPVKLLAEIS	LGVDGEGKEV	QPPSKDSGYG	IESCGHPIEV	QQTGFVKCQT	900
	LSGSQGSASL	SASGSVQPAV	SIPDPLQHGN	YLVETETYSAS	GSLVQPSSTAG	FDPLLTQNV	960
	VERTVICPIS	SVPGNLAGPT	QLRGSHTMLC	TEDPCSRLI			

Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 56-1642

25	1	11	21	31	41	51	
	AGTATCCCAG	GAGGAGCAAG	TGGCACGTCT	TGGGACCTAG	GCTGCCCTTG	CCGTTCATGTC	60
	GCAAGGGGATC	CTTTCTCCGC	CAGCGGGCTT	GCTGTCCGAT	GACGATGTCG	TAGTTTCTCC	120
	CATGTTTGAG	TCCACAGCTG	CAGATTGGGG	GTCTGTGGTA	CGCAAGAACC	TGCTATCAGA	180
30	CTGCTCTGTG	GTCTCTACCT	CCCTAGAGGA	CAAGCAGCAG	GTTCCTATCT	AGGACAGTAT	240
	GGAGAAGGTG	GAATATATCT	TGAGGGTTAG	GCCCTTGTTA	CCTTCAGAGT	TGGAACGACA	300
	GGAGATCAG	GGTGTGTCTC	GTATTGAGAA	TGTGGAGACC	CTTGTTCTAC	AAGCACCCAA	360
	GGACTCTTTT	GCCCTGAAGA	GCAATGAACG	GGGAATTGGC	CAAGCCACAC	ACAGTTTCAC	420
	CTTTTCCAG	ATCTTTGGGC	CAGAAGTGGG	ACAGGCATCC	TTCTTCAACC	TAACTGTGAA	480
35	GGAGATGGTA	TACATCGAAA	TCAAAGGGCA	GAACCTGGCTC	ATCTATACAT	ATGGAGTCAC	540
	TAACTCAGGG	AAAACCCACA	CGATTCAAGG	TACCATCAAG	GATGGAGGGA	TTCTCCCCCG	600
	GTCCCTGGCG	CTGATCTTCA	ATAGCCTCCA	AGGCCAATCT	CATCCACAC	CTGATCTGAA	660
	GCCCTTGCTC	TCCATATGAG	TAATCTGGCT	AGACAGCAAG	CAGATCCGAC	AGGAGGAAAT	720
	GAAGAAGCTG	TCCCTGTCAA	ATGGAGGCCT	CCAAGAGGAG	GAGCTGTCCA	CTTCTTGAA	780
40	GAGGAGTGTG	TACATCGAAA	GTGGATAGG	TACCAGCACC	AGCTTCGACA	GTGGCATTCG	840
	TGGGCTCTCT	TCTATCAGTC	AGTGATACAG	CAGTAGCCAG	CTGGATGAAA	CAAGTCATCG	900
	ATGGGCACAG	CCAGACATCG	CCCCACTACC	TGTCCCGGCA	AACATTGCGT	TCTCCATCTG	960
	GATCTCATTC	TTTGAGATCT	ACAACGAACT	GCTTTATGAC	CTATTAGAAC	CGCCTAGCCA	1020
	ACAGCGCAAG	AGGCGACTTT	TGCGGCTATG	CGAGGATCAA	AATGGCAATC	CCTATGTGAA	1080
45	AGATCTCAAC	TGGATTCTAG	TGCAAGATGC	TGAGGAGGCC	TGGAAGCTCC	TAAAAGTGGG	1140
	TGTAAGAAAC	CAGAGCTTTG	CCAGCACCCA	CCTCAACAGG	AACTCCAGCC	GCAGTCACAG	1200
	CATCTTCTCA	ATCAGGATCT	TACACCTTCA	GGGGGAAGGA	GATATAGTCC	CCAAGATCAG	1260
	CGAGCTGTCA	CTCTGTGATC	TGCTGTGCTC	AGAGCGCTGC	AAAGATCAGA	AGAGTGGTGA	1320
	ACGGTTGAAG	GAAGCAGGAA	ACATTAAACAC	CTCTCTACAC	ACCCCTGGGCC	GCTGTATTGC	1380
50	TGCCCTTCGT	CAAAACCCAG	AGAACCAGGC	AAAGCAGAAC	CTGGTTCCCT	TCCGTGACAG	1440
	CAAGTTGACT	CGAGTGTTC	AAGGTTTCTT	CACAGGCCGA	GGCCGTTTCT	GCATGATTGT	1500
	CAATGTGAA	CCCTGTGCAT	CTACCTATGA	TGAAACTCTT	CATGTGGCCA	AGTTCTCAGC	1560
	CATTGCTAGC	CAGGTGACTT	GTGCATGCCC	CACCTATGCA	ACTGGGATTC	CCATCCCTGC	1620
	ACTCGTTCAT	CAAGGAACAT	AGTCTTCAGG	TATCCCCCAG	CTTAGAGAAA	GGGGCTAAGG	1680
55	CAGACACAGG	CCTTGATGAT	GATATTGAAA	ATGAAGCTGA	CATCTCCATG	TATGGCAAG	1740
	AGGAGCTCTC	ACAAGTTGTG	GAAGCCATGA	AGACACTGCT	TTTGAAGGAA	CGACAGGAAA	1800
	AGCTACAGCT	GGAGATGCAT	CTCCGAGATG	AAATTGCAAA	TGAGATGGTA	GAACAGATGC	1860
	AACAGCGGGA	ACAGTGTGTC	AGTGAACATT	TGGACACCCA	AAAGGAACTA	TTGGAGGAAA	1920
	TGTATGAAGA	AAAACATAAT	ATCCTCAAGG	AGTCACTGAC	AAGTTTTTAC	CAAGAAGAGA	1980
60	TTCAGGAGCG	GGATGAAAAG	ATTGAAGAGC	TAGAAGCTCT	CTTGCAGGAA	GCCAGACAAC	2040
	AGTCAGTGGC	CCATCAGCAA	TCAGGGTCTG	AATTGGCCCT	ACGGCGGTCA	CAAAGGTTGG	2100
	CAGCTTCTGC	CTCCACCCAG	CAGCTTCAGG	AGGTTAAAGC	TAAATTACAG	CAGTGCAAG	2160
	CAGAGCTAA	CTCTACCACT	GAAGAGTTGC	ATAAGTATCA	GAAATGTGTA	GAACCAACC	2220
	CCTCAGCCAA	GCCCTTCACC	ATTGATGTGG	ACAAGAAGTT	AGAAGAGGGC	CAGAAGAATA	2280
65	TAAGGCTGTT	GCGGACAGAG	CTTCAGAAAC	TTGGTGAGTC	TCTCCAATCA	GCAGAGAGAG	2340
	CTTGTGTC	CAGCACTGGG	GCAGGAAAAC	TTGCTCAAGC	CTTGACCACT	TGTGATGACA	2400
	TCCTTAATCAA	ACAGGACCCAG	ACTCTGGCTG	AACTGCAGAA	CAACATGGTG	CTAGTGAAAC	2460
	TGGACCTTCG	GAAGAAGGCA	GCATGTATTG	CTGAGCAGTA	TCATACCTGT	TTGAAACTCC	2520
	AAGGCCAGGT	TTCTGCCAAA	AAGCGCCTTG	GTACCAACCA	GGAAAATCAG	CAACCAAAACC	2580
70	AACAACCACC	AGGGAAGAAA	CCATTCTTTC	GAAATTTACT	TCCCCGAACA	CCAACCTGCC	2640
	AAAGCTCAAC	AGACTGCAGC	CCTTATGCCC	GGATCCTACG	CTCAGCGCGT	TCCCCTTTAC	2700
	TCAAATCTGG	GCCTTTTGGC	AAAAAGTACT	AAGGCTGTGG	GGAAAGAGAA	GAGCAGTCAT	2760
	GGCCCTGAGG	TGGGTGAGCT	ACTCTCCTGA	AGAAATAGGT	CTCTTTTATG	CTTTACCATA	2820
	TATCAGGAAT	TATATCCAGG	ATGCAATACT	CAGACACTAG	CTTTTCTCTC	ACTTTTGTAT	2880
75	TATAACCACC	TATGTAATCT	CATGTTGTTG	TTTTTTTTTA	TTTACTTATA	TGATTCTTAT	2940
	GCACACAAA	ACAGTTATAT	TAAAGATATT	ATTGTTTACA	TTTTTTTATTG	AATTCCAAAT	3000
	GTAGCAAAA	CATTAAAAA	AATTATAAAA	GGGACAGAAA	AA		

Seq ID NO: 26 Protein sequence:
Protein Accession #: Eos sequence

80	1	11	21	31	41	51	
	MSQGILSPPA	GLLSDDDVVV	SPMFESTAAD	LGSVVRKNLL	SDCSVVSTSL	EDKQVPSSE	60
85	SMEKVKVYL	VRPLLPSELE	RQEDQGCVR	ENVETLVLQA	PKDSFALKSN	ERIGIQATHR	120
	FTFSQIFGPE	VQASFFNL	VKEMVKDVLK	GQNLVLYTYG	VTNSGKTHTI	QGTIKDGGIL	180
	PRSLALIFNS	LQGLHPPTD	LKPLLSNEVI	WLDKSKIRQE	EMKLSLLNG	GLQEELSTS	240
	LKRSVYIESR	IGTSTSPDSG	IAGLSSISQC	TSSSQLDETS	HRWAQPDTPA	LPVPANIRFS	300

INISPFIEIYN ELLYDLLEPP SQQRKRQTLR LCEDQNGNPF VKDLNWIHVQ DAEBAWKLLK 360
 VGRKNQSPAS THLNQNSSRS HSIFSRILH LQEGGDIVPK ISELSLCDLA GSERCKDQKS 420
 GERLKEAGNI NTSLHTLGRG IALRQNRQN RSKQNLVPR DSKLTRVFQ FFGTGRGRSCM 480
 IVNVNPCAST YDETLHVAKF SAIASQVTCA CPTYATGIPI PALVHQGT

Seq ID NO: 27 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 13-1424

10 1 11 21 31 41 51
 TAGAAGTTTA CAATGAAGTT TCTTCTAATA CTGCTCCTGC AGGCCACTGC TTCTGGAGCT 60
 CTTCCTCTGA ACAGCTCTAC AAGCCTGGAA AAAAATAATG TGCTATTGG TGAAGATAC 120
 15 TTAGAAAAAT TTATGCGCT TGAGATAAAC AAACCTCCAG TGACAAAAAT GAAATATAGT 180
 GGAAACTTAA TGAAGGAAAA AATCCAAGAA ATGCAGCACT TCTTGGGTCT GAAAGTGACC 240
 GGGCAACTGG ACACATCTAC CCTGGAGATG ATGCACGCAC CTCGATGTGG AGTCCCGGAT 300
 GTCCATCATT TCAGGGAAT GCCAGGGGGG CCCGTATGGA GGAACATTA TATCACTAC 360
 AGAATCAATA ATTACACACC TGACATGAAC CGTGAGGATG TTGACTACGC AATCCGAAA 420
 20 GCTTTCCAAG TCAAGAGTAA TGTACCCCT TTGAAATTCA GCAAGATTAA CACAGGCATG 480
 GGTGACATTT TGGTGGTTTT TGCCCGTGGA GCTCATGGAG ACTTCCATGC TTTGATGGC 540
 AAAGGTGGA TCTTAGCCCA TGCTTTTGGA CTGGATCTG GCATTGGAGG GGATGCACAT 600
 TTCGATGAGG ACGAATCTG GACTACACAT TCAGGAGGCA CAACTTGTG CTTCACTGCT 660
 GTTCAGGAGA TTGGCCATTC CTTAGGTCTT GGCCATTCTA GTGATCCAAA GGCCGTAATG 720
 25 TTCCCACTT ACATATCTGT TGACATCAAC ACATTTCCGC TCTCTGCTGA TGACATACGT 780
 GGCACTCAGT CCTGTATGG AGACCCAAA GAGAACCAAC GCTTGCCAAA TCCTGACAA 840
 TCAGAACCAG TCTCTGCTGA CCCCATTG AGTTTGTATG CTGTCACTAC CGTGGGAAAT 900
 AAGATCTTT TCTTCAAGA CAGGTTCTTC TGGCTGAAGG TTTCTGAGAG ACCAAGACC 960
 AGTGTATATT TAATTTCTTC CTATGGCCA ACCTTGCCAT CTGGCATTTA AGCTGCTTAT 1020
 30 GAAATGAAG CCAGAAATCA AGTTTTCTT TTTAAAGATG ACAAATCTG GTTAATTAGC 1080
 AATTTAAGAC CAGAGCCAAA TTATCCCAAG AGCATACATT CTTTGGTTT TCCTAACTTT 1140
 GTGAAAAAAA TTGATGCAGC TGTTTTTAAC CCAAGTTTTT ATAGGACCTA CTTCTTTGTA 1200
 GATAACCACT ATTGGAGGTA TGATGAAAG AGACAGATGA TGGACCTCG TTATCCCAA 1260
 CTGATTACCA AGAATTTCCA AGGAATCGGG CCTAAAATTG ATGCAGTCTT CTACTCTAAA 1320
 35 AACAAATCT ACTATTCTT CCAAGGATCT AACCAATTG AATATGACT CTACTCTCAA 1380
 CGTATCACA AAACACTGAA AAGCAATAGC TGGTTTGGTT GTTGAAATG GTGTAATTAA 1440
 TGGTTTTTGT TAGTTCAGT CAGCTTAATA AGTATTATG GCATATTGTC TATGCTCTCA 1500
 GTGTACCACT ACTTAGAGAT ATGTATCATA AAAATAAAAT CTGTAAACCA TAGGTAATGA 1560
 TTATATAAAA TACATAATAT TTTTCAATT TGAAAACTCT AATTGTCCAT TCTTGCTTGA 1620
 40 CTCTACTATT AAGTTTGA AAATAGTTACCT TCAAAGCAAG ATAATTCTAT TTGAAGCATG 1680
 CTCTGTAAGT TGCTTCCTAA CATCCTTGA CTGAGAAATT ATACTTACTT CTGGCATRAAC 1740
 TAAATTAAG TATATATATT TTGGCTCAA TAAATTTG

Seq ID NO: 28 Protein sequence:
 Protein Accession #: Eos sequence

45 1 11 21 31 41 51
 MKFLILLILQ ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKVSGNLM 60
 50 KEKIQEMQHF LGLKVTGQLD TSFLEMMHAP RCGVPDVHVF REMPGGPVWR KHYITYRINN 120
 YTPDMNRDQV DGAIRKAFQV WSNVTPPKFS KINTGMADIL VVPARGAHGD PHAFDGGKGI 180
 LAHAFPGSGG IGGDAHFDDE EFWTHSGGT NLPLTAVHEI GHSLLGLHSS DPKAVMPPY 240
 KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDENLSFDA VTTVGNKIEF 300
 FKDRPFWLKV SERPKTSVNL ISSLWPTLPS GIEAAVEIEA RNQVFLPKDD KYWLISNLRP 360
 55 EPNYPKSIHS GFPPNFVKKI DAAVFNPRFY RTYFVFDNQY WRYDERRQVM DPGYPKLITK 420
 NFQGGIPKID AVFYSKNKYY YFFQGSNQPE YDFLLQRITK TLKSNWFFGC

Seq ID NO: 29 DNA sequence
 Nucleic Acid Accession #: NM_006115.1
 Coding sequence: 236..1765

60 1 11 21 31 41 51
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 65 CGGGACACCC CACCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA 120
 ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGCCA ACAAGTGACT 180
 GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA 240
 ACGAAGGCGA TTTGGGGGTT CCATTAGAG CCGATACATC AGCATGAGTG TGTGGACAAG 300
 CCGACGGAGT CTGTGGAGG TGCGAGGCA GAGCCTGCTG AAGGATGAGG CCCTGGCCAT 360
 70 TGCCCGCCCTG GAGTTGCTGC CCAGGGAGCT CTTCGCCCA CTCTTCATGG CAGCCTTTGA 420
 CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGCGAGCC TGGCCCTTCA CTGCTCTCC 480
 TCTGGGAGTG CTGATGAAGG GACACATCT TCACTGGAG ACCTTCAAAG CTGTGCTTGA 540
 TGGACTTGAT GTGCTCTTGT CCCAGGAGGT TCGCCCCAGG AGGTGGAAC TTCAAGTGCT 600
 GGATTTACGG AAGAACTCTC ATCAGGACTT CTGGACTGTA TGGTCTGGAA ACAGGGCCAG 660
 75 TCTGTACTCA TTTCCAGAGC CAGAAGCAGC TCAGCCCATG ACAGAAGAGC GAAAAGTAGA 720
 TGGTTTGAGC ACAGAGGCAG AGCAGCCCTT CATTCAGTA GAGGTGCTCG TAGACCTGTT 780
 CCTCAAGGAA GGTCCCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA 840
 GAAAAATGTA CTACGCTGT GCTGTAAGAA GCTGAAGATT TTTGCAATGC CCATGCACGA 900
 TATCAAGATG ATCCTGAAAA TGGTGCAAGT GGACTCTATT GAAGATTGG AAGTGACTTG 960
 80 TACCTGGAAG CTACCCACCT TGGCGAAATT TTCTCCTTAC CTGGGCCAGA TGATTAATCT 1020
 GCGTAGACTC CTCCTCTCCC ACATCCATGC ATTTCTCTAC ATTTCCCGG AGAAGGAAGA 1080
 CGAGTATATC GCCCAGTTCA CCTCTCAGTT CACTGCTCG CAGTGCTCG AGGCTCTCTA 1140
 TGTGGACTCT TTATTTTCC TTAGAGGCCG CCTGGATCAG TTGCTCAGGC ACGTGATGAA 1200
 CCGCTTGGAA ACCCTCTCAA TAACTAACTG CCGGCTTTG GAAGGGGATG TGATGCATCT 1260
 85 GTCCAGAGT CCCAGCCTCA GTCAGCTAAG TGTCTGAGT CTAAGTGGGG TCATGCTGAC 1320
 CGATGTAAGT CCCGAGCCCC TCCAAGCTCT GCTGGAGAGA GCCTCTGCCA CCCTCCAGGA 1380
 CCTGGTCTTT GATGAGTGTG GGATCAGCTC CTTGCCCTCC TGCCTTCCCT 1440
 GAGCCACTGC TCCAGCTTA CAACCTTAAG CTTCTACGGG AATTCCATCT CCATATCTGC 1500

CTTGCAGAGT CTCTGCAGC ACCTCATCGG GCTGAGCAAT CTGACCCACG TGCTGTATCC 1560
 TGTCCCCCTG GAGAGTTATG AGGACATCCA TGGTACCCCT CACCTGGAGA GGCTTGCCCTA 1620
 TCTGCATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCACAGA TGGTCTGGCT 1680
 TAGTGCCAAC CCTGTCTCTC ACTGTGGGGA CAGAACTTTC TATGACCCGG AGCCCATCCT 1740
 GTGCCCTGT TTTATGCCCTA ACTAGCTGGG TGACATATC AAATGCTTCA TTCTGCATAC 1800
 TTGGACACTA AAGCCAGGAT GTGCATGCAT CTTGAAGCAA CAAAGCAGCC ACAGTTTCAG 1860
 ACAAATGTTT AGTGTGAGTG AGGAAACAT GTTCAGTGAG GAAAAACAT TCAGACAAAT 1920
 GTTCAGTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTGTACTTG AGGAGTTAAT 1980
 GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA 2040
 GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC 2100
 TGTGTAAAT AAAGAGAAGC AATGTGAAGC AAAAAAAAAA AAAAAAA

Seq ID NO: 30 Protein sequence:
 Protein Accession #: NP_006106.1

1 11 21 31 41 51
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 GCTTCAGGGT ACAGCTCCCC CGCAGCCAGA AGCCGGGGCT GCAGCGCCCT AGCACCCTC 60
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 ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGGCA ACAAGTGAAT 180
 GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA 240
 ACGAAGGCGT TTTGGGGT CCATTAGAG CCGATACATC AGCATGAGTG TGTGGACAAG 300
 CCCACGGAGA CTTGTGGAGC TGGCAGGCCA GAGCCTGCTG AAGGATGAGG CCCTGGCCAT 360
 TGGCGCCCTG GAGTTGCTGC CCAGGAGCT CTTCCGCCA CTCTTCATGG CAGCCTTTGA 420
 CGGGAGACAC AGGCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CCTGCCTCCC 480
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 GGAATTTACG AAGAATCTCT ATCAGGACTT CTGGACTGTA TGGTCTGGAA ACAGGGCCAG 660
 TCTGTACTCA TTTCCAGAGC CAGAAGCAGC TCAGCCCATG ACAAAGAAGC GAAAGTAGA 720
 TGGTTGAGC ACAGAGGCGA AGCAGCCCTT CATTCAGTA GAGGTGCTCG TAGACCTGTT 780
 CCTCAAGGAA GGTGCGTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA 840
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 TATCAAGATG ATCTGAAAA TGGTGCAGCT GGACTCTATT GAAGATTGG AAGTCACTTG 960
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 GCGTAGACTC CTCTCTCTCC ACATCCATGC ATCTCTCTAC ATTTCCCGG AGAAGGAAGA 1080
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 CGATGTAAGT CCGAGCCCCC TCAGAGCTCT GCTGGAGAGA GCCTCTGCCA CCCTCCAGGA 1380
 CCTGGTCTTT GGTGAGTGTG GATCACGGA TGATCAGCTC CTGCGCCCTC TGCCTTCCCT 1440
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 CTTGCAGAGT CTCTGCAGC ACCTCATCGG GCTGAGCAAT CTGACCCACG TGCTGTATCC 1560
 TGTCCCCCTG GAGAGTTATG AGGACATCCA TGGTACCCCT CACCTGGAGA GGCTTGCCCTA 1620
 TCTGCATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCACAGA TGGTCTGGCT 1680
 TAGTGCCAAC CCTGTCTCTC ACTGTGGGGA CAGAACTTTC TATGACCCGG AGCCCATCCT 1740
 GTGCCCTGT TTTATGCCCTA ACTAGCTGGG TGACATATC AAATGCTTCA TTCTGCATAC 1800
 TTGGACACTA AAGCCAGGAT GTGCATGCAT CTTGAAGCAA CAAAGCAGCC ACAGTTTCAG 1860
 ACAAATGTTT AGTGTGAGTG AGGAAACAT GTTCAGTGAG GAAAAACAT TCAGACAAAT 1920
 GTTCAGTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTGTACTTG AGGAGTTAAT 1980
 GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA 2040
 GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC 2100
 TGTGTAAAT AAAGAGAAGC AATGTGAAGC AAAAAAAAAA AAAAAAA

Seq ID NO: 31 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 64-2754

1 11 21 31 41 51
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 CTGACCCCTG TGATCTTCAG TCGTGATGGT GAAGCCTGCA AAAAGGTGAT ACTTAATGTA 180
 CCTTCTAAAC TAGAGGCAGA CAAAATAATT GGCAGAGTTA ATTTGGAAGA GTGCTTCAGG 240
 TCTGCAGACC TCAATCCGGTC AAGTGATCCT GATTTAGAG TTCTAAATGA TGGGTCACTG 300
 TACACAGCCA GGGCTGTTGC GCTGTCTGAT AAGAAAAGAT CATTTACCAT ATGGCTTCT 360
 GACAAAAGGA AACAGACACA GAAAGAGGTT ACTGTGCTGC TAGAACATCA GAAGAAGGTA 420
 TCGAAGACAA GACACACTAG AGAACTGTT CTCAGGCGTG CCAAGAGGAG ATGGGCACCT 480
 ATTCCTTGCT CTATGCAAGA GAATTCCTTG GGCCTTTCC CATTGTTTCT TCAACAAGTT 540
 GAATCTGATG CAGCAGAGAA CTATCTGTC TTCTACTCAA TAAGTGGAGC TGGAGTTGAT 600
 AAAGAACCCT TAAATTTGTT TTATATAGAA AGAGACACTG GAAATCTATT TTGCACTCGG 660
 CCTGTGGATC GTGAAGAATA TGATGTTTTT GATTGATTG CTTATGCGTC AACTGCAGAT 720
 GGATATTGAG CAGATCTGCC CCTCCACTA CCCATCAGGG TAGAGGATGA AAATGACAAC 780
 CACCCCTGTT TCACAGAAGC AATTTATAAT TTTGAAGTTT TGGAAAGTAG TAGACCTGGT 840
 ACTACAGTGG GGGTGGTTTG TGCCACAGAC AGAGATGAAC CGGACACAAT GCATACGCGC 900
 CTGAAATACA GCATTTTGCA GCAGACACCA AGGTCACTGA GGCTCTTTTC TGTGCATCCC 960
 AGCAGAGCGG TAATCCACAC AGTCTCTCAT TATTTGGACA GAGAGGTTGT AGACAAGTAC 1020
 TCATTGATAA TGAAGTACA AGACATGGAT GGCCAGTTT TGGATTGAT AGGCACATCA 1080
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 GAAATGGAC ATTTCAAAAT CAGCACAGAC AAAGAACTA ATGAAGGTGT TCTTTCTGTT 1320
 GTAAAGCCAC TGAATATGA AGAAACCGT CAAGTGAACC TGGAAATGG AGTAAACAAT 1380
 GAAGCGCCAT TTGCTAGAGA TATTCACAGA GTGACAGCCT TGAACAGAGC CTTGGTTACA 1440
 GTTCATGTGA GGGATCTGGA TGAGGGGCGT GAATGCACCT CTGCAGCCCA ATATGTGCGG 1500
 ATTAAGAAA ACTTAGCAGT GGGGTCAAAG ATCAACGGCT ATAAGGCATA TGACCCCGAA 1560

	AATAGAAATG	GCAATGGTTT	AAGGTACAAA	AAATTGCATG	ATCCTAAAGG	TTGGATCACC	1620
	ATTGATGAAA	TTTCAGGGTC	AATCATAACT	TCCAAAATCC	TGGATAGGGA	GGTTGAAACT	1680
	CCCAAAAATG	AGTTGTATAA	TATTACAGTC	CTGGCAATAG	ACAAAGATGA	TAGATCATGT	1740
5	ACTGGAAACAC	TTGCTGTGAA	CATTGAAGAT	GTAAATGATA	ATCCACCAGA	AATACTTCAA	1800
	GAATATGTAG	TCATTTGCAA	ACCAAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
	GATGAACCTG	TCCATGGAGC	TCCATTTTAT	TTCAAGTTTG	CCAATACTTC	TCCAGAAATC	1920
	AGTAGACTGT	GGAGCCTCAC	CAAAGTTAAT	GATACAGCTG	CCCGTCTTTC	ATATCAGAAA	1980
	AATGCTGGAT	TTCAAGAATA	TACCATTCTC	ATTACTGTAA	AAGACAGGGC	CGGCCAAGCT	2040
10	GCAACAAAAT	TATTGAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACTCA	GTGTCGTGGG	2100
	ACTTCAAGGA	GTACAGGAGT	AATACTTGGA	AAATGGGCAA	TCCTTGCAAT	ATTACTGGGT	2160
	ATAGCACTGC	TCTTTTCTGT	ATTGCTAACT	TTAGTATGTG	GAGTTTTTGG	TGCAACTAAA	2220
	GGGAAACGTT	TTCTGAAGA	TTTAGCACAG	CAAAACTTAA	TTATATCAAA	CACAGAAGCA	2280
	CCTGGAGAGC	ATAGAGTTGT	CTCTGCCAAT	GGATTTATGA	CCCAAACTAC	CAACAACTCT	2340
	AGCCCAAGGT	TTTGTGGTAC	TATGGGATCA	GGAATGAAAA	ATGGAGGGCA	GGAAACCAT	2400
15	GAAATGATGA	AAGGAGGAAA	CAGACCTTGG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
	ACCCTGAGCT	CCTGCAGGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACCTACTCG	2520
	GAGTGGCACA	GTTTTACTCA	ACCCCGTCTC	GGTGA AAAAT	TGCATCGATG	TAATCAGAA	2580
	GAAGACCGCA	TGCCATCCCA	AGATTATGTC	CTCACTTATA	ACTATGAGGG	AAGAGGATCT	2640
	CCAGCTGGTT	CTGTGGGCTG	CTGCAGTGAA	AAGCAGGAAG	AAGATGGCCT	TGACTTTTAA	2700
20	AATAATTGGG	AACCCAAAT	TATTACATTA	GCAGAAGCAT	GCACAAAGAG	ATAATGTCAC	2760
	AGTGCTACAA	TATGGTCTTT	CTCAGACATT	CTGGAGGTTT	CCAAAAATAA	TATTGTAAAG	2820
	TTCAATTTCA	ACATGTATGT	ATATGATGAT	TTTTTCTCA	ATTTTGAATT	ATGCTACTCA	2880
	CCAATTTATA	TTTTTAAAGC	CAGTGTGTGC	TTATCTTTTC	CAAAAAGTGA	AAAATGTTAA	2940
25	AACAGACAAC	TGTAATAATC	CAAACTCCAG	CACCTGGAAT	AAGGTCTCTA	AAGCATCTGC	3000
	TCTTTTTTTT	TTTTAGCGAT	ATTTTAGTAA	TAAATATGCT	GGATAAATAT	TAGTCCAACA	3060
	ATAGCTAAGT	TATGCTAATA	TACATTATT	ATGTATTAC	TTTTAAGTAT	AGTTTAAAAA	3120
	ATAAACAAAG	AATATTGAGT	ATCACTATGT	GAAGAAAGTT	TTGAAAAAGA	AACAATGAAG	3180
	ACTGAATTTA	ATTAAAAAAT	TTGCAGCTCA	TAAAGAAATG	GGACTCACCC	CTACTGCATC	3240
30	ACCAGAAATC	TTTTGACTTG	GAGGCAAAAT	GTGTTGAAGT	GCCCTATGAA	GTAGCAATTT	3300
	TCTATAGGAA	TATAGTTGGA	AATAAATGTG	TGTTGTGATA	TTATTATTAA	TCAATGCAAT	3360
	ATTTTAAATG	AAATAGAAAC	AAGAGGAAA	ATGGTAAAAA	CTTGAATGAA	GGCTGGGGTA	3420
	TAGTTTGTCC	TACAATAGAA	AAAAGAGAGA	GCTTCCCTAGG	CCTGGGCTCT	TAAATGCTGC	3480
	ATTATAACTG	AGTCTATGAG	GAAATAGTTC	CTGTCCAATT	TGTGTAATTT	GTTTAAAAAT	3540
35	GTAAATAAAT	TAAACTTTTC	TGGTTTCTGT	GGGAAGGAAA	TAGGGAAATC	AATGGAACAG	3600
	TAGCTTTGCT	TTGCAGTCTG	TTTCAAGATT	TCTGCATCCA	CAAGTTAGTA	GCAAACTGGG	3660
	GAATACTCGC	TGCAGCTGGG	TTTCCCTGCT	TTTTGGTAGC	AAGGGTCCAG	AGATGAGGTG	3720
	TTTTTTTCGG	GGAGCTAATA	ACAAAAACAT	TTTAAACTTT	ACCTTTACTG	AAGTTAAATC	3780
	CTCTATTGCT	GTCTTATTC	TCTCTATAG	TGACCAACAT	CTTTTAAATT	TAGATCCAAA	3840
40	TAACCATGTC	CTCCTAGAGT	TAGAGGGCTA	GAGGGAGCTG	AGGGGAGGAT	CTTACTGAAA	3900
	GCACCTGGGG	GAGATTGATT	GTCCCTTAAAC	CTAAGCCCCA	CAAACTTGAC	ACCTGATCAG	3960
	GTCTGGGAGC	TACAAAAATT	CATTTTCTC	CTCACTGCCC	TTCTTCTGAG	TGGCATTTGG	4020
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	ACCTCCAGCA	GAGATTCCCT	TAAGTGACTC	CAGGTTTTCC	ACCATCCTTC	AGCGTGAATT	4140
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	TTGAATGTAT	AAAAGAAAAA	GATCAAGTTG	TCATTTTAGA	ACAGAGGGAA	CTTTGGGAGA	4260
	AAGCAGCCCA	AGTAGGTTAT	TTGTACAGTC	AGAGGGCAAC	AGGAAGATGC	AGGCCTTCAA	4320
	GGGCAAGGAG	AGGCCACAAG	GAATATGGGT	GGGAGTAAAA	GCAACATCGT	CTGCTTCATA	4380
	CTTTTTCTTA	GGCTTGGCAC	TGCCTTTTCC	TTTCTCAGGC	CAATGGCAAC	TGCCATTGAA	4440
50	GTCCGGTGAG	GGATCAGCCA	ACCTCTTCTC	TATGGCTCAC	CTTATTGGA	GTGAGAAATC	4500
	AAGGAGACAG	AGCTGACTGC	ATGATGAGTC	TGAAGGCATT	TGCAGGATGA	GCCTGAACTG	4560
	GTGTGTGAGA	ACAAAACAAG	CATTCAATGG	AATGTGTGTA	TTCTTCTGCG	AGCCCTCCTT	4620
	CTGGGCACCTA	AGAAGGCTTA	TGAATTAAT	GCCTATCTAA	AATTCGTGAT	TATTCTTACA	4680
	TTTTCTGTTT	TCTAATTTGA	CCTAAAAATC	TATGTGTTTT	AGACTTAGAC	TTTTTATTGC	4740
55	CCCCCCCCCT	TTTTTTTTTG	AGACGGAGTC	TCGCTCTGAC	GCACAGGCTG	GAGTGCAGTG	4800
	GCTCCGATAG	CTGCTCACTG	AAAGCTCCGC	CTCCCGGGTT	CATGCCATTG	TCCTGCCTCA	4860
	GCCTCCTGAG	TAGCTGGGAC	TACAGGCGCC	CACCACCAAG	CCCGGCTAAT	TTTTGTATT	4920
	TTTAATAGAG	ACGGGGTTTC	ACTGTGTTAG	CCAGGATGGT	CTCGATCTCC	TGACCTCGTG	4980
	ATCCCGCTGC	CTCGGCTCC	CAAGTGCTG	GGATTACAGG	CATGACCCAC	CGCTCCCGGC	5040
	CTTGTTTTCC	GTTTAAAGTC	GTCTTCTTTT	AATGTAATCA	TTTTGAACAT	GTGTGAAAGT	5100
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	GGGAGAAAAG	AACTAGGGCA	CAAAAATTG	GTCTGAGAA	GGAATTCCTC	GTAAGCCTAG	5220
	TTGCTGAAAT	TTCTGCTGT	AACCAGAAGC	CAGTTTATC	TAACGGCTAC	TGAAACACCC	5280
	ACTGTGTTTT	GCTCACTCCC	TCACTCACCG	ATCAAAACCT	GCTACCTCCC	CAAGACTTTA	5340
65	CTAGTGCCGA	TAACTTTCT	CAAAGAGCAA	CCAGTATCAC	TTCCCTGTTT	ATAAAACCTC	5400
	TAACCATCTC	TTTGTCTTT	GAACATGCTG	AAAACCACT	GGTCTGCATG	TATGCCCGAA	5460
	TTTGAATTC	TTTTCTCTCA	AATGAAAAAT	TAATTTTAGG	GATTCATTTT	TATATTTTCA	5520
	CATATGTAGT	ATTATTATTT	CCTTATATGT	GTAAGGTGAA	ATTTATGGTA	TTTGAGTGTG	5580
	CAAGAAAATA	TATTTTAAAA	GCTTTCAATT	TTCCCCAGT	GAATGATTTA	GAATTTTITA	5640
70	TGTAATATA	CAGAATGTTT	TTTCTTACTT	TTATAAGGAA	GCAGCTGTCT	AAAATGCAGT	5700
	GGGGTTTGT	TTGCAATGTT	TTAAACAGAG	TTTTAGTATT	GCTATTAAAA	GAAGTTACTT	5760
	TGCTTTTAAA	GAAACTTGGC	TGCTTAAAAAT	AAGCAAAAAAT	TGGATGCATA	AAGTAATATT	5820
	TACAGATGTG	GGGAGATGTA	ATAAAACAAT	ATTAACCTGG	TTTCTGTGTT	TTGCTGTATT	5880
	TAGAGATTAA	ATAATTCTAA	GATGATCACT	TTGCAAAATT	ATGCTTATGG	CTGGCATGGA	5940
75	AATAGAAATA	CTCAATTATG	TCTTTGTTGT	ATTAATGGGG	AATATTTTGG	ACAATGTTTC	6000
	ATTATCAAA	TGTCGACATC	ATTAATATAT	ATTGTAATGT	TGGGAAGAGA	TCACTATTTT	6060
	GAAGCACAGC	TTTACAGATG	AGTATCTATG	ATACATATGT	ATAATAAATT	TTGATCGGGT	6120
	ATTAAGAAAT	TAGAAAGGTG	GTTATAATTG	CAGAGTATTC	CATGAATAGT	ACACTGACAC	6180
	AGGGGTTTAA	CTTTGAGGAC	CAGTGTAGTC	AAGGGA AAAAC	ATGAGTTAAA	AAGAAAAGCA	6240
80	GGCAATATTG	CAGTCTTGAT	TCTGCCACTT	ACAGGATAGA	TAATGCCTGA	ACTTTAATGA	6300
	CAAGATGATC	CAACCAATAA	GGTGCTCTGT	GCTTCACAGT	GAATCTTTTC	CCCATGCAGG	6360
	AGTGTGCTCC	CCTACAAACG	TTAAGACTGA	TCATTTCAAA	AATCTATTAG	CTATATCAAA	6420
	AGCCTTACAT	TTTAATATAG	GTTGAACCAA	AATTTCAATT	CCAGTAACTT	CTATTGTAA	6480
	CATTATTTTT	GTTGATGTCT	TCAAGAAATG	TCATTGGATT	TTTGTGTTGA	ATAGTAAAA	6540
85	ACCGGATACA	TTTCAAGTGT	CCTTCAGTAT	TGATTGGGTT	GAATATTGGG	TCATAATGGT	6600
	TGAGAAGCAT	GGACACTAGA	GCCAGAATGC	TTGGATATGA	ATCCTGGATC	TGTCACTTAC	6660
	TTCTGTGTGA	CCTTTGAAAG	GCTACTTATT	TCCTCTCTTA	GCTTTCTCAT	TAAATCAAT	6720
	GAACAAATGCC	AGCCTCATGG	GTTTGTGAA	TGATTAAATT	AGTTAATATA	CCTAAAGTAC	6780

ATAGAACACT GCCTGCACAT AGTAAAGAA TTATAAGTGT GAGGTAGTTG GTAAATATAT 6840
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 TATATATAAT CCCGAAACAT G

5 Seq ID NO: 32 Protein sequence:
 Protein Accession #: NP_001932.1

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KTRHTRETVL	RRAKRRWAPI	PCSMQENSLG	PFPLFLQQVE	SDAAQNYTVF	YSISGRGVDK	180
EPLNLFYIER	DTGNLFCRTP	VDREEDYDVF	LIAYASTADG	YSADLPLPLP	IRVEDENDNH	240
PVFTEAIYNF	EVLESSRPGT	TGVVVCATDR	DEPDTMHTRL	KYSILQQTFR	SPGLFSVHPS	300
TGVITTVSHY	LDREVVDKYS	LIMKVQDMDG	QFFGLIGTST	CIITVTSND	NAPTRQONAY	360
EAFVEENAFN	VELLRIBIED	KDLINTANWR	VNFTILKGNE	NGHFKISTDK	ETNEGVLSSV	420
KPLNYEENRQ	VNLEIGVNNE	APFARDIPRV	TALNRALVTV	HVRDLDEGPE	CTPAAQYVRI	480
KENLAVGSKI	NGYKAYDPEN	RNGNGLRYKK	LHDPKGWITI	DEISGSIITS	KILDREVETP	540
KNELYNITVL	ATDKDDRSCT	GTLAVNIEDV	NDNPPFELQS	YVVICPKPMG	YTDILAVDPD	600
EPVHGAPFPY	SLPNTSPEIS	RWSLTKVND	TAARLSYQKN	AGFQETIPI	TVKDRAGQAA	660
TKLLRVNLCE	TLHRTQCRAT	SIRSTGVILGK	WAILAILLGI	ALLFSVLLTL	VCGVFGATKG	720
KRFPEDLAQQ	NLIISNTEAP	GDDRVCSANG	FMTQTNNSS	QGFCTMGSG	MQNGGQETIE	780
MMKGNGQTL	SCRGAGHHT	LDSCRGGHTE	VDNCRYTYSE	WHSFTQPRLG	EKLHRCNQNE	840
DRMPSQDYVL	TYNYEGRGSP	AGSVGCCSEK	QEDGLDPLN	NLEPKFITLA	EACTKR	

Seq ID NO: 33 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 64-2583

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CTGACCCCTG	TGATCTTCAG	TGCTGATGGT	GAAGCCTGCA	AAAAGGTGAT	ACTTAATGTA	180
CCTTGTAAC	TAGAGGCAGA	CAAAATAATT	GGCAGAGTTA	ATTGGAAGA	GTGCTTCAG	240
TCTGCAGACC	TCATCCGCTC	AAGTGATCCT	GATTTCAGAG	TTCTAAATGA	TGGTTCAGTG	300
TACACAGCCA	GGGCTGTGTC	GCTGTCTGAT	AAGAAAAGAT	CATTTACCAT	ATGGCTTTCT	360
GACAAAAGGA	AACAGACACA	GAAAGAGGTT	ACTGTGCTGC	TAGAACATCA	GAAGAAGGTA	420
TGGAAGACAA	GACACACTAG	AGAAACTGTT	CTCAGGCGTG	CCAAGAGGAG	ATGGGCACCT	480
ATTCCTTGCT	CTACGACAGA	GAATTCCTTG	GGCCCTTTCC	CATTGTTTCT	TCAACAAGTT	540
GAATCTGATG	CAGCACAGAA	CTATACTGTC	TTCTACTCAA	TAAGTGGACG	TGGAGTTGAT	600
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GGATATTGAG	CAGATCTGCC	CCTCCCACTA	CCCATCAGGG	TAGAGGATGA	AAATGACAA	780
CACCCCTGTT	TTCACGAAGC	AATTTATAAT	TTTGAAGTTT	TGGAAGTAG	TAGACCTGTT	840
ACTACAGTGG	GGGTGTTTGG	TGCCACAGAC	AGAGATGAAC	CGGACACAAT	GCATACGCGC	900
CTGAATACAC	GCAATTTGCA	GCAGACACCA	AGGTCACCTG	GGCTCTTTTC	TGTGCATCCC	960
AGCACAGGCG	TAATCACACC	AGTCTCTCAT	TATTTGGACA	GAGAGGTTGT	AGACAAGTAC	1020
TCATTGATAA	TGAAAGTACA	AGACATGGAT	GGCCAGTTTT	TTGGATTGAT	AGGCACATCA	1080
ACTTGATATC	AGATTCAAA	GATAATGCAC	CCACTTTTCA	ACAAAATGCT	ACAAAATGCT	1140
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CCCAAAAATG	AGTTGTATAA	TATTACAGTC	CTGGCAATAG	ACAAAGATGA	TAGATCATGT	1740
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ACTTCAAGGA	GTACAGGAGT	AATACTTGA	AAATGGGCAA	TCCTTGCAAT	ATTACTGGGT	2160
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GGGAAACGTT	TTCTGGAAGA	TTTAGCACAG	CAAAACTTAA	TTATATCAAA	CACAGAAGCA	2280
CCTGGAGACG	ATAGAGTGTG	CTCTGCCAAT	GGATTATGA	CCCAAACTAC	CAACAACTCT	2340
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ACCCTGGACT	CCTGCAGGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACCTACTCG	2520
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	ACCATTATT	TTGTGTATGT	CTTCAAGAA	GTTCAATGGA	TTTTTGTGTT	TAATAGTAAA	6660
	ATACCGGATA	CATTTCACGT	GTCCTTCAGT	ATTGATTGGG	TTGAATATTG	GGTCATAATG	6720
	GTTGAGAGC	ATGAGACATA	GAGCCAGAA	GCTTGGATAT	GAATCCTGGA	TCTGTCACTT	6780
60	ACTTCTGTGT	GACCTTTGAA	AGGCTACTTA	TTTCTCTCT	TAGCTTTCTC	ATTAAATCA	6840
	ATGAACAATG	CCAGCCTCAT	GGGGTTGTTG	AATGATTAAA	TTAGTTAATA	TACCTAAAGT	6900
	ACATAGAAC	CTGCCCTGAC	ATAGTAAAG	AATTATAAGT	GTGAGGTAGT	TGGTAAATTT	6960
	ATGTAGTTGG	ATATACTACC	GAACAATATC	TAATCTCTTT	TTAGGGAAT	AAAGTTTGTG	7020
	CATATATATA	ATCCCGAAAC	ATG				

Seq ID NO: 34 Protein sequence:
Protein Accession #: NP_077741.1

	1	11	21	31	41	51	
70	MAAAGPRRSV	RGAVCLHLLL	TLVIFSRDGE	ACKKVILNVP	SKLEADKIIG	RVNLEECFRS	60
	ADLIRSSDPD	FRVLNDGSVY	TARAVALSDK	KRSFTIWLSD	KRKQTQKEVT	VLLHQKKVS	120
	KTRHTRFVTL	RRAKRRWAPI	PCSMQENSLG	PFPLFLQQVE	SDAAQNYTVF	YSISGRGVDK	180
	EPLNLFYIER	DTGNLPCTRP	VDREYDVFD	LIAYASTADG	YSADLPLPLP	IRVEDENDNH	240
75	PVFTETAYNF	EVLESSRPGT	TGVVVCATDR	DEPDTHMTRL	KYSILQQTFR	SPGLFSVHPS	300
	TGVITTVSHY	LDREVVDKYS	LIMKVDMDG	QFGLIGTST	CIITVDSND	NAPTFRONAY	360
	EAPVEENAFN	VEILRIPIED	KDLINTANWR	VNFTILKMGNE	NGHFKISTDK	ETNBSVLVSV	420
	KPLNYENNRQ	VNLEIGVNNE	APFARDIPRV	TALNRALVTV	HVRDLDEGPE	CTFAAQYVRI	480
	KENLAVGSKI	NGKAYDPEN	RNGNGLRYKK	LHDPKGWITI	DEISGSIITS	KILDREVETP	540
80	KNELYNITVL	AIDKDRSCT	GTLANVIEDV	NDNPPEILQE	YVVIKPKPMG	YTDILAVDPD	600
	EPVHGAPPFY	SLPNTSPFIS	RLWSLTKVND	TAARLSYOKN	AGFOEYTIPI	TVKDRAGQAA	660
	TKLLRVNLCE	CTHPTQCRAT	SRSTGVILGK	WAILAILLGI	ALLFSVLLTL	VCGVFGATKG	720
	KRFPEDLAQQ	NLIISNTEAF	GDGDRVCSANG	FMTQTTNNSS	QGFCGTMGSG	MKNGGQETIE	780
	MMKGGNQTLB	SCRGAGHHHT	LDSRGGHTE	VDNCRYTISE	WHSFTQPRLG	EESIRGHTG	

Seq ID NO: 35 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 146-1273.

	1	11	21	31	41	51	
	GGGAGTGGGC	GTGGCGGTGC	TGCCCAGGTG	AGCCACCGCT	GCTTCTGCCC	AGACACGGTC	60
5	GCCTCCACAT	CCAGGTCTTT	GTGCTCCTCG	CTTGCTGTGT	CCTTTTCCAC	GCATTTTCCA	120
	GGATAACTGT	GACTCCAGGC	CCGCAATGGA	TGCCCTGCAA	CTAGCAAATT	CGGCTTTTGC	180
	CGTTGATCTG	TTCAAACAAC	TATGTGAAAA	GGAGCCACTG	GGCAATGTCC	TCTTCTCTCC	240
	AATCTGTCTC	TCCACCTCTC	TGTCACTTGC	TCAAGTGGGT	GCTAAAGGTG	ACACTGCAAA	300
10	TGAAATTGGA	CAGGTTCTTC	ATTTTGAAAA	TGTCAAAGAT	ATACCCCTTG	GATTTCAAAC	360
	AGTAACATCG	GATGTAAACA	AACTTAGTTC	CTTTTACTCA	CTGAAACTAA	TCAAGCGGCT	420
	CTACGTAGAC	AAATCTCTGA	ATCTTTCTAC	AGAGTTCATC	AGCTCTACGA	AGAGACCCCTA	480
	TGCAAAAGGAA	TTGAAAACCTG	TTGACTTCAA	AGATAAATG	GAAGAAACGA	AAGGTGAGAT	540
	CAACAACTCA	ATTAAGGATC	TCACAGATGG	CCACTTTGAG	AACATTTTAG	CTGACAACAG	600
	TGTGAACGAC	CAGACCAAAA	TCCTTGTTGT	TAATGCTGCC	TACTTTGTTG	GCAAGTGGAT	660
15	GAAGAAATTT	CCTGAATCAG	AAACAAAAGA	ATGTCCTTTC	AGACTCAACA	AGACAGACAC	720
	CAAAACCACTG	CAGATGATGA	ACATGGAGGC	CACGTTCTGT	ATGGGAAACA	TTGACAGTAT	780
	CAATTGTAAAG	ATCATAGAGC	TTCTTTTTC	AAATAAGCAT	CTCAGCATGT	TCATCCTACT	840
	ACCCAAGGAT	GTGGAGGATG	AGTCCACAGG	CTTGGAGAAG	ATTGAAAAAC	AACTCAACTC	900
20	AGAGTCACTG	TCACAGTGGG	CTAATCCCG	CACCATGGCC	AATGCCAAGG	TCAAACCTC	960
	CATTCCAAAA	TTTAAGGTGG	AAAAGATGAT	TGATCCCAAG	GCTTGTCTGG	AAAACTTAGG	1020
	GCTGAAACAT	ATCTTCAGTG	AAGACACATC	TGATTTCTCT	GGAATGTCAG	AGACCAAGGG	1080
	AGTGGCCCTA	TCAAATGTTA	TCCACAAAGT	GTGCTTAGAA	ATAACTGAAG	ATGGTGGGGA	1140
	TTCCATAGAG	GTGCCAGGAG	CACGGATCCT	GCAGCACAAAG	GATGAATTGA	ATGCTGACCA	1200
25	TCCCTTTATT	TACATCATCA	GGCACAACAA	AACTCGAAAC	ATCATTTTCT	TTGGCAAAAT	1260
	CTGTTCTCCT	TAGTGGCATC	AGCCCATGTT	AAGTCCTCCC	TGACTTTTCT	GTGGATGCCG	1320
	ATTTCTGTAA	ACTCTGCATC	CAGAGATTCA	TTTCTAGAT	ACAATAAATT	GCTAATGTTG	1380
	CTGGATCAGG	AAGCCGCCAG	TACTTGTCT	ATGTAGCCTT	CACACAGATA	GACCTTTTTT	1440
	TTTTTCCAAT	TCATCTTTT	GTTCCTTTT	TTCCCAATAG	ACAATGACAT	ACGCTTTTAA	1500
30	TGAAAAGGAA	TCACGTTAGA	GGAAAAATAT	TTATTCATTA	TTTGTCAAA	TGTCCGGGGT	1560
	AGTTGGCAGA	AATACAGTCT	TCCACAAAGA	AAATTCCTAT	AAGGAAGATT	TGGAAGCTCT	1620
	TCTTCCAGC	ACTATGCTTT	CCTTCTTGG	GATAGAGAAT	GTTCCAGACA	TTCTCGCTTC	1680
	CCTGAAAGAC	TGAAGAAAGT	GTAGTGCATG	GGACCCACGA	AACTGCCCTG	GCTCCAGTGA	1740
	AACTTGGGCA	CATGCTCAGG	CTACTATAGG	TCCAGAAGTC	CTTATGTTAA	GCCCTGGCAG	1800
35	GCAGGTGTTT	ATTAAATTC	TGAATTTTGG	GGATTTTCAA	AAGATAATAT	TTTACATACA	1860
	CTGTATGTTA	TAGAACTTCA	TGGATCAGAT	CTGGGGCAGC	AACCTATAAA	TCAACACCTT	1920
	AATATGCTGC	AACAAAATGT	AGAATATTCA	GACAAAATGG	ATACATAAAG	ACTAAGTAGC	1980
	CCATAAGGGG	TCAAAATTTG	CTGCCAAATG	CGTATGCCAC	CAACTTACAA	AAACACTTCG	2040
	TTCCGAGAGC	TTTTAGATT	GTGGAATGTT	GGATAAGGAA	TTATAGACCT	CTAGTAGCTG	2100
40	AAATGCAAGA	CCCAAGAGG	AAGTTCAGAT	CTTAATATAA	ATTCACCTTC	ATTTTGTATA	2160
	GCTGTCCCAT	CTGGTCAATG	GGTTGGCACT	AGACTGGTGG	CAGGGGCTTC	TAGCTGACTC	2220
	GCACAGGGAT	TCTCACAATA	CCCGATATCA	GAATTTGTGT	TGAAGGAAC	TGTCTCTTCA	2280
	TCTAATATGA	TAGCGGAAAA	AGGAGAGGAA	ACTACTGCCT	TTAGAAAATA	TAAGTAAAGT	2340
	GATTAAAGTG	CTCACGTTAC	CTTGACACAT	AGTTTTCAG	TCTATGGGTT	TAGTTACTTT	2400
45	AGATGGCAGT	GTGTAACCT	ATATTAATAG	TAATTTGTAA	AGTTGGGTGG	ATAAGCTATC	2460
	CCTGTTGCGG	GTTCACTGGAT	TACTTCTCTA	TAAAAAATAT	ATATTACCA	AAAAATTTTG	2520
	TGACATTCTC	TCTCCATCT	CTTCTTGAC	ATGCATTGTA	AATAGGTTCT	TCTTGTCTCG	2580
	AGATTCAATA	TTGAATTTCT	CCTATGCTAT	TGACAAATAA	ATATTATTGA	ACTACC	

Seq ID NO: 36 Protein sequence:
Protein Accession #: NP_002630.1

	1	11	21	31	41	51	
	MDALQLANSA	FAVDLPKQLC	EKEPLGNVLF	SPICLSTSL	LAQVGAKGDT	ANEIGQVLHF	60
55	ENVVDIPFGF	QTVTSVNVKL	SSFYSLKLIK	RLYVDKSLNL	STEFISSTKR	PYAKELETVD	120
	FKDKLEETKG	QINNSIKDLT	DGHFENILAD	NSVNDQTKIL	VVNAAYFVGK	WMKKFPESET	180
	KECPFRLNKT	DTKPVQMMNM	EATPCMGNID	SINCKIIELP	FQNKHLSMFI	LLPKDVEDES	240
	TGLEKIEKQL	NSESLSQWTN	PSTMANAKVK	LSIPKFKVEK	MIDPKACLEN	LGLKHIFSED	300
60	TSDPSGMSBT	KVGLNSNVII	KVCLEITEBG	GDSIEVPGAR	ILQHKDELNA	DHPFIYIIRH	360
	NKTRNIIFFG	KFCSP					

Seq ID NO: 37 DNA sequence
Nucleic Acid Accession #: NM_0168583
Coding sequence: 72-842

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	GGAGTGGGGG	AGAGAGAGGA	GACCAGGACA	GCTGCTGAGA	CCTCTAAGAA	GTCCAGATAC	60
70	TAAGAGCAAA	GATGTTTCAA	ACTGGGGGCC	TCATGTGCTT	CTACGGGCTG	TTAGCCGAGA	120
	CCATGGCCCA	GTTTGGAGGC	CTGCCCGTGC	CCCTGGACCA	GACCCCTGCC	TTGAATGTGA	180
	ATCCAGCCCT	GCCCTTGAGT	CCACAGGTC	TTGCAGGAAG	CTTGACAAAT	GCCCTCAGCA	240
	ATGGCTGTCT	GTCCTGGGGC	CTGTTGGGCA	TTCTGGAAAA	CCTTCCGCTC	CTGGACATCC	300
75	TGAAGCCTGG	AGGAGTACT	TCTGGTGGCC	TCCTTGGGGG	ACTGCTTGGG	AAAGTGACGT	360
	CAGTGATTCC	TGGCCTGAAC	AAACATCATT	ACATAAAGGT	CAGTGACCCC	CAGCTGCTGG	420
	AACTTGGCCT	TGTGCAAGAG	CCTGATGGCC	ACCGTCTCTA	TGTCAACCAT	CCTCTCGGCA	480
	TAAAGCTCCA	AGTGAATACG	CCCTGGTTCG	GTGCAAGTCT	GTTGAGGCTG	GCTGTGAAGC	540
	TGGACATCAC	TGCAAAATC	TTAGCTGTGA	GAGATAAGCA	GGAGAGGATC	CACCTGGTCC	600
80	TTGGTGACTG	CACCCATTCC	CCTGGAAGCC	TGCAAAATTC	TCTGCTTGAT	GGACTTGGCC	660
	CCCTCCCAT	TCAAGGTCTT	CTGGACAGCC	TCACAGGGAT	CTTGAATAAA	GTCTGCTGCT	720
	AGTTGGTTCA	GGGCAACGTG	TGCCCTCTGG	TCAATGAGGT	TCTCAGAGGC	TTGGACATCA	780
	CCCTGGTGCA	TGACATTGTT	AACATGCTGA	TCCACGGACT	ACAGTTTGTG	ATCAAGGTCT	840
	AAGCCTTCCA	GGAGGGGCTG	GGCCTCTGCT	GAGCTGCTTC	CAGTGCTCA	CAGATGGGCT	900
85	GCCCATGTGC	TGGAAGATGA	CACAGTTGCC	TTCTCTCCGA	GGAACTGGCC	CCCTCTCCTT	960
	TCCCACACAG	CGTGTGTAAC	ATCCCATGTG	CCTCACCTAA	TAAATGGCT	CTTCTTCTGC	1020
	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA				

WO 02/086443

PCT/US02/12476

Seq ID NO: 38 Protein sequence:
Protein Accession #: NP_057667

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5      1      11      21      31      41      51
MFQTGGGLIVF YGLLAQMAQ FGLFVPLDQ TLPLNVNPAI PLSPTGLAGS LTNALSNGLL 60
SGGLLGILEN LPLLDILKPG GGTSGGLLGG LLGKVTSVIP GLNNIIIDIKV TDPQLLELGL 120
VQSPDGHRLY VTTPGLGKIQ VNTPLVGASL LRLAVKLDIT AEILAVRDQK ERIHLVLGDC 180
THSPGSLQIS LLDGLGPLPI QGLLDSLTI LNKVLPVLVQ GNVCPLVNEV LRGLDITLVH 240
10 DIVNMLINGL QFVIKV

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Seq ID NO: 39 DNA sequence
Nucleic Acid Accession #: NM_004363.1
Coding sequence: 115-2223

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15      1      11      21      31      41      51
CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT 60
TCCTGGAAGT CAAGCTCTTC TCACAGAGGG AGGACAGAGC AGACAGCAGA GACCATGGAG 120
TCTCCCTCGG CCCCTCCCCA CAGATGGTGC ATCCCTTGGC AGAGGCTCCT GCTCACAGCC 180
TCACTTCTAA CCTTCTGGAA CCCGCCACC ACTGCCAAGC TCACTATTGA ATCCAACGCC 240
TTCAATGTCT CAGAGGGGAA GGAGGTGCTT CTACTTGTC ACATCTGCC CCAGCATCTT 300
TTTGGCTACA GCTGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT 360
GTAATAGGAA CTCAACAAGC TACCCAGGG CCCGCATACA GTGGTCGAGA GATAATATAC 420
CCCAATGCAT CCTGTCTGAT CCAGAACATC ATCCAGAATG ACACAGGATT CTACACCCTA 480
CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTCCG GGTATACCCG 540
GAGCTGCCCA AGCCCTCCAT CTCCAGCAAC AACTCCAAAC CCGTGAGGA CAAGGATGCT 600
GTGGCCTTCA GCTGTGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAAT 660
CAGAGCCTCC CGTGCAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720
TTCAATGTCA CAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAGT 780
GCCAGGCGCA GTGATTCACT CATCTGAAT GTCCTCTATG GCCCGATGC CCCACCACTT 840
TCCCTCTTAA ACACATCTTA CAGATCAGGG GAAAATCTGA ACCTCTCTTG CCACGCAGCC 900
TCTAACCCAC CTGTGAGTA CTCTTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 960
GAGCTCTTTA TCCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020
AACTCAGACA CTGGCCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA 1080
CCCAAACCTT TCATCACCAG CAACAACCTC AACCCCGTGG AGGATGAGGA TGCTGTAGCC 1140
TTAAGCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC 1200
CTCCCGGTCA GTCCAGGCTC CAGCTGTGCC AATGACRACA GGACCTCAC TCTACTCAGT 1260
GTCACAAGGA ATAGTGTAGG ACCCTATGAG TGTGGAATCC AGAAGCAAT AAGTGTGAC 1320
CACAGCGACC CAGTCACTCT GAATGTCCTT TATGGCCAG ACAGCCCAAC CATTTCCCTC 1380
TCATACACCT ATTACCGTCC AGGGGTGAAC CTCAGCCTCT CCGCCTATGC AGCCTCTAAC 1440
CCACCTGCAC AGTATTCTTG GCTGATTGAT GGGAACTACC AGCAACACAC ACAAGAGCTC 1500
TTTATCTCCA ACATCACTGA GAAGAACAGC GGACTCTATA CCGCCAGGC CAATAACTCA 1560
GCCAGTGCCG ACAGCAGGAC TACAGTCAAG ACAATCAGAG TCTCTGCGGA GCTGCCCAAG 1620
CCCTCCATCT CCGTCAACAA CTCAAAACCC GTGGAGGACA AGGATGCTGT GGCCTTCAAC 1680
TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740
GTCAGTCCCA GGCTGCAGCT GTCCAATGGC AACAGSACCC TCACTCTATT CAATGTCA 1800
AGAAATGACG CAGAGGCTTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCGCAGT 1860
GACCCAGTCA CCTTGGATGT CCTCTATGGG CCGGACACCC CCATCATTTT CCCCCCAGAG 1920
TCGTCTTACC TTTCGGGAGC GAACCTCAAC CTCTCCTGCC ACTCGGCCTC TAACCCATCC 1980
CCGCACTATT CTGGCGGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC 2040
GCCAAATCA CGCCAAATAA TAACGGGACC TATGCTGTGT TTGTCTCTAA CTGGCTACT 2100
GGCCGCAATA ATTCCATAGT CAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCTGGT 2160
CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGGTTGGGGT TGCTCTGATA 2220
TAGCAGCCCT GGTGTAGTTT CTTCATTTC GGAAGACTGA CAGTTGTTTT GCTTCTTCT 2280
TAAAGCATTT GCAACAGCTA CAGTCTAAAA TTGCTTCTT ACCAAGGATA TTACAGAAA 2340
AGACTCTGAC CAGAGATCGA GACCATCCTA GCCAACATCG TGAAACCCCA TCTCTACTAA 2400
AAATACAAAA ATGAGCTGGG CTGTGTGGCG CGCACCTGTA GTCCAGTTA CTGGGAGGC 2460
TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC 2520
ACTGCATCTC AGTCTGCACA CAGAGCAAGA CTCATCTCA AAAAGAAAAG AAAAGAAAGC 2580
TCTGACCTGT ACTCTGAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCAC 2640
AACTTTAATG ACCTAAGTGA CAGCTTCATG AAACGTGTTA CCAAGATCAA GCAGAGAAAA 2700
TAATTAATTT CATGGGACTA AATGAACATA TGAGGATTGC TGATTCTTTA AATGTCTTGT 2760
TTCCAGATT TCAGGAAACT TTTTCTTT TAAGCTATCC ACTCTTACAG CAATTGTGATA 2820
AAATATACCT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGGTCGCTCC 2880
AGACTTGGGA AACTATTTCAT GAATATTTAT ATTGTATGGT AATATAGTTA TTGCACAAAT 2940
70 TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

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Seq ID NO: 40 Protein sequence:
Protein Accession #: NP_004354.1

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75      1      11      21      31      41      51
MESPSAPPHR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEKGE VILLVHNLQ 60
HLFGYSWKYK ERVDGNRQII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFY 120
TLHVIKSLDV NEEATGQFRV YPELPKPSIS SNNSKPFVDEK DAVAFTEPEE TQDATYLMWV 180
NNQSLPVSPR LQLSNVNRLL TLFNVTRNDT ASYKCBTQNP VSARRSDSVI LNVLYGPDAP 240
TISPLNTSYR SGENLNLSCH AASNPPAQYS WFNVTGFPQS TOELFIPNIT VNNSGSYTCQ 300
AHNSDTGLNR TTVTTITVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NTTYLWVWNN 360
QSLPVSFRLQ LSNDRNLTL LSVTRNDVGF YECGIQNELS VDHSDPVILN VLYGPDPTI 420
SPSYTYRREG VNLSLSCHAA SNPPAQYSWL IDGNIQHTQ ELFIINITEK NSGLYTCQAN 480
NSAGHSRTT KLTFTVBAEL PKFSISSNNS KPVEDKDAVA FTCEPEAQNT TYLWVWNGQS 540
LPVSPRLQLS NGNRTLTLFN VTRNDARAYV CGIQNSVSAV RSDPVTLDVL YGPDPTIISP 600
PDSSYLSGAN LNLSCASNS PSPQYSWRIN GIPOQHTQVL FIAKITPNNN GTYACFVSNL 660
85 ATGRNNSIVK SITVASGTS PGLSAGATVG IMIGVLVGA LI

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Seq ID NO: 41 DNA sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11-793

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1	11	21	31	41	51	
AATCCCGACA	ATGGCGAAAG	ACAACTCAAC	TGTTGGTTGC	TTCCAGGGCC	TGCTGATTTT	60
TGGAATGTG	ATTATTGGTT	GTTCGGCAT	TGCCCTGACT	GCGGAGTGCA	TCTTCTTTGT	120
ATCTGACCAA	CACAGCCTCT	ACCCACTGCT	TGAAGCCACC	GACAAAGATG	ACATCTATGG	180
GGCTGCCTGG	ATCGGCATAT	TTGTGGGCAT	CTGCCTCTTC	TGCTGTCTG	TCTAGGCAT	240
TGTAGGCATC	ATGAAGTCCA	GCAGGAAAT	TCTTCTGGCG	TATTTTCATC	TGATGTTTAT	300
AGTATATGCC	TTTGAAGTGG	CATCTTGTAT	CACAGCAGCA	ACACAACGAG	ACTTTTTCAC	360
ACCCAACTCT	TTCTCGAAGC	AGATGCTAGA	GAGGTACCAA	AACAACAGCC	CTCCAAACAA	420
TGATGACCAG	TGGAATAACA	ATGAGTCAAC	CAAAACCTGG	GACAGGCTCA	TGCTCCAGGA	480
CAATTGCTGT	GGCGTAAATG	GTCCATCAGA	CTGGCAAAAA	TACACATCTG	CCTTCCGGAC	540
TGAGAATAAT	GATGCTGACT	ATCCCTGGCC	TCGTCAATGC	TGTTTATGA	ACAATCTTAA	600
AGAACCTCTC	AACCTCGAGG	CTTGTAAACT	AGGCGTGCTT	GGTTTTATC	ACAATCAGGG	660
CTGCTATGAA	CTGATCTCTG	GTCCAATGAA	CCGACACGCC	TGGGGGGTTG	CCTGGTTTGG	720
ATTTGCCATT	CTCTGCTGGA	CTTTTGGGT	TCTCTGGGT	ACCATGTTCT	ACTGAGCAG	780
AATTGAATAT	TAAGAA					

Seq ID NO: 42 Protein sequence:
Protein Accession #: NP_008883.1

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MAKDNSTVRC	FQGLLIPGNV	IIGCCGIALT	AECIFFVSDQ	HSLYPLLEAT	DNDDIYGAAW	60
IGIFVGLCLF	CLSVLGLVGI	MKSSRKILLA	YFILMPFIVYA	FEVASCITAA	TQRDFPTPNL	120
FLKQMLERYQ	NNSPFNDDQ	WKNNGVTKTW	DRLMLQDNCC	GVNGPSDWQK	YTSAFRTENN	180
DADYFWPRQC	CVMNNLKEPL	NLEACKLGVP	GFYHNQGCYE	LISGPMNRHA	WGVANFGFAI	240
LCWTFWVLLG	TMFYWSRIEY					

Seq ID NO: 43 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 83-2605

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GCCGGACAGA	TCTGCGGTA	TCCTGGAGCC	GGCCCAAGTTG	TGAAGTAGGA	GAGCTTTGGG	60
ACCTCTGTCC	CAAGCAAGAG	AGATGAATGG	AGAGTATAGA	GGCAGAGGAT	TTGGACGAGG	120
AAGATTTCAA	AGCTGGAAAA	GGGGAAGAGG	TGGTGGGAAC	TTCTCAGGAA	AATGGAGAGA	180
AAGAGAACAC	AGACTCTGATC	TGAGTAAAC	CACAGGAAAA	CGTACTTCTG	AACAAACCCC	240
ACAGTTTTTG	CTTTCAACAA	AGACCCCA	GTCATGTCAG	TCAACATTGG	ATCGATTTCAT	300
ACCATATGAA	GGCTGGGAAGC	TTTATTCTC	TGAAGTTTAC	AGCGTAGCT	CTCCTTTGAT	360
TGAGAAGATT	CAAGCATTTG	AAAAATTTT	CACAAGGCAT	ATTGATTTGT	ATGACAAGGA	420
TGAAATAGAA	AGAAGGGGAA	GTATTTTGGT	AGATTTTAAA	GAAGTGACAG	AAGGTGGTGA	480
AGTAACTAAC	TTGATACCA	ATATAGCAAC	TGAAGTAAAG	GATGCACCTG	AGAAAACTT	540
GGCTTGCAAT	GGTTTGCAAA	TACATCAGGT	GTTAACTAAG	GACCTTGAAA	GGCATGCAAG	600
TGAGTTACAA	GCCCAAGGAG	GATTGTCTAA	TGATGGAGAA	ACAATGGTAA	ATGTGCCCAA	660
TATTCATGCA	AGGCGTACAA	ACTATGAGCC	TTTGACACAG	CTCAAGAAATG	TCAGAGCAAA	720
TTACTATGGA	AAATACATTG	CTCTAAGAGG	GACAGTGGTT	CGTGTGAGTA	ATATAAGGCC	780
TCCTTGCAAC	AAGATGGCTT	TTCTTTGTGC	TGCATGTGGA	GAAATTCAGA	GCTTTCTCT	840
TCCAGATGGA	AAATACAGTC	TTCCCAACAA	GTGTCTCTGT	CCTGTGTGTC	GAGGCAGGTC	900
ATTTACTGCT	CTCCGCAAGT	CTCCTCTCAC	AGTTACGATG	GACTGGCAGT	CAATCAAAAT	960
CCAGGAATTG	ATGTCTGATG	ATCAGAGAGA	AGCAGGTCGG	ATTCCACGAA	CAATAGAAATG	1020
TGAGCTTGTT	CATGATCTTG	TGGATAGCTG	TGTCCCGGGA	GACACAGTGA	CTATTACTGG	1080
AATTGTCAAA	GTCTCAAAATG	CGGAAGAAGG	TTCTCGAAAT	AAGAATGACA	AGTGTATGTT	1140
CCTTTTGTAT	ATTGAAGCAA	ATTCTATTAG	TAATAGCAAA	GGACAGAAAA	CAAAGAGTTC	1200
TGAGGATGGG	TGTAAGCATG	GAATGTTGAT	GGAGTTCTCA	CTTAAAGACC	TTTATGCCAT	1260
CCAAGAGATT	CAAGCTGAAG	AAAACCTGTT	TAAACTCATT	GTCAACTCGC	TTTGCCCTGT	1320
CATTTTGTGT	CATGAACCTG	TTAAAGCAGG	TTTGGCATT	GCACTCTTTG	GAGGAAGCCA	1380
GAAATACGCA	GATGACAAAA	ACAGAATTCC	AATTCCGGGA	GACCCCAACA	TCCTTGTTGT	1440
TGGAGATCCA	GGCCTAGGAA	AAAGTCAAAT	GCTACAGGCA	GCGTGCAATG	TTGCCCCACG	1500
TGGCGTGAT	GTTTGTGGTA	ACACCACGAC	CACCTCTGGT	CTGACGGTAA	CTCTTTCAAA	1560
AGATAGTTCC	TCTGGAGATT	TTGCTTTGGA	AGCTGGTGCC	CTGGTACTTG	GTGATCAAGG	1620
TATTTGTGGA	ATCGATGAAT	TTGATAAGAT	GGGGAATCAA	CATCAAGCCT	TGTTGGAAGC	1680
CATGGAGCAG	CAAAGTATTA	GTCTTGCTAA	GGCTGGTGTG	GTTTGTAGCC	TTCTTGCAAG	1740
AACCTTCCATT	ATTGCTGCTG	CAAATCCAGT	TGGAGGACAT	TACAATAAAG	CCAAAACAGT	1800
TTCTGAGAA	TTAAAAATGG	GGAGTGCACT	ACTATCCAGA	TTTGATTGG	TCTTTATCCT	1860
GTTAGATACT	CCAAATGAGC	ATCATGATCA	CTTACTCTCT	GAACATGTGA	TTGCAATAAG	1920
AGCTGGAAG	CAGAGAACCA	TTAGCAGTGC	CACAGTAGCT	CGTATGAATA	GTCAAGATT	1980
AAATACTTCC	GTACTTGAAG	TAGTTTCTGA	GAAGCCATTA	TCAGAAAGAC	TAAAGGTGGT	2040
TCCTGGAGAA	ACAATAGATC	CCATTCCCCA	CCAGCTATTG	AGAAAGTACA	TTGGCTATGC	2100
TGGGAGATAT	TGTATACCAA	GGCTATCCAC	AGAAGCTGCT	CGAGTTCTTC	AAGATTTTTA	2160
CCTTGAGCTG	CGGAAAACAG	GCCAGAGGTT	AAATAGCTCA	CCAATCACTA	CCAGGCAGCT	2220
GGAATCTTTG	ATTCTGTCTGA	CAGAGGCACG	AGCAAGGTTG	GAATTGAGAG	AGGAAGCAAC	2280
CAAAGAAGAC	GCTGAGGATA	TAGTGGAAAT	TATGAAATAT	AGCATGCTAG	GAACCTACTC	2340
TGATGAATTT	GGGAACCTAG	ATTTGAGCG	ATCCAGCAT	GGTCTGGAA	TGAGCAACAG	2400
GTCAACAGCG	AAAAGATTTA	TTTCTGCTCT	CAACCAAGTT	GCTGAAAGAA	CTTATAATAA	2460
TATATTTCAA	TTTCATCAAC	TTGCGCAGAT	TGCCAAAGAA	CTAAACATTC	AGGTTGCTGA	2520
TTTTGAAAT	TTTATTTGAT	CACATAATGA	CCAGGTTTAC	CTCTTGAAAA	AAGGCCAAAA	2580
AGTTTACCAG	CTTCAAACTA	TGTAAAGGA	CTTCAACAG	TTAGGGCTCT	CTGGGTTTAT	2640
TGCAGATTAA	AGCCATCTCA	GTGAAGATAT	GCSTGCACGC	ACAGACAGAC	AGACACACAC	2700
ACACACACAC	ACACACACAC	ACACACACAC	AAATACTGTT	CTCTGAAAAA		2760
TGATGTCCCA	AAAGTATTAT	AATAGGAAAA	AAGCATTAAG	TATAATAAAC	TAATTTAAGA	2820

AGTGATAAAG TCTCCAGATG CAGTAGCTCA CACTGTAATC ACGTAGACTC AGGAGGCTGA 2880
 GGTGAGAGGA TTCCTTGAGG CCAGGGTTGG AGACCAACCT TGGGCAACAT AGCAAGACCC 2940
 CATTTCCTAA AAAAAAATAA AAAAAATTTA AACTTAGCTG GGTATGGTGG CACATGCCTA 3000
 TAGTCTCAGC TACTTGTGAG GCTGAGGCGAG GAGGATTCTT TGAGCCGAGG AGTTTGAGGT 3060
 TACAGTGAGC CACAATCACA CCAATCACTG CACTCCAGCC TGGGCAATAA AGTAACTCTT 3120
 GACTCAAAAA AATAAAAAAA ATTGTAGTGG TAGCCATGTG TTAATTGTTA AATAAATTCT 3180
 CCAAAGGGCT AAAAGTAAAT TACTTATAAA TTTTATTATG TTGTATTTT GACCTGCCTT 3240
 TTATATGTAT GAATATTTC A TAGTTTTGCA TATCAGATGT AGGCATACAG ACAAAATACAT 3300
 AAACCAATGA ATATATTACA TATTCTGTGT TCCAATAAAA CTTTATTAT GGACACTAAA 3360
 ATTTGAATTT CATAAATTT TCCCATGTGA AGAATACAAA ATACTTGAGT TTTGTTTTTA 3420
 GCTATTAAAT AATAGGCTCT ATTTATTCCA CAGGCTGTAG TTTGTAGTCT TGCTTGAAAC 3480
 AATAGAAACA GACTGATTAA GCAGGAGAAG TTTTGTGAAA GAATTTTGTG TGGCTCACGG 3540
 AATTATTAGA AGGCAGGTGA ACCAGGAGGG TAAGCTTCCA GCAGCAATTT GTAAAAACCT 3600
 GCCTTAGAAT TGGAGCTTGC AAGAAGCTGC TGACACTCCA CTGCCACACA GGGCACTGGA 3660
 AGAAAGTGCT GCTGCCTCCC TGCCCCACCT TTGCCACTTC TGCAGCAGGA ATAGGTAGAA 3720
 GAATGCCCCC ACCCGCACCG GAACAGCAAC AAAAGGATTC TGCATGAGAT GCCTCCCTAA 3780
 ATTGCTGAAT TCAAAAAAGA AGTTGCATAC AAAGACATCT GATTGAAAAA GGGTATGTTA 3840
 TATGCCCTCT TCATAGGCTG CTAGGGAGTT TTCTGGTTC TACTTTCAGG TGGTGGGATC 3900
 AATAAGACGA GAATTTCTCA TATGTTGTGA GAGGATTCAA ATGTTACAGG GTTGCCAGCC 3960
 AAACATCAAA TCATGTATAA ATCCAACAAA CACTTTGTAA CATAACAGAA CTCAGGAAAT 4020
 GTGAACCAAT TGTGGAGAAT TACTAAAAAT ACGGCTTCCC GCAACGAAAG ATGAATGGAA 4080
 AATGTAAATA AAAAGAACTG GCAGTGTATA TCAGATGTTT AACTATAGGA CCAGAACTAA 4140
 GATGTGGAGA CTATTGTCAT AGACCAACAAT GTAAATTTT AAGTGAGGAA GGAATAATCA 4200
 GGAATCAAAA GGGGCCAGGT GCAGTGGCTC ACATCTATAA TCCCAGAGCT TTGGGAGTTC 4260
 GAGGCAGGAG GATCACTTGA AGCCAGTTTT GAGACCAGCC TATGCAACAC ATTGAGACCC 4320
 TATCTCTACA AAAAATAGAT TAGCTGGGCA CGGTGGTGCA TGCCTATTGT CCTACCTACT 4380
 GTGGAGGCTG AAGTAGGAAA TCACITGAGC CCGAGAGTTT GAGGTTACAG TGAGCTATGA 4440
 TTATACCACT GCACCTCAGC CTGGGCAAGA GAGCAAGACC TTGCTCTCT

Seq ID NO: 44 Protein sequence:
 Protein Accession #: CAB55276.2

1 11 21 31 41 51
 | | | | |
 MNGEYRGRGF GRGRFQSWKR GRGGGNFSGK WREREHRPDL SKTTGKRTSE QTPQFLLSTK 60
 TPQSMQSTLD RFIPYKGWKL YFSEVYSDSS PLIEKIQAFE KFFTRHIDLY DKDEIERKGS 120
 ILVDFKELTE GGEVTNLIPD IATELRDAPE KTLACMGLAI HQVLTKDLER HAAELQAQEG 180
 LSNDETGMVN VPHIHARVYN YEPLTQLKNV RANYYGKYIA LRGTVVVRVN IKPLCTKMAP 240
 LCAACGEQTS FPLPDGKYSL PTKCPVPVCR GRSFTALRSS PLVTMDWQS IKIQLMSDD 300
 QREAGRIPRT IECBLVEDLV DSCVPGDVT ITGIVKVSNA EEGSRNKNK CMFLLYIEAN 360
 SISNSKGQKT KSESDGCKHG MMEFSLKDL YAIQEIQAEE NLFKILVNSL CPVIFGHELV 420
 KAGLALALFG GSQKYADDKN RPIRGDPHI LVVGDPLGK SMLQAACNV APRGVVYCGN 480
 TTTTSGLTVT LSKDSSSGDF ALEAGALVLG DQICIGIDEF DKMGNOHQAL LEAMEQQSIS 540
 LAKAGVVCSL PARTSIIAAA NPVGGHYNKA KTVSENLMKG SALLSRFDLV FILLDTFNEH 600
 HDHLLSEHVI AIRAGKQRTI SSATVARMNS QDSNTSVLEV VSEKPLSERL KVPVGETIDP 660
 IPHQLLRKYI GYARQVYVPR LSTEARVLQ DFYLELRKQS QRLNSSPITT RQLESILRLT 720
 EARARLEIRE EATKEDAEI VEIMKYSLG TYSDEFNLD FERSQHGSGM SNRSTAKRFI 780
 SALNNVAERT YNNIFQPHQL RQIAKELNIQ VADFENFIGS LNDQGYLLKK GPKVYQLQTM

Seq ID NO: 45 DNA sequence
 Nucleic Acid Accession #: NM_005416.1
 Coding sequence: 149..658

1 11 21 31 41 51
 | | | | |
 ACCAGATCCC AGAGGCTGAA CACCTCGACC TTCTCTGCAC AGCAGATGAT CCCTGAGCAG 60
 CTGAAGACCA GAAAAGCCAC TAAGACTTTC TGCTTAATTC AGGAGCTTAG AGGATTCTTC 120
 AAAGAGTGTG TCCACGATCC TTTGAAGCAT GAGTTCTTAC CAGCAGAAGC AGACCTTTAC 180
 CCCACCACCT CAGCTTCAAC AGCAGCAGGT GAAACAACCC AGCCAGCCTC CACCTCAGGA 240
 AATATTGTGT CCCACAACCA AGGAGCCATG CCACTCAAAG GTTCCACAAC CTGGAAACAC 300
 AAAGATTCCA GAGCCAGGCT GTACCAAGGT CCCTGAGCCA GGCTGTACCA AGGTCCCTGA 360
 GCCAGGCTGT ACCAAGGTCC CTGAGCCAGG TTGTACCAAG GTCCCTGAGC CAGGCTGTAC 420
 CAAGGTCCCT GAGCCAGGTT GTACCAAGGT CCCTGAGCCA GGCTACACCA AGGTCCCTGA 480
 ACCAGGCGAG ATCAAGGTCC CTGACCAAGG CTTTCATCAAG TTTCTGAGC CAGGTGCCAT 540
 CAAAGTTTCT GAGCAAGGAT ACACCAAGT TCCTGTGCCA GGCTACACAA AGCTACCAGA 600
 GCCATGTCTT TCAACGGTCA CTCCAGGCCC AGCTCAGCAG AAGACCAAGC AGAAGTAATT 660
 TGGTGACAGT ACAAGCCCTT GAGAAGCCAA CCACCAGATG CTGGACACCC TCTTCCCATC 720
 TGTTCCTGTG TCTTAATTGT CTGTAGACCT TGTAATCAGC ACATTGTAC CCCAAGCCAT 780
 AGTCTCTCTC TTATTGTAT CCTAAAAATA CGTACTATAA AGCTTTTGTG CACACACACT 840
 CTGAAGAATC CTGTAAGCCC CTGAATTAG CAGAAAGTCT TCATGGCTTT TCTGGTCTTC 900
 GGCTGCTCAG GGTTCATCTG AAGATTCGAA TGAAAGAAA TGATGTTTC CTGCTCTTCC 960
 CTCATTAAAT TGCTTTTAAT TECA

Seq ID NO: 46 Protein sequence:
 Protein Accession #: NP_005407.1

1 11 21 31 41 51
 | | | | |
 MSSYQKQKTF TPPPQLQQQQ VKQPSQPPPO EIFVPTTKEP CHSKVPQPGN TKIPEPGCTK 60
 VPEPGCTKVP EPGCTKVPEP GCTKVPEPGC TKVPEPGCTK VPEPGYTKVP EPGSIKVPDQ 120
 GFIKFPEPGA IKVPEQGYTK VVPVGYTKLP EPCPSTVTPG PAQQKTKQK

Seq ID NO: 47 DNA sequence
 Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 5 GCGTCGTGTG CAGGCGTCCC CGGGCTGTGG ATAATTAGAC ACGTTCCTCC CTCATTGCC 60
 AAGGCTCGTT AGAATTGCGC CTAGAGCTGT ATCATGTATT TTCTTTCAAA TTAACCTTGC 120
 TTGCAATTAA GCTTAGGGAA CCAGCAACAA AAGCAAACCT GGCCCGAGGT CGTTCACCGC 180
 GAAAATGGAT TAGAGAACT TCTTCCCGA TTTAAGGGGA AAGATTCTCTG CGGCCAGCGC 240
 TTTGGGGAAA GTGCCCCGAC CGCAGAGGCG ACGACAGGGG AGCAGGAAGC TGCTCACGGT 300
 AGTCGGCGTT GGCGGCAGCG GTGGCCTTCC TCATCTGGGC GATGTGGGCT CCTAGAAGAG 360
 10 TAAGGATAAC ATCTCTGAAA TGACTTCTGT ACGGTTTGAG CCCAACTGCA CACTCATGAC 420
 TTGGAGCTGC CCTGTGGAGT TACAGTTTAC CAAACACATT CATGAACATA ATCTCATTTA 480
 CTA AAAACTT TGTGAGAA TTCTTTTACT AAAATTTTCT CTTATTACAA A

Seq ID NO: 48 DNA sequence:
 Nucleic Acid Accession #: CAT cluster

15 1 11 21 31 41 51
 20 TTCCAAATTT TTTTCTTGT AATAAGAAAA AATTTTAGTA AAAGAAAATT CTCACAAAGT 60
 TTTTAGTAAA TGAGATTATG TTCATGAATG TGTTTGGTAA ACTGTAACCT CACAGGGCAG 120
 TCCCAAGTCA TGAGTGTGCA GTTGGGCTCA AACCGTACAG AAGTCATTTC CAGGATGTTA 180
 TCCTTACTCT TCTGGAGGCC CACATCGCCC AGATGAGGAA GGCCACCGCT GCCGCCAACG 240
 CCGACTACCG TGAGCAGCTT CCTGCTCCCC TGTCGCTGCC TCTGCGGTGC GGGCACTTTC 300
 25 CCGAAAGCGC TGGCCGAGG AATCTTTCCC CTTAAATCGG GGAAGAAAGT TCTCTAATCC 360
 ATTTTCGGCG TGAACGACCT CGGGCCAAAG TTGCTTTTGT TGCTGTGTCC CTAAGCTTAA 420
 TTGCAAGCAA AGTTAAATTTG AAAGAAAATA CATGATACAG CTCTAGGGCG AATTCTAACG 480
 AGCCTTGGGC AATGAGGGAA GAACGTGTCT AGTTATCCAC AGCCCGGGGA CGCCTGCACA 540
 CGACGCT

Seq ID NO: 49 DNA sequence
 Nucleic Acid Accession #: CAT cluster

30 1 11 21 31 41 51
 35 TCTTCTTCT GCTGCTCGTT TGCTCTCTCT GTGCTCTTCT TCTTCTTCT CCTCGCGCT 60
 CCTGCGGACC TCTGTGTCT CTCTCTGAT GGCGGGGGG GGGAGAAAGT GACCGGTGAG 120
 ACCGTAGACC CGAAACCAT GGGTGTGACA AGCCGCTGCG CGGCTTTTTT GGGAGAACCC 180
 GACACATGCA GACCAGTTTT CCTGGAACNG CATGACCATG TTATTACTAT GGGCCGCTTC 240
 40 CCGAACCAA GTGTTTAAAA CTTTTTAGGG CACCCCAAAT ATTTTCTTTT TTTTCTTTT 300
 TTCAATTAAA AACTCTAAT ATTTATATTA AATACAAAGA TACCCAAACC CTTTATGCTT 360
 TTTCTCTGTA TCTGTGCTT TTTCTTTGA CAGCATCTCC ATTTTCTTTC TGCTGCTTCA 420
 TCGCTGTAGC CATGGGAATC CGTTTCATTA TTATGGTAGC AATATGGAGT GCTGTATTCC 480
 TAAAGAAATC GACACAGGAG AATCACTTGA ACTTGGGAGG CAGAGTTTGC AGTGAGCCGA 540
 45 GATTGAACCA GTGCACTCCA GCCTTGGCAG CGGAGCAAGA TTCTGTACCA GTTCTGAAG 600
 TGCTGGTATC GTCCCTGAGC CCCATCCTCG GTTCCATTGC GCTGCCAGGC AGGGTGTCTG 660
 GACGTGGGGA GAGCTGTGCT ATATATCCGG GTGAAGCTCA GCTGTGGCAC ACCTTGGATG 720
 CCGGTGCTCT CCTGGCCCGG GGAACCTAGT ATTTTGTCCA CGAGTGTACA CCAACCAAAG 780
 GAGACAGCAT CATTTATGAG CCTGCAGCAT CCACCTTACT GCTGTATCCA GTTTCATTG 840
 ACTG

Seq ID NO: 50 DNA sequence
 Nucleic Acid Accession #: L05187
 Coding sequence: 1991..2260

55 1 11 21 31 41 51
 CTGCAGGAG GCAGGTAGAA AAGGCTTTT GGTTTTCAGG TGGGGGGCAG TCTAGCCTGA 60
 TCAGAAAGGA GGAAGAGGCC AGGGCAGATG TCTGGGTGGA GTGAAGGGAA AAAGTGTATG 120
 60 CAGAAAGAGG ATTAGCCCTT GAAAGTCCCT GAAAGTAGGAG AAGGGTAAAG GTGTGGTTGG 180
 TGAAAGAAAG CAGGTTTTTC CAGATTAGCA ACCAGTCAGG GGGAGGAAGG TGAGAGTGGG 240
 AGAGTCATAA GTAATATTAT CTGAATGTGT GTAGTTTAAAT GGAATTGGGA AAAAGATGGG 300
 GGAATGGAT GGAAGGTCTT GGAATCTGAG ACAAGGGGTC TATAATCAGT CCATTTCATT 360
 ATTTCTAGCT TCCACCTTCA CCAAGGCAGA CAAGGAGGOC CCACCTCAGC TCCTCTGCTC 420
 65 CCCCCTCCCT TCCCACCTAT TCATGTGTGC AAGAGTGCCC TGTCCCACAG AACACGGGGA 480
 ACAACCATCT CAATGACAAG GACAGCAGGT GGCAAGGCTC AACAGGACTC AGATGTCCCC 540
 CCAGGGTTAA CTCATGAAAC CCTCCATGAA GCCTGCTGCT CACCCCTCCC TCAAGGCAAG 600
 CCCTGCACCT GGGTCTGAGG ATGAGGGTGG CAGTGAAAT TAGGCCAGTG ACATCATTTT 660
 CAGCCAGCTA GTGCCAAAAA ATATCAGGTG GTGTTTATCA AATAAGCCGA GCCAACCGGT 720
 70 GATGAGGATG GTAGTGTGAG TCATGTGTGA CAGGTGAGGA ATGAAAACAG AGTGCCCGAG 780
 AGCTTCTATT TCCTTAGGAG AGGGCTCAT TCATCTATAA AAGCCAGCTG GCCATGTGCT 840
 TCACACCAAA CCCAAGGGAC CACACAGCCC ATTTCTGCTC GTATACCAGG TAAGTCTCTG 900
 ATTGCAACAA ACTGGCAATT CTAGTGTACT TTTTCATTAT TAGAAATTAG CTAAGGGCAA 960
 75 ATATGTGTAA GCAGGTTAAT CCAGGTTTTC AATGGGAGAT AGAGAATAGT GGAATATCTT 1020
 TATTTTAAGT TAAATTACAG TCTGGATTTC AAAGGACCTT AGAGATGGTT AGGCTCCCA 1080
 CCTCAGTAGA TAGTCATTGA ACTGGGAGTC CTGGAGAAGA TTGTTCAAAAT GCCCATGGGA 1140
 AGTTTCATAGC AGAATAGAG CTGAGGCCAG AGCACTCTCA GTAACACTGC AATTTCCTCC 1200
 TGACAAGATA TTTATAGAAA TTTTAATTTA TTAGATGGAT CTCTACTGAG CATTTATTCC 1260
 ATTTAAGGCA GTATGTCTAGG CACTTTGGAC AAATCAATGC CCTAACGTAC TTACTTAACA 1320
 80 AACATAAAC CTAGCAGGAA GGTAAATAC ATATATAAAT AATGAAATG CAAAGTAGAT 1380
 AGTAATTGGC ATGACGGAGA TGGGCAGAGA AGGGCTGTGC ACTTTGGGA GACTTGCTCA 1440
 AGGAGACCTC TAGGGTGTCA AGTGATGTGA GCTATGATGG AGGGGTATTT GGACAAGCAG 1500
 AGATGGGAG AAAAGCATTT GGAAGGGACT GTGTAAAGCAC AGACCAGAAAG CAAAACCATTA 1560
 GAGGCTTAGA TGAATGTAAA GCCATCCTAT AAGTCACAGG CTTTCTCAT GGTACTAGGA 1620
 85 GAGGAAAGTG GTCTGATGCC ATTTTCCAAA AGACCTAATA TGCGGACCTC ATGTCCCTCA 1680
 GAAGCCAGCT TTAGTAGGCG ATTTTCCAG AACAGATATA AGGTGCTTTC GGTAGGAAGC 1740
 GAGCAAGAA GAGCACTCCA ATAAATTTGA GCAGAAGAAA TTGCTTTTAA GCTCCTCTC 1800
 TCAAGGGC CTGAAATTA TCCAAGCTTA TTTCTTTT AAATGTAATG GGGGAGCTAA 1860

GGGAGATGAA AGGCTTTCTC TTCTAAAGGG TCCTGAAATA AAATCTGTTT GGCATTGAAT 1920
TTGTATCCAT CTTTCTTTAA TTGAATCACT GTGTGAGCTT TCTGTCTCTA GAAAAAACA 1980
CATTTTGAAGC ATGAATTTCTC AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA 2040
GCAGCAGCAG GTGAAACAAC CTTGCCAGCC TCCACCCAG GAACCATGCA TCCCCAAAC 2100
CAAGGAGCCC TGCCAAACCA AGGTGCCTGA GCCCTGCCAC CCCAAAGTGC CTGAGCCCTG 2160
CCAGCCCAAG ATCCAGAGC CCTGCCAGCC CAAGGTGCCT GAGCCCTGCC CTTCAACGGT 2220
CACTCCAGCA CCAGCCAGC AGAAGACCAA GCAGAAATAA TGTGGTCCAC AGCCATGCCC 2280
TTGAGGAGCT GGCACCTGGA TACTGAACAC CCTACTCCAT TCTGCTTATG AATCCCATT 2340
GCCTATTGAC CCTGCAGTTA GCATGCTGTC ACCCTGAATC ATAATCGCTC CTTTGACCT 2400
CTAAAAAGAT GTCCCTTACC CTCACTCTGG AGGCTCCTGA GCCTCTGCGT AAGGCTGAAC 2460
GTCTCACTGA CTGAGCTAGT CTTCTGTTG CTCGGGTGCA TTTGAGGATG GATTGGGGA 2520
AGGTCAAGTG ACCATCCCTA G

Seq ID NO: 51 Protein sequence:
Protein Accession #: AAC26838

1 11 21 31 41 51
MNSQQKQKPC TPPPQPQQQQ VKQPQPQQPQ EPCIPKTKEP CQPKVPEPCH PKVPEPCQPK 60
IPEPCQPKVP EPCPSTVTPA PAQKQTKQK

Seq ID NO: 52 DNA sequence
Nucleic Acid Accession #: NM_002638.1
Coding sequence: 120-473

1 11 21 31 41 51
CAATACAGCT AAGGAATTAT CCCTTGTAAT TACCACAGAC CCGCCCTGGA GCCAGGCCAA 60
GCTGGAGTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG 180
AGGCAGCTGT CACGGGAGTT CCTGTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCACTTAA AGGTCAAGAT AAAGTCAAAG 300
CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360
TCCGGTGGCG CATGTTGAAT CCCCTAACCC GCTGCTTAA AGATACCTGAC TGCCAGGAA 420
TCAAGAAATG CTGTGAAGGC TCTTGGCGGA TGGCCTGTTT CGTTCGCCG TGAAGGGAGC 480
CGGTCTTTCG TGACCTGTG CCGTCCCCAG AGCTACAGGC CCGATCTGGT CCTAAGTCCC 540
TGCTGCCCTT CCCCTTCCCA CACTGTCCAT TCTTCTCTCC ATTCAAGATG CCCACGGCTG 600
GAGCTGCCCT TCTCATCCAC TTTCCAAATA A

Seq ID NO: 53 Protein sequence:
Protein Accession #: NP_002629.1

1 11 21 31 41 51
MRASSFLIVV VPLIAGTLVL EAAVTGVFVK GQDTPVGRVP FNGQDPVKQ VSVKGQDKVK 60
AQEPVKGPVS TKPSCPIIL IRCAMLNPPN RCLKDTPCPG IKKCCGSCG MACFPVQ

Seq ID NO: 54 DNA sequence
Nucleic Acid Accession #: NM_019618
Coding sequence: 75-584

1 11 21 31 41 51
GGCAGGAGCC ACAGTTCACT CCCCTGGACT GTAGATAAAG ACCCTTCTCT GCCAGGTGCT 60
GAGACAACCA CACTATGAGA GGCACCTCCAG GAGACGCTGA TGGTGGAGGA AGGGCCGTCT 120
ATCAATCAAT GTGTAAACCT ATTAAGTGGG CAATTAATGA TTTGAATCAG CAAGTGTGGA 180
CCCTTCAGGG TCAGAACCTT GTGGCAGTTC CACGAAGTGA CAGTGTGACC CCAGTCACTG 240
TTGCTGTTAT CACATGCAAG TATCCAGAGG CTCTTGAGCA AGGCAGAGGG GATCCCATTT 300
ATTTGGGAAT CCAGATCCCA GAAATGTGTT TGTATTGTGA GAAGGTGGA GAACAGCCCA 360
CAATGCAGCT AAAGAGAGCAG AAGATCATGG ATCTGTATGG CCAACCCGAG CCGGTGAAAC 420
CCTTCTCTTT CTACCTGGCC AAGACTGGTA GGACCTCCAC CCTTGAGTCT GTGGCCTTCC 480
CGGACTGGTT CATTGCCCTC TCCAAGAGAG ACCAGCCCAT CATTCTGACT TCAGAACTTG 540
GGAAGTCATA CAACACTGCC TTTGAATTAA ATATAAATGA CTGAACCTAG CCTAGAGGTG 600
GCAGCTTGGT CTTTGTCTTA AAGTTTCTGG TTCCCAATGT GTTTTCGTCT ACATTTCTT 660
AGTGTCAATT TCACGCTGGT GCTGAGACAG GGGCAAGGCT GCTGTTATCA TCTCATTTTA 720
TAATGAAGAA GAAGCAATTA CTTATAGCA ACTGAAGAAC AGGATGTGGC CTCAGAAGCA 780
GGAGAGCTGG GTGATATAAG GCTGCTCTCT CAAGCTGGTG CTGTGTAGGC CACAAGGCAT 840
CTGCATGAGT GACTTTAAGA CTCAAAGACC AAACACTGAG CTTTCTTCTA GGGGTGGGTA 900
TGAAGATGCT TCAGAGCTCA TGCGGTTTAC CCACGATGGC ATGACTAGCA CAGAGCTGAT 960
CTCTGTTTCT GTTTTGCTTT ATTCCCTCTT GGGATGATAT CATCCAGTCT TTATATGTTG 1020
CCAATATACC TCATTGTGTG TAATAGAACCT TTCTTAGCAT TAAGACCTTG TAAACAAAAA 1080
TAATCTTGT GTTAAGTTAA ATCATTTTGT TCCTAATGT AATGTGTAAT CTTAAAGTTA 1140
AATAAACTTT GTGTATTAT ATAATAAAAA AAAAAAAAAA AAA

Seq ID NO: 55 Protein sequence:
Protein Accession #: NP_062564

1 11 21 31 41 51
MRGTPGDADG GGRAVYQSMC KPITGTINDL NQQVWTLQGG NLVAVPRSDS VTPVTVAVIT 60
CKYPEALEQG RGPDIYLIQ NPMECLYCEK VGEQPTLQK EQKIMDLVYQ PEPVKPFLFY 120
RAKTGRTSTL ESWAFPDWFI ASSKRDQPII LTSELGKSYN TAFELNIND

Seq ID NO: 56 DNA sequence
Nucleic Acid Accession #: NM_003125
Coding sequence: 65-334

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1      11      21      31      41      51
|      |      |      |      |      |
5  AGCAGTTCTA AGGGACCATA CAGAGTATTC CTCTCTTCAC ACCAGGACCA GCCACTGTTG 60
   CAGCATGAGT TCCAGCAGCC AGAAGCAGCC CTGCATCCCA CCCCCTCAGC TTCAGCAGCA 120
   GCAGGTGAAA CAGCCTTGCC AGCCTCCACC TCAGGAACCA TGCAATCCCA AAACCAAGGA 180
   GCCCTGCCAC CCCAAGGTGC CTGAGCCCTG CCACCCCAAA GTGCCGTGAGC CCTGCCAGCC 240
   CAAGCTTCCA GAGCCATGCC ACCCCAAGGT GCCTGAGCCC TGCCCTTCAA TAGTCACTCC 300
10 AGCACCAGCC CAGCAGAAGA CCAAGCAGAA GTAATGTGGT CCACAGCCAT GCCCTTGAGG 360
   AGCCGGCCAC CAGATGCTGA ATCCCTATC CATCTCTGTG TATGAGTCCC ATTTGCCCTG 420
   CAATTAGCAT TCTGTCTCCC CCAAAAAGA ATGTGCTATG AAGCTTTCTT TCCTACACAC 480
   TCTGAGTCTC TGAATGAAGC TGAAGTCTT AGTACCAGAG CTAGTTTCA GCTGCTCAGA 540
   ATTATCTGTA AGAGAGACTT AAGATGAAAG CAAATGATTG AGCTCCCTTA TACCCCAATT 600
15 AAATTCATT TCAATTCCA

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Seq ID NO: 57 Protein sequence:
Protein Accession #: NP_003116

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20      1      11      21      31      41      51
|      |      |      |      |      |
   MSSQQQKQPC IPPPQLQQQQ VKQPCQPPPP EPCIPKTKEP CHPKVPEPCH PKVPEPCQPK 60
   LPEPCHPKVP EPCPSVTPA PAQKTKQK

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Seq ID NO: 58 DNA sequence
Nucleic Acid Accession #: NM_001793.2
Coding sequence: 71-2560

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30      1      11      21      31      41      51
|      |      |      |      |      |
   AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCCGTGCG GGCAGCTGCT TCACCCCTCT 60
   CTCTGCAGCC ATGGGGCTCC CTGCTGAGCC TCTGCGCTCT CTCTCTCTTC TCCAGGTTTG 120
   CTGGCTGCAG TCGCGCGCCT CCGAGCCGTC CCGGGCGGTC TTCAGGAGG CTGAAGTGAC 180
   CTTGGAGGCG GGAGGCGCGG AGCAGGAGCC CGGCCAGCGC CTGGGGAAAG TATTTCATGGG 240
   CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
   TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
   ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
   TGAAAATGGC AAGGGTCCCT TCCCCAGAG ACTGAATCAG CTCAAGTCTA ATAAAGATAG 480
   AGACACCAAG ATTTTCTACA GCATCACGGG GCGGGGGGCA GACAGCCCCC CTGAGGGTGT 540
   CTTGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
   GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTCAGAG AATGGTGCCT CAGTGGAGGA 660
   CCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
   GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTTACCA GGTACTTCTG TGATGCAGGT 780
   GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAA GTGGTGGTTG CTTACTCCAT 840
   CCATAGCCAA GCGTGGCGTG ACCCAACAGG CCTCATGTTT ACCATTCAAC GGAGCACAGG 900
   CACCATCAGC GTCATCTCCA GTGGCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC 960
   CATCCAGGCC ACAGACATGG ATGGGACCGG CTCACCAACC ACGGCAGTGG CAGTAGTGA 1020
   GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
   GCCTGAGAAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140
   CAACTCACCA CCGTGGCGTG CACCTACCT TATCATGGGC GGTGACGACG GGGACCAATT 1200
   TACCATCACC ACCCAACCTG AGAGCAACCA GGGCATCCTG ACAACAGGAG AGGGTTTGA 1260
   TTTTGAAGCC AAAAACCCAG ACACCTGTA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320
   GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
   ACCTGTGTTT GTCCACCCCT CCAAGTCTGT TGAGGTCCAG GAGGGCATCC CCACTGGGAG 1440
   GCCTGTGTT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAAGA TCAGTACCG 1500
   CATCTGAGA GACCCAGCAG GGTGGCTAGC CATGACCCCA GACAGTGGGC AGGTCAACGC 1560
   TGTGGGCACC CTCGACCTGT AGGATGAGCA GTTTGTGAGG AACAACATCT ATGAAGTCAT 1620
   GGTCTTGGCC ATGACAAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680
   ACTGATTGAT GTCAATGACC ATGGCCCACT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
   CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
   CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
   GGAAGGTGAC ACAGTGGTCT GTTCCCTGAA GAAGTTCTCT AAGCAGGATA CATATGACGT 1920
   GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
   GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAAGGAG GTTTCATCCT 2040
   CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGGTGCTGC TTTTGTGTTG 2100
   GAGAAAGGAG CGGAAGATCA AGGAGCCCTT CTTACTCCCA GAAGATGACA CCCGTGACAA 2160
   CBTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
   GCTCCACCGA GGTCTGGAGG CAGGCGCGGA GGTGGTCTC CGCAATGACG TGGCACCAAC 2280
   CATCATCCCG ACACCCATGT ACGTCTCTCG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
   TATAATTGAG AACCTGAAGG CGCTTAACAC AGACCCCA CAACCCGCCCT ACGACACCTT 2400
   CTGTGTTTCT GACTATGAGG GCAGCGGCTC CGACGCGCGC TCCCTGAGCT CCCTCACCTC 2460
   CTCGCTCCAC ACCCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCCCTTCAA 2520
   GAAGCTGGCA GACATGTACG GTGGCGGGGA GACGACTAG GCGGCTGCCC TGCAAGGCTG 2580
75 GGGACCAAAC GTCAAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCTCC TTCAGCTGAG 2640
   GACTTCGGAG CTTGTAGGGA AGTGGCCGTA GCAACTTGCC GAGACAGGAG TATGAGTCTG 2700
   ACGTTAGAGT GGTGTGCTTC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
   AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCTCAG AGGCCAAGTT TCCAGAAGCT 2820
   TCTTACCTGC CGTAAATGTC TCAACCTGT GTCTGGGCC TGGGCTGCT GTGACTGACC 2880
80 TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGTGCA ACTTAATTTT 2940
   TTTTTTAAT GCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000
   GCTGGGCCCA CTGGCCGTCC TGCAATTCTG GTTCCAGAG CCAATGCGCT CCCATTCCGA 3060
   TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTT TATTTTCCCT 3120
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   TAAAGAACT TTTCCAGAA AAAAA

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Seq ID NO: 59 Protein sequence:

Protein Accession #: NP_001784.2

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	QEPALFSTDN	DDFTVRNGET	VQERRSLKER	NPLKIFPSKR	ILRRHKRDWV	VAPISVPENG	120
	KGPFPQRLNQ	LKSNKDRDTK	IFYSITGPGA	DSPPEGVFAV	EKETGWLLLN	KPLDREEIAK	180
	YELFGHAYSE	NGASVEDPMN	ISIIIVTDQND	HKPKFTQDTF	RGSVLEGVLP	GTSVMQVTAT	240
10	DEDDAIYTYN	GVVAYSISHSQ	EPKDPHDLMF	TIHRSTGTIS	VISSGLDREK	VPEYTLTIQA	300
	TDMDGDGTTT	TAVAVVEILD	ANDNAPMDFP	QKYEAHVPEN	AVGHEVQRLT	VTDLDAPNSP	360
	AWRATYILMG	GDDGDHFTIT	THPESNQIL	TRKGLDFEA	KNQHTLYVEV	TNEAPFVLKL	420
	PTSTATIVVH	VEDVNEAPVF	VPPSKVVEVQ	EGIPTGEPVC	VYTAEDPDKE	NQKISYRILR	480
	DPAGWLAMP	DSGQVTAVGT	LDREDEQFVR	NNIYEVMLA	MDNGSPPTTG	TGTLTLLTLD	540
	VNDHGPVPEP	RQITICNQSP	VRQVLNITDK	DLSPHTSPFQ	AQLTDDSDIY	WTAEVNEEGD	600
15	TVVLSLKKFL	KQDTYDVHLS	LSDHGNKEQL	TVIRATVCDC	HGHVETCPGP	WKGGFILPVL	660
	GAVLALLPLL	LVLALLVRKK	RKIKPELLLP	EDDTRDNVYF	YGEEGGGEED	QDYDITQLHR	720
	GLEARPEVVL	RNDVAPTIIIP	TPMYRPRPAN	PDEIGNFIE	NLKAANTDPT	APPYDTLLVF	780
	DYEGSGSDAA	SLSLTSSAS	DQDQDYDYLN	EWGSRFKKLA	DMYGGGEDD		

Seq ID NO: 60 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 162-428

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	AGCACCTCGG	AAGCTGAGGC	AGCTGGTACT	TGACAGAGAG	GATGGCGCTG	TCGACCATAG	180
	TCTCCCAAG	GAACGAGATA	AAGCGGAAGG	CTCCCGTGG	CTTTCTAAAG	CGAGTCTTCA	240
30	AGCGAAAGAA	GCCTCAACTT	CGTCTGGAGA	AAAGTGGTGA	CTTATTGGTC	CATCTGAAC	300
	GTTTACTGTT	TGTTTACTGA	TTAGCAGAAG	AGTCCAGGAC	AAACGCTTGT	CGAGTAAAT	360
	GTAGAGTCAT	TAACAAGGAG	CATGTACTGG	CCGCAGCAAA	GGTAATTCTA	AAGAAGAGCA	420
	GAGGTTAGAA	GTCAAGAAGC	ATATTCTTGA	AAGTTATGAT	GCATTCTTTT	GGGTGGTAAC	480
	AGATCATAAA	GACATTTTTT	ACACATCAGT	TAATATGGGA	TTATTAAATA	TTGG	

Seq ID NO: 61 Protein sequence:
Protein Accession #: Eos sequence

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40	MALSTIVSQR	KQIKRKAPRG	FLKRVFKRKK	PQLRLEKSGD	LLVHLNCLLF	VHRLAESRT	60
	NACASKCRVI	NKERVLAAAK	VILKKSRRG				

Seq ID NO: 62 DNA sequence
Nucleic Acid Accession #: NM_000094.2
Coding sequence: 99-8933

	1	11	21	31	41	51	
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	GAGGCGGGGG	TCCTAGCTGA	CGGCTTTTAC	TGCCTAGGAT	GACGCTGCGG	CTTCTGGTGG	120
	CGCGCTCTG	CGCCGGGATC	CTGGCAGAGG	CGCCCCGAGT	GCGAGCCAG	CACAGGGAGA	180
	GAGTGACCTG	CACGCGCTT	TACGCGCTG	ACATTGTGTT	CTTACTGGAT	GGCTCCTCAT	240
	CCATTGGCCG	CAGCAATTTC	CGCGAGGTCC	GCAGCTTCT	CGAAGGGCTG	GTGCTGCCTT	300
55	TCTCTGGAGC	AGCCAGTGCA	CAGGCTGTGC	GCTTTGCCAC	AGTGCACTAC	AGCGATGACC	360
	CACGGACAGA	GTTCCGGCTG	GATGCACCTG	GCTCTGGGGG	TGATGTGATC	CGCGCCATCC	420
	GTGAGCTTAG	CTCAAGGGGG	GGCAACACTC	GCACAGGGGC	TGCAATCTCT	CATGTGGCTG	480
	ACCATGTCTT	CCTGCCCCAG	CTGGCCCGAC	CTGGTGTCCC	CAAGGTCTGC	ATCCTGATCA	540
	CAGACGGGAA	GTCCGAGGAC	CTGGTGGACA	CAGCTGCCCA	AAGGCTGAAG	GGGACGGGGG	600
60	TCAAGCTATT	TGCTGTGGGG	ATCAAGAATG	CTGACCCCTG	GGAGCTGAAG	CGAGTTGCCT	660
	CACAGCCAAAC	CTCCGACTTC	TTCTTCTTCG	TCAATGACTT	CAGCATCTTG	AGGACACTAC	720
	TGCCCTCTGT	TTCCCGGAGA	GTGTGCACGA	CTGCTGGTGG	CGTGCCCTGT	ACCCGACCTC	780
	CGGATGACTC	GACCTCTGCT	CCACGAGACC	TGGTGTCTGC	TGAGCCCAAGC	AGCCAACTCT	840
	TGAGAGTACA	GTGGACAGCG	GCCAGTGGCC	CTGTGACTGG	CTACAAGGTC	CAGTACACTC	900
65	CTCTGACGGG	GCTGGGACAG	CCACTGCCGA	GTGAGCGGCA	GGAGGTGAAC	GTCCGAGCTG	960
	GTGAGACCAG	TGTGCGGCTG	CGGGTCTTCC	GGCCACTGAC	CGAGTACCAA	GTGACTGTGA	1020
	TTGCCCTCTA	CGCCAAACAGC	ATCGGGGAGG	CTGTGAGCGG	GACAGCTCGG	ACCACTGCCC	1080
	TAGAAGGGCC	GGAATGACCC	ATCCAGAATA	CCACAGCCCA	CAGCCTCTCT	GTGGCTGGGC	1140
	GGAGTGTGCC	AGGTGCCACT	GGCTACCGTG	TGACATGGCG	GCTCCTCAGT	GGTGGGCCCA	1200
70	CACAGCAGCA	GGAGCTGGGC	CCTGGGCAGG	GTTTCACTGT	GCTGCGTGAC	TTGGAGCCTG	1260
	GCACGGACTA	TGAGGTGACC	GTGAGCACCC	TATTTGGCCG	CAGTGTGGGG	CCCGCACTT	1320
	CCCTGATGGC	TCGCACCTGAC	GCTTCTGTTG	AGCAGACCTT	GCGCCCGGTC	ATCCTGGGCC	1380
	CCACATCCAT	CCTCTTTTCC	TGGAACCTGG	TGCCTGAGGC	CGGTGGCTAC	CGGTTGGAAT	1440
	GGCGGCGTGA	GACTGGGCTTG	GAGCCACCGC	AGAAGGTGGT	ACTGCCCTCT	GATGTGACCC	1500
75	GCTACCAATT	GGATGGGCTG	CAGCCGGGCA	CTGAGTACCG	CCTCACACTC	TACACTCTGC	1560
	TGGAGGGCCA	CGAGGTGGCC	ACCCCTGCAA	CCGTGGTTCC	CAGTGGACCA	GAGCTGCCTG	1620
	TGAGCCCTGT	AACAGACCTG	CAAGCCACCG	AGCTGCCCGG	GCAGCGGGTG	CGAGTGTCTT	1680
	GGAGCCCACT	CCCTGGTGCC	ACCCAGTACC	GCATCAITGT	GCGCAGCACC	CAGGGGGTTG	1740
	AGCGGACCTT	GGTGCTTCTT	GGGAGTCAGA	CAGCATTCGA	CTTGATGATC	GTTCAGGCTG	1800
80	GGCTTAGCTA	CAGTGTGCGG	GTGTCTGCTC	GAGTGGGTCC	CCGTGAGGGC	AGTGCCAGTG	1860
	TCCTCACTGT	CCGCGGGGAG	CCGGAACACT	CAGTGTGCTG	TCCAGGGCTG	CGGGTGTGGG	1920
	TGTACAGTGC	AACCGAGTGC	AGGGTGGCCT	GGGGACCCGT	CCCTGGAGAG	AGTGGATTTC	1980
	GGATTAGCTG	GAGCACAGGC	AGTGGTCCGG	AGTCCAGCCA	GACACTGCCC	CCAGACTCTA	2040
	CTGCCACAGA	CATCACAGGG	CTGCAGCCTG	GAACCACTTA	CCAGGTGGCT	GTGTGGGTAC	2100
85	TGCGAGGCAG	AGAGGAGGGC	CCTGCTGCAG	TCATCGTGGC	TGGAACGGAC	CCACTGGGGC	2160
	CAGTGAGGAC	GGTCCATGTG	ACTCAGGCCA	GCAGCTCATC	TGTCACCACT	ACCTGGACCA	2220
	GGGTTCCTGG	CGCCACAGGA	TACAGGGTTT	CCTGGCACTC	AGCCACGGCC	CCAGAGAAAT	2280

	CCCAGTTGGT	TTCTGGGGAG	GCCACGGTGG	CTGAGCTGGA	TGGACTGGAG	CCAGATACTG	2340
	AGTATACGGT	GCATGTGAGG	GCCCATGTGG	CTGGCGTGGA	TGGGCCCCCT	GCCTCTGTGG	2400
	TTGTGAGGAC	TGCCCCCTGAG	CCTGTGGGTC	GTGTGTGAGG	GCTGCAGATC	CTCAATGCTT	2460
5	CCAGCGACGT	TCTACGGATC	ACCTGGGTAG	GGGTCACTGG	AGCCACAGCT	TACAGACTGG	2520
	CCTGGGGCCG	GAGTGAAGGC	GGCCCCATGA	GGCACCAGAT	ACTCCCAGGA	AACACAGACT	2580
	CTGCAGAGAT	CCGGGGTCTC	GAAGGTGGAG	TCAGCTACTC	AGTCCGAGTG	ACTGCACTTG	2640
	TCGGGGACCG	CGAGGGCACA	CCTGTCTCCA	TTGTTGTAC	TACGCCCGCT	GAGGCTCCGC	2700
	CAGCCCTGGG	GACGCTTCAC	GTGGTGCAGC	GCGGGGAGCA	CTCGCTGAGG	CTCGCTGGG	2760
10	AGCCGGTGCC	CAGAGCGCAG	GGCTTCTTTC	TGCATGGCA	ACCTGAGGGT	GGCCAGGAAC	2820
	AGTCCCGGGT	CCTGGGGCCC	GAGCTCAGCA	GCTATCACCT	GGACGGGCTG	GAGCCAGCGA	2880
	CACAGTACCG	CGTAGAGCTG	AGTGTCTTAG	GGCCGGCTGG	AGAAGGGGCC	TCTGCAGAGG	2940
	TGACTGCGCG	CACTGAGTCA	CCTCGTGTTC	CAAGCATTGA	ACTAGTGTGT	GTGGACACCT	3000
	CGATCGACTC	GGTGACTTTG	GCCTGGACTC	CAGTGTCCAG	GGCATCCAGC	TACATCCTAT	3060
15	CCTGGCGGGC	ACTCAGAGGC	CCTGGCCAGG	AAGTGCCTGG	GTCCCCGAG	ACACTTCCAG	3120
	GGATCTCAAG	CTCCACGGCG	GTGACAGGGC	TAGAGCCTGG	CGTCTCTTAC	ATCTTCTCCC	3180
	TGACGCTGT	CTCGGGGTCT	GTGCGGGTCT	CTGAGGCATC	TGTACACAG	ACGCCAGTGT	3240
	GCCCCCTGG	CCTGGCGGAT	GTGGTGTTC	TACCACATGC	CACTCAAGAC	AATGCTCACC	3300
	GTGCGGAGGC	TACAGGAGG	GTCTGGAGC	GTCTGGTGT	GGCACTTGG	CCTCTTGGGC	3360
20	CACAGGCGAT	TCAGGTGGC	CTGCTGTCTT	ACAGTCATCG	GGCTTCCCCA	CTGTTCCAC	3420
	TGAATGGCTC	CCATGACCTT	GGCATTATCT	TGCAAGGAT	CCGTGACATG	CCCTACATGG	3480
	AGCAAGTGT	GAAACAACCT	GGCACAGCCG	TGGTCACAGC	TCACAGATAC	ATGTTGGCAC	3540
	CAGATGCTCC	TGGCGCCGCG	CAGCACGTAC	CAGGGGTGAT	GGTCTGTCTA	GTGGATGAAC	3600
	CCTTGAGAGG	TGACATATTC	AGCCCCATCC	GTGAGGCCCA	GGCTTCTGGG	CTTAATGTGG	3660
25	TGATGTGGG	AATGAGCTGA	GCTGAGCCAG	AGCAGCTGCG	TGCTTGGCG	CCGGGTATGG	3720
	ACTCTGTCCA	GACCTTCTTC	GCCGTGGATG	ATGGGCCAAG	CCTGGACGAG	GCAGTCAGTG	3780
	GTCTGGCCAC	TGAGGCTGTG	CAGGCATCTT	TCACACTCA	GCCCCGGCCA	GAGCCCTGCC	3840
	CAGTGTATTG	TCCAAAGGGC	CAGAAGGGGG	AACCTGGAGA	GATGGGCTGT	AGAGGACAAG	3900
	TTGGGCTCC	TGGCGACCTT	GGCCTCCCGG	GCAGGACCGG	TGCTCCCGGC	CCCCAGGGGC	3960
30	CCCTGGGAAG	TGCCACTGCG	AAGGGCGAGA	GGGGCTTCCC	TGGAGCAGAT	GGGCGTCCAG	4020
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	CAGGGTTGCC	TGGCCCTCGT	GGGACCCCGG	GAGAGCGAGG	ACCTCGAGGC	CCAAAGGGGG	4140
	AGCCGGGGGC	TCCCGGACAA	GTGATCGGAG	GTGAAGGACC	TGGGCTTCTT	GGGCGGAAAG	4200
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35	GTGGCCCCCC	AGGGCTTCTT	GGAAACAGCCA	TGAAGGTGTA	CAAAAGCGAT	CGTGGGGAGC	4320
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	GTGACTCTGA	GGATGGAGCT	CCAGGCCCTC	CAGGACAACC	TGGGTCTCCG	GGTGAGCAGG	4500
	GCCCCAGGGG	ACCTCCTGGA	GCTATTGGCC	CCAAAGGTGA	CCGGGGCTTT	CCAGGGCCCC	4560
40	TGGGTGAGGC	TGGAGAGGAG	GGCGAACGTC	GACCCCCAGG	CCCAGCGGGA	TCCCGGGGGC	4620
	TGCCAGGGGT	TGCTGGACGT	CCTGGAGCCA	AGGGTCTCTA	AGGGCCACCA	GGACCCACTG	4680
	GCGCCCAAGG	AGAGAAAGGG	GAGCCTGGTC	GCCCTGGGGA	CCCTGCAGTG	GTGGGACCTG	4740
	CTGTGTCTGG	ACCCAAAGGA	GAAAGGGGAG	ATGTGGGGCC	CGCTGGGGCC	AGAGGAGCTA	4800
	CCGGAGTCCA	AGGGGAACCG	GGCCACCCCG	GCTTGGTTCT	TCCTGGAGAC	CCTGGCCCCA	4860
45	AGGAGAGACC	TGGAGACCGG	GGTCCCATTC	GCCTTACTGG	CAGAGCAGGA	CCCCCAGGTG	4920
	ACTCAGGGCC	TCCTGGAGAG	AAGGGAGACC	CTGGGCGGCC	TGGCCCCCTA	GGACCTGTTG	4980
	GCCCCCGAGG	ACGAGATGGT	GAAGTTGGAG	AGAAAGGTGA	CGAGGGCTCT	CCGGGTGACC	5040
	CGGGTTTGCC	TGGAAGAGCA	GCGAGCGGTG	GCCTTCGGGG	GGCACCTGGA	GTTCGGGGGC	5100
	CTGTGGGTGA	AAAGGGGAGC	CTGGAGAGATC	TGGAGAGGTA	TGGACGAAAT	GGCAGCCCTG	5160
50	GATCATCTGG	ACCCAAGGGT	GACCGTGGGG	AGCCGGGTCC	CCCAGGACCC	CCGGGACGCG	5220
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	GTCTCGAGG	GCCCAAGGGT	GATCCTGGCC	TCCTTGGAGC	CCCTGGGGAA	AGGGGCATTG	5340
	AAGGGTTTCG	GGGACCCCCA	GGCCACAGG	GGGACCCAGG	TGTCGAGGCG	CCAGCAGGAG	5400
	AAAAGGGTGA	CCGGGGTCCC	CTGGGGCTGG	ATGGCCGGAG	CGGACTGGAT	GGGAAACCCG	5460
55	GAGCCGCTGG	GCCCTCTGGG	CCGAATGGTG	CTGCAGGCCA	AGCTGGGGAC	CCAGGGAGAG	5520
	ACGGGCTTCC	AGGCCTCCGT	GGAGAACAAAG	GCCTCCCTGG	CCCCCTCTGT	CCCCCTGGAT	5580
	TACCGGAAAG	GCCCGGCGAG	GATGGGAAAC	CTGGCCCTGAA	TGGAAGAAAG	GGAGAACCTG	5640
	GGGACCTGG	AGAGAGCGGG	AGGAAGGGAG	AGAAAGGAGA	TTCAGGCGCC	TCTGGGAGAG	5700
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60	CTCCAGGCCCT	CCCAGGGCCA	GTGGGCCCTC	CTGGCCAGGG	TTTTCTCTGT	GTCCAGGAG	5820
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	CTGCTGGCAT	CAAGGCATCT	GCCCTGCGGG	AGATCGTGGA	GACCTGGGAT	GAGAGCTCTG	6000
	GTAGCTTCTT	GCCTGTGCCC	GAACGGCGTC	GAGGCCCCAA	GGGGGACTCA	GGCGAACAGG	6060
65	GCCCCCAGG	CAAGGAGGGC	CCCATCGGCT	TTCTTGAGGA	ACGCGGGCTG	AAGGGCGACC	6120
	GTGGAGAGCC	TGGCCCTCAG	GGGCCACCTG	GTCTGGCCCT	TGGGGAGAGG	GGCCCCCCG	6180
	GGCCTTCCGG	CCTTGCCCGG	GAGCCTGGAA	AGCCTGGTAT	TCCCGGGCTC	CCAGGCAGGG	6240
	CTGGGGGTGT	GGGAGAGGCA	GGAAGGCCAG	GAGAGAGGGG	AGAACGGGGA	GAGAAAGGAG	6300
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70	GACCCCTCTG	CCCCAAGGTG	TCTGTGGATG	AGCCAGGTCC	TGGAATCTCT	GGAGAACAGG	6420
	GACCCCTCTG	ACTCAAGGGT	GCTAAGGGGG	AGCCGGGCGG	CAATGGTGAC	CAAGGTCCCA	6480
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75	CTGGTCCCCC	GGGTCTTGCT	GGCCCTGCAG	GACCCCAAGG	ACCTTCTGGC	CTGAAGGGGG	6720
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	AGGGAGATCT	GGGCTTCCCT	GGCCTGCCCG	GTGCTCCTGG	TGTTGTTGGG	TTCCCGGGTC	7320
85	AGACAGGCCC	TCGAGGAGAG	ATGGGTGAGC	CAGGCCCTAG	TGGAGAGCGG	GGTCTGGCAG	7380
	GCCCCCAGG	GAGAGAAGGA	ATCCAGGAC	CCCTGGGGCC	ACCTGGACCA	CCGGGTCTAG	7440
	TGGGACACCC	TGGGGCTCTT	GGACTCAAAG	GAGACAAGGG	AGACCTGGA	GTAGGGCTGC	7500

	CTGGGCCCCG	AGGCGAGCGT	GGGGAGCCAG	GCATCCGGGG	TGAAGATGGC	CGCCCCGGCC	7560
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	GTGATGTTGG	GAGTGCAGGA	CTAAAGGGTG	ACAAGGGAGA	CTCAGCTGTG	ATCCTGGGGG	7680
5	CTCCAGGGCC	ACCGGGTGCC	AAGGGGACA	TGGGTGAACG	AGGGCCTCGG	GGCTTGGATG	7740
	GTGACAAAGG	ACCTCGGGGA	GACAAATGGG	ACCTCTGGTA	CAAGGGCAGC	AAGGGAGAGC	7800
	CTGGTGACAA	GGGCTCAGCC	GGGTGCCAG	GACTGCGTGG	ACTCCTGGGA	CCCCAGGGTC	7860
	AACCTGGTGC	AGCAGGGATC	CCTGGTGACC	CGGGATCCCC	AGGAAAGGAT	GGAGTGCCTG	7920
	GTATCCGAGG	AGAAAAAGGA	GATGTTGGCT	TCATGGGTCC	CCGGGGCCTC	AAGGGTGAAC	7980
10	GGGGAGTGAA	GGGAGCCTGT	GGCCTTGATG	GAGAGAAGGG	AGACAAGGGA	GAAGCTGGTC	8040
	CCCCAGGCGC	CCCCGGGCTG	GCAGGACACA	AAGGAGAGAT	GGGGGAGCCT	GGTGTGCCGG	8100
	GCCAGTCGGG	GGCCCTGGC	AAGGAGGGCC	TGATCGGTCC	CAAGGGTGAC	CGAGGCTTTG	8160
	ACGGGCAGCC	AGGCCCCAAG	GGTGACCAGG	GCAGAAAGG	GGAGCGGGGA	ACCCAGGAA	8220
	TTGGGGGCTT	CCCAGGCCCC	AGTGGAAATG	ATGGCTCTGC	TGGTCCCCCA	GGGCCACCTG	8280
	GCAGTGTGG	TCCAGAGGAC	TTCAGGGCCA	GAAGGGTGAG	CGAGGTCCCC	CGAGGTCCCC	8340
15	CCGGAGAGAG	AGTGGTGGGG	GCTCCTGGGG	TCCTGGGAGC	TCCTGGGCGG	AGAGGGGAGC	8400
	AGGGGCGGCC	AGGCTCTGCC	GGCTCTCGAG	GCGAGAAGGG	AGAAGCTGCA	CTGACGGAGG	8460
	ATGACATCCG	GGGCTTTGTG	CGCCAAGAGA	TGAGTCAGCA	CTGTGCCTGC	CAGGGCCAGT	8520
	TCATCGCATC	TGGATCAGGA	CCCTCCCTTA	GTTATGCTGC	AGACACTGCC	GGCTCCCAGC	8580
20	TCATGCTGTG	CGCTGTGCTC	CGCGTCTCTC	ATGCAGAGGA	GGAAGAGCGT	GTACCCCTCG	8640
	AGGATGATGA	TGACTCTGAA	TACTCCGAGT	ATTCTGTGGA	GGAGTACCAG	GACCCCTGAAG	8700
	CTCCTTGGGA	GTAGTCTGAC	CCCTGTTCCC	TGCCACTGGA	TGAGGGCTCC	TGCACTGCCT	8760
	ACACCTCTGC	CTGTGACCAT	CGGGCTGTGA	CAGGCAGCAC	AGAGGCCTGT	CACCCCTTTG	8820
	TCTATGGTGG	CTGTGGAGGG	AATGCCAACCC	GTTTTGGGAC	CCGTGAGGCC	TGCGAGCGCC	8880
25	GTCTGCCACC	CCGGGTGGTC	CCGAGCCAGG	GGACAGGTAC	TGCCCAGGAG	TGAGGCCCCAG	8940
	ATAATGAGCT	GAGATTGAGC	ATCCCTTGGA	GGAGTCCGGG	TCTCAGCAGA	ACCCCACTGT	9000
	CCCTCCCTCT	GGTCTGAGAG	GCTTGTGTGC	ACGTGAGCGT	GCGAGTGAC	GTCCGTATT	9060
	TCAGTGACTT	GGTCCCGTGG	GTCTAGCCTT	CCCCCTGTGT	GACAAACCCC	CATTGTGGCT	9120
	CTGCGCACCC	TGGCAGATGA	CTCACTGTGG	GGGGGTGGCT	GTGGGCACTG	AGCGGATGTG	9180
30	ACTGGCGTCT	GACCCGCCCC	TTGACCCAAG	CCTGTGATGA	CATGGTGCTG	ATTCCTGGGG	9240
	GCATTAAAGC	TGCTGTTTAA	AAAGGCAAAA	AA			

Seq ID NO: 63 Protein sequence:
Protein Accession #: NP_000085.1

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	AAILHVAHV	FLPLQARPGV	PKVCILITDG	KSQDLVDTA	QRLKGQGVKL	FAVGIKNADP	180
40	EELKRVASQP	TSDFFFVND	FSILRTLPL	VSRVCTTAG	GVPTRPDD	STAPRDLVL	240
	SEFSSQSLRV	QWDAAAGPVT	GKQVYPTPL	GLGQPLPSE	QEVNVPAGET	SVRLRLRL	300
	TEYQVTVIAL	VANSIGEA	GTARTALEG	PELTIQNTTA	HSLLVANRSV	PGATGYRVW	360
	RVLSSGGPTQ	QELPGQGSV	LLRDLPEGTD	YEVTVSTLFG	RSVGPATSLM	ARTDASVEQT	420
	LRPVILGPTS	ILLSNVLPVE	ARGYRLEWRR	ETGLEPPQKV	VLPSTDVTRYQ	LDGLQPGTEY	480
45	RLTLTYLLEG	HEVATPATVV	PTGPELFPVSP	VTDLQATELP	GQVRVRSWSP	VPATQYRII	540
	VRSTQGVERT	LVLDTQAGLS	YTVRVSAVVG	PREGSAVLT	VRRREPETPLA		600
	VPGLRVVSD	ATRVRVANGP	VPASGFRIS	WSTGSGPSS	QTLPPDSTAT	DITGLQPGTT	660
	YQVAVSVLRG	REEGPAIVV	ARTDPLGPVR	TVHVTQASS	SVTITWTRVP	GATGYRVSWH	720
	SAHGPEKSQL	VSGEATVAEL	DGLEPDTEYT	VHVRHVAVG	DGPPASVVVR	TAPEPVGRVS	780
50	RLQILNASSD	VLRTTWGVT	GATAYRLANG	RSEGGPMRQ	ILPGNTDSAE	IRGLEGGVSY	840
	SVRVTLVGD	REGTFVSIHV	TTPEAPPAL	GLHVVQRGE	HSLRLRWEPV	PRAQGLLHV	900
	QPEGQEQESR	VLGPELSSYH	LDGLEPATQY	VRVLSVLGPA	GEGPSAEVTA	RTESPRVPSI	960
	ELRVVDTSID	SVTLAWTFVS	RASSYILSNR	PLRGPGQEV	GSPQTLPGIS	SSQRTVGLPE	1020
55	GVSYIFSLTP	VLDGVRGPEA	SVTQTFVCP	GLADVVFLEH	ATQDNAHRAE	ATRRVLERLV	1080
	LALGPLGQPA	VQGALLSYSH	RPSPLFPLNG	SHDLGILQIR	IRDMFYMDPS	GNNLGTAVVT	1140
	AARYMLAPDA	PQRQHVPGV	MVLLVDEPLR	GDIFSPIREA	QASGLNVVML	GMAGADPEQL	1200
	RRLAPGMDG	QTFPAVDG	SLDQAVSGLA	TALCQASFTT	QPRPEPCFVY	CPKGGKGEFG	1260
	EMGLRGQVGP	PGDPLGPRG	GAPGPGQPPG	SATKGERGF	PGADGRPGSP	GRAGNPGTGP	1320
60	APGLKGSPLG	PGPRGDPGER	GPRGPKGEPG	APGQVIGGEG	PGLPGRKGDP	GPSGPPGPRG	1380
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	PGKKGEKGDS	EDGAPGLPGQ	PGSPGEQGP	GPPGAIGPKG	DRGFPGLGE	AGEKGERGPP	1500
	GPAGSRGLFG	VAGRPQAKGP	EGPFGPTGRQ	GKGEPRGPRG	DPAVVGPAVA	GPKEKGDPVG	1560
	PAGPRGATGV	QGERGPPGLV	LPDGPQPKGD	PGDRGPIGLT	GRAGPPGDSG	FPGEKGDPR	1620
65	PGPPGVPGR	GRDGEVGEKG	DEGPPGDPGL	PGKAGERGLR	GAPGVRGPRG	EKGDPQDPGE	1680
	DGRNGSPGSS	GPKGDRGEPG	PPGPPGRLVD	TGPGAREKGE	PGDRGQEGPR	GPKGDPGLPG	1740
	APGERGIEGF	RGPFGPPGDP	GVRGPAGEKG	DRGPPGLDGR	SGLDGKFGAA	GPSGPNGAAG	1800
	KAGDPGRDGL	PGLRGEQGLP	GPSGPPGLPG	KPGEDGKPLG	NGKNGEPGDP	GEDGRKGEKG	1860
	DSGASGRER	DGPKGERGAP	GILGPQGGPG	LPGPVGPPGQ	GFPVGVGGTG	PKGDRGETGS	1920
70	KGEQGLPGER	GLRGEPGSPV	NVDRLLETAG	IKASALREIV	ETWDESSGSF	LPVPERRRGP	1980
	KGDSGEQGGP	GKEGPIGFP	ERGLKGDGRD	PGPQGPGLA	LGERGPPGPS	GLAGEPGKPG	2040
	IPGLPGRAGG	VGEAGRPGER	GERGEKGERG	EQGRDGPPLG	PPTPGPPGPF	GPKVSVDEPG	2100
	PGLSGEQGPP	GLKAKGEPG	SNGDQGPXGD	RGVPGIKGDR	GEPGPRGQDG	NPLPGERGM	2160
	AGFEGKPLGL	GPRGPPGPGV	GHGDPGPPGA	PGLAGPAGPQ	GPSGLKGEPE	ETGPPGRGLT	2220
75	GPTGAVGLPG	PPGPGSLVGP	QSSPGLPCQV	GETGKPGAPG	RDGASGKGDG	RGSFPGVPGSP	2280
	GLPFPVGPKG	EPGPTGAPGQ	AVVGLPGAAG	EXGAPGGLAG	DLVGEPAKAG	DRGLPGRPRG	2340
	KGEAGRAGEP	APGPKGPKGD	PGVGVPGSPG	PPGPPGVKGD	LGLPGLGAP		2400
	GVVGFPPGQT	PRGEMQPGP	SGERGLAGPP	GREGIPGPLG	PPGPPGSPVG	PGASGLKGDK	2460
	GDPPGVLPGR	RGSRGEPGIR	PRGLTGPPGS	RGERGEKGDV	GSAGLKGDGP		2520
80	DSAVILGPPG	PRGAKGDMGE	RGRGLDGDG	GPRGNDGDFG	DKGSKGEPGD	KGSAGLFLGR	2580
	GLLGPQGGPG	AAGIPGDPGS	PGKGVPGIR	GEKGVDFGPG	PRGLKGERGV	KGACGLDGEK	2640
	GDKGEAGPFG	RPGLAGHKGE	MGEPPGVPGS	GAPGKEGLIG	PKGDRGFDGQ	PGPKGDQGEK	2700
	GERGTPTGIG	PPGSGNDGGS	AGPPGPPGSP	GPRGPEGLQG	QKGERGPPGE	RVVGAAPVGP	2760
	APGERGEGRG	PPGAPGRGEG	GEAALTEDDI	RGFVRQEQMS	HCACQGGQTA	SGSRPLPSYA	2820
85	ADTAGSQHLA	VPVLRVSHAE	EEERVPPEDD	EYSEYSEYSV	EEYQDPEAPW	DSDDPCSLPL	2880
	DEGSTAYTTL	RWYHRAVTGS	TEACHPFVYG	GCGGNANRFG	TREACERRCP	PRVVQSQGTG	2940
	TAQD						

WO 02/086443

PCT/US02/12476

Seq ID NO: 64 DNA sequence
Nucleic Acid Accession #: NM_006945
Coding sequence: 1-219

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TGTCACAGC CCGCCACC TCAGCAGTGC CAGCAGAAAT ATCCTCCTGT GACACCTTCC 180
10 CCACCTGCC AGCCAAAGTA TCACCGAAG AGCAAGTAA

Seq ID NO: 65 Protein sequence:
Protein Accession #: NP_008876

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1 11 21 31 41 51
MSYQQQQCKQ PCQPPVPCPT PKCPEPCPPP KCPEPCPPPK CPQPCPPQCC QQKYPPVTPS 60
PPCQPKYPPK SK

Seq ID NO: 66 DNA sequence
Nucleic Acid Accession #: NM_005629.1
Coding sequence: 639-2546

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CCGCCCGCCG CACCGCCACC GGAGTGCGCG GCCAGCCGGG CAGCCTCGCG GGGCCCCCGG 180
30 CCGGGCGGGG GGGCGCGGCC ACAGGCCCTT GCTCCGCGCG TCGTTTGCAG ACCCGGGGGC 240
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GCCGCCCGCC GAGCCGCGGG CAGGAGCCTC GGGAGCCGCC GCGCCGCGCG CCGCGCGCCG 360
GCCGGCCCCC GACGCCCGCC GCGCGCCCCC GGGCCCCCGA CACACATGAG ATTCTTCAGG 420
CTCATTTCAT AGTGCTTCGT GGAAGCTCTT TGAAGTGCCT GCGCCCGCCC CGCACCCCGC 480
CGTCGCGCCG CCGCGCGGTC CCGCGCCCCG GCGCCCGCCC GCGCCCGCCC CCGCGCGCCC 540
35 CCTCGGGGCG CTCGCCGGTG CCGCGCGTGC CCGCCCGCTG ACCCGCGCCC CCGGTGAGGC 600
GCCGCGAGCC CGCGCCGCGC GTGCGGCCCG CCGGGGCCAT GCGAAGAAAG AGCGCCGAGA 660
ACGGCATCTA TAGGCTGTCC GCGACGAGA AGAAGGGCCC CCTCATCGCG CCGGGGCCCG 720
AOGGGCCCCC GGCAGAGGCG GACCGCCCCG TGGGCTTGGG GACACCCGCG GCGCGCCTGG 780
CGGTGCCCGC GCGCGAGACC TGSAGCGGCC AGATGGACTT CATCATGTCT TCGGTGGGCT 840
40 TGCGCGTGGG TTTGGGCAAC GTGTGGCGCT TCCCTACCTT GTGCTACAAG AACCGCGGAG 900
GTGTGTCTCT TATTCCCTAC CTCTGATCG CCCTGGTTGG AGGAATCCCC ATTTTCTTCT 960
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CCCTGTTCAA AGGCTTGGCG TACGCTCTCA TGGTGATCGT CTCTACTGCG AACACCTACT 1080
45 ACATCATGGT GCTGGCCTGG GGCTTCTATT ACCTGGTGAA GTCTTTTACC ACCACGCTGC 1140
CCTGGGCCAC ATGTGGCCAC ACCTGGAAAC CTCGCGACTG CGTGGAGATC TTCGCCCATG 1200
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CCCTGTGATC CAGGTTCTGG GAGAACAAAG TCTTGAGGCT GTCTGGGGA CTGGAGGTGC 1320
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50 TCTGTGCTG GAAGGGGGTC AAATCCACCG GAAAGATCGT GTACTTCACT GCTACATTCC 1440
CCTAGCTGCT CCGGTGCTG CTGCTGGTGC GTGGAGTGTG GTCGCTGGC GCCCTGGATG 1500
GCATCATTTA CTATCTCAAG CCGTACTGGT CAAAGCTGGG GTCCCCCTAG GTGTGGATAG 1560
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GCAGCTACAA CCGCTTCAAC AACAACTGCT ACAAGGACGC CATCATCTCT GCTCTCATCA 1680
55 ACAGTGGGAC CAGCTTCTTT GCTGGCTTCG TGGTCTTCTC CATCTTGGGC TTCATGGCTG 1740
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60 CCCTCTGTTG TGCCCTCTGC TTTGTCTATG ATCTCTCCAT GGTGACTGAT GCGGGGATGT 2040
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65 ACAACACCTA CGTGTACCGG TGGTGGGGTG AGGCCATGGG CTGGGCTTTC GCCTGTCTCT 2340
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CTGAGCGCTG GCAGCACTG ACCAGCCCA TCTGGGGCCT CCACCACTG GAGTACCGAG 2460
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70 GCCATAGCAG CCGCTGCTTC AGCCCCACCG CACCCCTCCA GGGGGCCTGC CTTTCCCTGA 2640
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85 GCTGTCCCTT TGCCACAAGT CTGTGGGGCA AGAGGCTGCA ATATTCCGTC CTGGGTGTCT 3600
GGGCTGCTAA CCTGGCCTGC TCAGGCTTCC CACCTGTGTC GGGGCACACC CCCAGGAAGG 3660
GACCTTGGAC ACGCTCCCA CGTCCAGGCT TAAGGTGGAT GCATTCCTCG CACCTCCAGT 3720

CTTCTGTGTA GCAGCTTTAA CCCACGTTTG TCTGTACGCT CCAGTCCCGA GACGGCTGAG 3780
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5

Seq ID NO: 67 Protein sequence:
 Protein Accession #: NP_005620.1

10 1 11 21 31 41 51
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 CVEIFRHEDC ANASLANLTC DQLADRRSPV IEFWENKVLK LSGGLEVPGA LNWEVTLCLL 240
 15 ACWLVLVFCV WKGVKSTGKI VYFTATFPYV VLVLVLRGV LLPGALDGI IYLLKPDWSKL 300
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 20 TTLWQAEAF DRFMDDIACM IGYRCPWMK WCNWSPFTPLV CMGIFIPNVV 540
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25 Seq ID NO: 68 DNA sequence
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 Coding sequence: 178-2469

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 35 AATGCCCCAA GTGAAACATC AGAGGAGGAA CCTAAGAGAT CCGCTGCCCA ACAGGAGTCT 300
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 40 GGACCAAAAC CTGCAGCTAG GGATGTGAAT CTTCCTAGAC CACCTGGAGC CCTTTGCGAG 660
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 80 TTGATAGAA GGAAGACCTG CAGTGACCGG TTTCTTCCG GCTGAGGTAC CTGGATCTG 3000
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Seq ID NO: 69 Protein sequence:
Protein Accession #: NP_068772.1

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	LRPQTQTSYD	AKRTEVTLET	LGPKPAARDV	NLPRPPGALC	EQKRETCADG	EAAGCTINNS	180
10	LSNIQWLKRM	SSDGLGRSRI	KQEMEKEKNC	HLEQRQVKVE	EPSRPSASWQ	NSVSRPPYS	240
	YMAMIQFAIN	STERKRMTLK	DIYTWIEDHF	PYFKHIAKPG	WKNSIRHNL	LHDMFVRETS	300
	ANGKVSFWTI	HPSANRYLTL	DQVFKPLDPG	SPQLPEHLES	QOKRPNPELR	RNMTIKTELP	360
	LGARRKMKPL	LPRVSSYLVP	IQFPVNSLV	LQPSVKVPLP	LAASLMSSSL	ARHSKRVRIA	420
	PKVLLAEEGI	APLSSAGPGK	EEKLLFGEGR	SPLLPVQTIK	EEETQPGHEM	PHLARPIKVE	480
15	SPPLEEWSP	APSPKESSSH	SWEDSSQSPT	PRPKKSYGSL	RSPTRCVSEM	LVIQHRERRE	540
	RSRSRRKQHL	LPPCVDEPEL	LFSEGPSTSR	WAAELFPFAD	SSDPASQLSY	SQEVGGPFKT	600
	PIKETLPISS	TPSKSVLPRT	PESWRLTPPA	KVGGDLDFSPV	QTSQASDPL	PDPLGLMDLS	660
	TTPLQSAFPL	ESQORLLISE	FLDLISVPFG	NSSPSDIDVP	KPGSPREPQVS	GLAANRSLTE	720
20	GLVLDTMNDS	LSKILLDISF	PGLDEDPLGF	DNINWSQFIP	ELQ		

Seq ID NO: 70 DNA sequence
Nucleic Acid Accession #: BC006529.1
Coding sequence: 178-2424

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	GGCAGGAGGG	GGACCCGGCC	GGTCCGGCGC	GAGCCCCCGT	CCGGGGCCCT	GGCTCGGCC	60
	CCAGGTTTGG	GGAGCCCGGA	CCCGCCTTC	GGAGCTACGG	CCTAACGGCG	GCGGCGACTG	120
30	CAGTCTGAGC	GGTCCACACT	TGTGATCTTC	AATGAGAGAT	GAAACGCGAG	ATTCTAATAG	180
	AAAACATAGC	CCCTCGGCG	ACTGATTCTC	AAAAGACGGA	GGCTGCCCTC	TCCTGTTCAA	240
	AATGCCCCAA	GTGAACATC	AGAGGAGGAA	CCTAAGAGAT	CCCTCGCCCA	ACAGGAGTCT	300
	AATCAAGCAG	AGGCTCCCAA	GGAAGTGCCA	GAGTCCAACT	CTTGCAAGTT	TCCAGCTGGG	360
	ATCAAGATTA	TTAACCACCC	CACCATGCCC	AACACGCAAG	TAGTGGCCAT	CCCCAACACT	420
35	GCTAATATTC	ACAGCATCAT	CACAGCACTG	ACTGCCAAGG	GAAAGAGAG	TGGCAGTAGT	480
	GGGCCCAACA	AATCTCTCTC	CATCAGCTGT	GGGGGAGCCC	CAACTCAGCC	TCCAGGACTC	540
	CGGCCTCAAA	CCCAAAACCAG	CTATGATGCC	AAAAGGACAG	AAGTGACCTC	GGAGACCTTG	600
	GGACCAAAAC	CTGCAGCTAG	GGATGTGAAT	CTTCTAGAC	CACCTGGAGC	CCTTTGCGAG	660
40	CAGAAACCGG	AGACCTGTGC	AGATGGTGAG	GCAGCAGGCT	GCACATCAA	CAATAGCCTA	720
	TCCAACATCC	AGTGGCTTCG	AAAGATGAGT	TCTGATGGAC	TGGGCTCCCG	CAGCATCAAG	780
	CAAGAGATGG	AGGAAAGGGA	GAAATGTGAC	CTGGAGCAGC	GACAGGTTAA	GGTTGAGGAG	840
	CCTTCGAGAC	CATCAGCGTC	CTGGCAGAAC	TCTGTGTCTG	AGCGCCACCC	CTACTCTTAC	900
	ATGGCCATGA	TCAATTCGCG	CATCAACAGC	ACTGAGAGGA	AGCGCATGAC	TTTGAAGAGC	960
45	ATCTATAGCT	GGATTGAGGA	CCACTTTCCC	TACTTTAAGC	ACATTGCCAA	GCCAGGCTGG	1020
	AAGAACTCCA	TCCGACCAAA	CCTTTCCCTG	CACGACATGT	TTGTCCGGGA	GACGCTGCCC	1080
	AATGGCAAGG	TCTCTTCTGT	GACCATTCAC	CCCAGTGCCA	ACCGCTACTT	GACATTGGAC	1140
	CAGGTGTTTA	AGCAGCAGAA	ACGACCGAAT	CCAGAGCTCC	GCCGGAACAT	GACCATCAAA	1200
	ACCGAACTCC	CCCTGGGCGC	ACGGCGGAAG	ATGAAGCCAC	TGCTACCACG	GGTCAGCTCA	1260
50	TACCTGGTAG	CTATCCAGTT	CCCGGTGAAC	CAGTCACTGG	TGTTGCAGCC	CTCGGTGAAG	1320
	GTGCCATTGC	CCCTGGGCGC	TTCCCTCATG	AGCTCAGAGC	TTGCCCGCCA	TAGCAAGCGA	1380
	GTCCGCAATG	CCGCAAGGTC	GCTGCTAGCT	GAGGAGGGGA	TAGCTCCTCT	TTCTTGTGCA	1440
	GGACCAAGGA	AAGAGGAGAA	ACTCCTGTTT	GGAGAAAGGT	TTTCTCCTTT	GCTTCCAGTT	1500
	CAGACTATCA	AGGAGGAAGA	AATCCAGCCT	GGGGAGGAAA	TGCCACACTT	AGCGAGACCC	1560
55	ATCAAGTGG	AGAGCCCTCC	TTGGAAGAG	TGGCCCTCCC	CGGCCCATC	TTTCAAGAG	1620
	GAATCATCTC	ACTCCTGGGA	GGATTCTGTC	CAATCTCCCA	CCCCAAGACC	CAAGAAGTCC	1680
	TACAGTGGGC	TTAGGTCCCC	AACCCGGTGT	GTCTCGGAAA	TGCTTGTGAT	TCAACACAGG	1740
	GAGAGGAGGG	AGGAGAGCCG	GTCTCGGAGG	AAACAGCATC	TACTGCTCCC	CTGTGTGGAT	1800
	GAGCCGGAGC	TGCTCTTCTC	AGAGGGGCC	AGTACTTCCC	GCTGGGCCCG	AGAGCTCCCG	1860
60	TTCCAGCAG	ACTCCTCTGA	CCCTGCCTCC	CAGCTCAGCT	ACTCCCAGGA	AGTGGGAGGA	1920
	CCTTTTAAGA	CACCCATTAA	GGAAACGCTG	CCCATTCTCT	CCACCCCGAG	CAAACTCTGT	1980
	CTCCCCAGAA	CCCCCTGATC	CTGGAGGCTC	ACGCCCCCAG	CCAAAGTAGG	GGGACTGGAT	2040
	TTAGCCAGCA	TACAAACCCC	CCAGGGTGCC	TCTGACCCCT	TGCTGACCC	CCTGGGGCTG	2100
	ATGGATCTCA	CTGCAAAAGT	GCTCCCCCCC	TTGAATCACC	GCAAAGGCTC		2160
65	CTCAGTTCAG	AACCCCTAGA	CCTCATCTCC	GTCCCTTTTG	GCAACTCTTC	TCCCTCAGAT	2220
	ATAGACGTCC	CCAAGCCAGG	CTCCCGGAG	CCACAGGTTT	CTGGCCTTGC	AGCCAAATCGT	2280
	TCTCTGACAG	AAGGCTGGGT	CTGGACACA	ATGAATGACA	GCCTCAGCAA	GATCCTGTCT	2340
	GACATCAGCT	TTCTTGCCCT	GGACGAGGAC	CCACTGGGCC	CTGACACAT	CAACTGGTCC	2400
	CAGTTTATTC	CTTGCAAAAGT	GCTCCCCCCC	TTGAATCACC	GCAAAGGCTC		2460
70	ATCCCGGGCA	CTCCAAGGCT	CAGTGCAACC	CAAGCCTCTG	AGTGAGGACA	GCAGGCAGGG	2520
	ACTGTTCTGC	TCCTCATAGC	TCCTGCTGTC	CTGATTATGC	AAAAGTAGCA	GTCAACCCCT	2580
	AGCCACTGCT	GGGACTGTGT	GTCCCCCAAG	AGTATCTGAT	TCCTCTGTCT	TCCCTGCCAG	2640
	GAGCTGAAGG	GTGGGAACAA	CAAAGGCAAT	GGTGAAAAGA	GATTAGGAAC	CCCCCAGCCT	2700
	GTTTCCATT	TCTGCGGAGC	AGTCTCTTAC	CTTCCCTGAT	CTTTGCAGGG	TGGTCCGCTG	2760
75	AAATAGTATA	AATTCTCCAA	ATTATCCTCT	AATTATAAAT	GTAAGCTTAT	TTCTTAGAT	2820
	CATTATCCAG	AGACTGCCAG	AAAGTGGGTA	GGATGACCTG	GGGTTTCAAT	TGACTTCTGT	2880
	TCCTTGCTTT	TAGTTTGTAT	AGAAGGGAAG	ACCTGCAGTG	CACGGTTTCT	TCCAGGCTGA	2940
	GGTACCTGGA	TCTTGGGTTT	TTCACTGCAG	GGACCCAGAC	AAGTGGATCT	GCTTGCCAGA	3000
	GTCCCTTTTG	CCGCTCCCTG	CCACCTCCCT	GTGTTTCCAA	GTCAGCTTTC	CTGCAAGAGA	3060
80	AAATCCTGGT	TAAAAAAGTC	TTTTGTATTG	GGTCAGGAGT	TGAATTGGGG	GTGGGAGGAT	3120
	GGATGCAACT	GAAGCAGAGT	GTGGGTGCC	AGATGTGCGC	TATTAGATGT	TTCTCTGATA	3180
	ATGTCCCAAC	TCATACCAAG	GAGACTGGCA	TTGACGAGAA	CTCAGGTGGA	GGCTTGAGAA	3240
	GGCCGAAGG	GCCCTGACCC	TGCCTGGCTT	CCTTAGCTTG	CCCCCTCAGT	TTGCAAGAG	3300
	CCACCTTAGG	CCCGAGCTGA	CCGATGGGTT	GTGAGCCAGC	TTGAGAACAC	TAACTACTCA	3360
85	ATAAAAGCGA	AGGTGGAATA	AAAAAATAAA	AAAAAATA			

Seq ID NO: 71 Protein sequence:
Protein Accession #: AAH06529.1

	1	11	21	31	41	51	
5	MKTSPPRLPI	LKRRRLPLPV	QNAPSETSEE	EPKRSPAQQE	SNQAEASKEV	AESNSCKFFA	60
	GKIINHPTM	ENTQVVAIPN	NANIHSIITA	LTAKGKESGS	SGPNKFILIS	CGGAPTQPPG	120
	LRPQTQTSYD	AKRTEVTLET	LGPKAARDV	NLPRPPGALC	EQKRETCADG	EAAGCTINNS	180
	LSNIQWLKRM	SSDGLGSRSI	KQEMEKEKENC	HLEQRQVKVE	EPSRPSASWQ	NSVSRPPYS	240
	YMAMIQFAIN	STERKRMILK	DIYTWIEDHF	PYFKHIAKPG	WKNSIRHNLS	LHDMFVRETS	300
10	ANGKVSFWTI	HPSANRYLTL	DQVPKQKRP	NPELRRNMTI	KTELPLGARR	KMKPLLPVRS	360
	SYLVPIQFPV	NQSLVLQPSV	KVPLPLAASL	MSSELARHSK	RVRIAPKVL	AEEGIAPLSS	420
	AGPGKEEKLL	FGEGFSPLLP	VOTIKEEIQ	PGEEMPHLAR	PIKVESPPLE	EWSPAPSFK	480
	EESHSWEDS	SQSPTPRPKK	SYSGLRSPTR	CVSEMLVIQH	RERRERSRSR	RKQHLPLPCV	540
	DEPELLFSEG	PSTRWAAEL	FPADSSDPA	SQLSYSQEVG	GPFKTPIKET	LPISSTPSKS	600
15	VLPRTPESWR	LTPPAKVGGL	DFSPVQTFQG	ASDPLDPLG	LMDLSTPLQ	SAPPLESPQR	660
	LLSSEPLDLI	SVFPGNSPSS	DIDVPKPGSP	EPQVSGLAAN	RSLTEGLVLD	TMNDSLKIL	720
	LDISPPGLDE	DPLGPDNINW	SQFIPELQ				

Seq ID NO: 72 DNA sequence
Nucleic Acid Accession #: U74612.1
Coding sequence: 178-2583

	1	11	21	31	41	51	
25	GGCAGGAGGG	GGACCCGGCC	GGTCCGGCGC	GAGCCCCCGT	CCGGGGCCCT	GGCTCGGCCC	60
	CCAGGTGTGA	GGAGCCCGGA	GCCCGCCTTC	GGAGCTACGG	CCTAACGGCG	GCGGCGACTG	120
	CAGTCTGGAG	GGTCCACACT	TGTGATTCTC	AATGGAGAGT	GAAACCGCAG	ATTCTAATG	180
	AAAACTAGCC	CCCGTCGGCC	ACTGATTCTC	AAAAGACGGA	GGCTGCCCCC	TCCTGTTCAA	240
	AATGCCCCAA	GTGAAACATC	AGAGGAGGAA	CCTAAGAGAT	CCCTGCCCCA	ACAGGAGTCT	300
30	AATCAAGCAG	AGGCGTCCAA	GGAAGTGGCA	GAGTCCAACT	CTTGCAAGTT	TCCAGCTGGG	360
	ATCAAGATTA	TTAACACACC	CACCATGCC	AACACGCAAG	TAGTGGCCAT	CCCCAACAA	420
	GCTAATATTC	ACAGCATCAT	CACAGCACTG	ACTGCCAAGG	GAAAGAGAG	TGGCAGTAGT	480
	GGGCCCAACA	AATTCATCCT	CATCAGCTGT	GGGGGAGCCC	CAACTCAGCC	TCCAGGACTC	540
	CGGCCTCAAA	CCCAAAACAG	CTATGATGCC	AAAAGGACAG	AAGTGACCTT	GGAGACCTTG	600
35	GGACCAAAAC	CTGCAGCTAG	GGATGTGAAT	CTTCTAGAC	CACCTGGAGC	CCTTTGCGAG	660
	CAGAAACGGG	AGACCTGTGC	AGATGGTGAG	GCAGCAGGCT	GCATATCAA	CAATAGCCTA	720
	TCCAACATCC	AGTGGCTTCG	AAAGATGAGT	TCTGATGGAC	TGGGCTCCCG	CAGCATCAAG	780
	CAAGAGATGG	AGGAAAAGGA	GAATTGTAC	CTGGAGCAGC	GACAGGTTAA	GGTTGAGGAG	840
	CCTTCGAGAC	CATCAGCTC	CTGGCAGAAC	TCTGTGCTG	AGCGGCCACC	CTACTCTTAC	900
40	ATGGCCATGA	TACAAATCGC	CATCAACAGC	ACTGAGAGGA	AGCGCATGAC	TTTGAAGAGC	960
	ATCTATACGT	GGATTGAGGA	CCACTTTCCT	TACTTTAAGC	ACATTGCCAA	GCCAGGCTGG	1020
	AAGAACTCCA	TCCGCCACAA	CCTTCCCTG	CACGACATGT	TTGTCCGGGA	GACGCTCTGC	1080
	AATGGCAAGG	TCTCCTTCTG	GACCATTAC	CCCAGTGCCA	ACCGCTACTT	GACATTGGAC	1140
	CAGGTGTTTA	AGCCACTGGA	CCAGGGTCT	CCACAATTGC	CCGAGCACTT	GGAATCAGAG	1200
45	CAGAAACGAC	CGAATCCAGA	GCTCCGCCGG	AACATGACCA	TCAAACCGA	ACTCCCCCTG	1260
	GGCGCACGGC	GGAAGATGAA	GCCACTGCTA	CCACGGGTCA	GCTCATACCT	GGTACCTATC	1320
	CAGTTCGCCG	TGAACCAATC	ACTGGTGTG	CAGCCCTCGG	TGAAGGTGCC	ATTGCCCTTG	1380
	GCGGCTTCCC	TCATGAGCTC	AGAGCTTGCC	CGCCATAGCA	AGCGAGTCCG	CATTGCCCCC	1440
	AAGGTTTTTG	GGGAACAGGT	GGTGTGTTG	TACATGAGTA	AGTTCCTTAG	TGGCGATCTG	1500
50	CGAGATTTTG	GTACACCCAT	CACCGACTTG	TTTAATTTTA	TCTTCTTTTG	TTTATCAGTG	1560
	CTGCTAGCTG	AGGAGGGGAT	AGCTCCTCTT	TCTTCTGAG	GACCAAGGAA	AGAGGAGAAA	1620
	CTCCTGTTTG	GAGAAGGGTT	TTCTCCTTTG	CTTCCAGTTC	AGACTATCAA	GGAGGAAGAA	1680
	ATCCAGCCTG	GGGAGGAAAT	GCCACACTTA	GCGAGACCCA	TCAAAGTGGA	GAGCCCTCCC	1740
	TTGGAAGAGT	GGCCCTCCCC	GGCCCCATCT	TTCAAAGAGG	AATCATCTCA	CTCCTGGGAG	1800
55	GATTGCTCCC	AATCTCCACC	CCCAAGACCC	AAGAAGTCTT	ACAGTGGGCT	TAGGTCCCCA	1860
	ACCCGGTGTG	TCTCGGAAT	GCTTGTGATT	CAACACAGGG	AGAGGAGGGA	GAGGAGCCGG	1920
	TCTCGGAGGA	AACAGCATCT	ACTGCCCTCC	TGTGTGGATG	AGCCGGAGCT	GCTCTTCTCA	1980
	GAGGGGCCCA	GTACTTCCCG	CTGGGCCGCA	GAGCTCCCGT	TCCAGCAGAG	CTCCTCTGAC	2040
	CCTGCCCTCC	AGCTCAGCTA	CTCCCAAGAA	GTGGGAGGAC	CTTTAAGAC	ACCCATTAA	2100
60	GAAACGCTGC	CCATCTCCTC	CACCCGAGC	AAATCTGTCC	TCCCAAGAAC	CCCTGAATCC	2160
	TGGAGGCTCA	CGACCCACAG	CAAAGTAGGG	GGACTGGATT	TCAGCCCACT	ACAAACCTCC	2220
	CAGGGTGCC	CTGACCCCTT	GCCTGACCCC	CTGGGGCTGA	TGGATCTCAG	CACCACTCCC	2280
	TTGCAAGATG	CTCCCCCTCT	TGAATCACCG	CAAAGGCTCC	TCAGTTTCAG	ACCCCTAGAC	2340
	CTCATCTCCG	TCCCTTTTGG	CAACTCTTCT	CCCTCAGATA	TAGACGTCCC	CAAGCCAGGC	2400
65	TCCCCGGAGC	CACAGGTTTC	TGGCCTTGCA	GCCATCGTT	CTCTGACAGA	AGGCCCTGGT	2460
	CTGGACACAA	TGAATGACAG	CCTCAGCAAG	ATCCTGCTGG	ACATCAGCTT	TCTTGGCCTG	2520
	GACGAGGACC	CAGTGGGCCC	TGACAAATC	AACTGGTCCC	AGTTTATTCC	TGAGCTACAG	2580
	TAGAGCCCTG	CCCTTGGCCC	TGTGCTCAAG	CTGTCCACCA	TCCGGGGCAC	TCCAAGGCTC	2640
	AGTGACCCCC	AAGCCTCTGA	GTGAGGACAG	CAGGCAGGGA	CTGTTCTGCT	CCTCATAGCT	2700
70	CCCTGCTGCC	TGATTATGCA	AAAGTAGCAG	TCACACCCTA	GCCACTGCTG	GGACCTTGTG	2760
	TTCCCCAAGA	GTATCTGATT	CCTCTGCTGT	CCCTGCCAGG	AGCTGAAGGG	TGGGAACAAC	2820
	AAAGGCAATG	GTGAAAAGAG	ATTAGGAACC	CCCCAGCCTG	TTTCCATTCT	CTGCCAGACA	2880
	GTCTCTTATG	TTCCCTGATC	TTTGACGGGT	GGTCCGTGTA	AATAGTATAA	ATTCTCCAAA	2940
	TTATCCTCTA	ATTATAAATG	TAAGCTTATT	TCCTTAGATC	ATTATCCAGA	GACTGCCAGA	3000
75	AGGTGGGTAG	GATGACCTGG	GGTTTCAATT	GACTTCTGTT	CCTTGGCTTT	AGTTTGTATA	3060
	GAAGGGAAGA	CCTGCAGTGC	ACGGTTTCTT	CCAGGCTGAG	GTACCTGGAT	CTTGGGTTCT	3120
	TCACTGACAG	GACCCAGACA	AGTGGATCTG	CTTGCCAGAG	TCCTTTTTCG	CCCTCCCTGC	3180
	CACCTCCCGG	TGTTTCCAAG	TCAGCTTTCC	TGCAAGAAGA	AATCCTGGTT	AAAAAGTCT	3240
	TTTGATTTGG	GTCAGGAGTT	GAATTTGGGG	TGGGAGGATG	GATGCAACTG	AAGCAGAGTG	3300
80	TGGGTGCCCA	GATGTGCGCT	ATTAGATGTT	TCTCTGTATA	TGTCCCAAT	CATACCAAGG	3360
	AGACTGGCAT	TGACGAGAAC	TCAGGTGGAG	GCTTGAGAAG	GCCGAAAGGG	CCCCTGACCT	3420
	GCCTGGCTTC	CTTAGCTTGC	CCCTCAGCTT	TGCAAGAGAC	CACCTTAGGC	CCCAGCTGAC	3480
	CGCATGGGTG	TGAGCCAGCT	TGAGAACACT	AACTACTCAA	TAAAGCGGAA	GGTGACACAA	3540
85	AAAAAAAAAA	AAAAA					

Seq ID NO: 73 Protein sequence:
Protein Accession #: AAC51128.1

1 11 21 31 41 51
 5 MKTSPRRPLI LKRRRLPLPV QNAPSETSEE EFKRSPAQQE SNQAEASKEV AESNSCKPPA 60
 GIKIINHPTM ENTQVVAIPN NANIHSIITA LTAKGKESGS SGNPKFILIS CGGAPTQPPG 120
 LRPQTQTSYD AKRTEVTLET LGPKPAARDV NLPRPPGALC EQKRETCADG EAAGCTINNS 180
 LSNIQWLRLM SSDGLGSRSI QMEMEEKENC HLEQRQVKVE EPSRPSASWQ NSVSERPPYS 240
 YMAMIQFALN STERKRMTLK DIYTWIEDHF PYFKHIAKPG WKNSIRHNL LHMDFVRETS 300
 10 ANGKVSFWTI HPSANRYLTL DQVFKPLDPG SFQLPEHLES QQKRPNPRL RNMTIKTEL 360
 LGARRKMKPL LPRVSSYLVP IQFPVNQSLV LQPSVKVPLP LAASLMSSEL ARHSKRVRIA 420
 PKVPGEQVVF GYMSKFFSGD LRDFGTPTS LFNPIFLCLS VLLAEEGIAP LSSAGPGKEE 480
 KLLFGEQFSP LLFVQTIKEE EIQFGEEMPH LARPIKVESP PLEEWSPAP SPKEESSHSW 540
 EDSSQSPTFR FKKSYSGLRS PTRCVSEMLV IQHRRERS RSRRKQHLLP PCVDEPELLF 600
 15 SEGSPSTRWA AELFFPADSS DPASQLSYSQ EVGGPFKTP I KETLPISSSTP SKSVLPRTP 660
 SWRLTPPAKV GGLDFSPVQT SQGASDPLPD PLGLMDLSTT PLQSAPPLES PQRLLSSSEPL 720
 DLISVFFGNS SPSPIDVPKP GSPEPQVSGL AANRSLTEGL VLDTMNDSL KILLDISPPG 780
 LDEDFLGPEN INWSQFIPEL Q

20 Seq ID NO: 74 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 111-416

1 11 21 31 41 51
 25 GGGAAGAGCC AGGCTGAGCC TTATAAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
 TCATCCTTCT ACTCGTGACG CTCCCAGCT CTGGCTTTT GAAAGCAAAG ATGAGCAACA 120
 CTCGAAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCAGACGTG 180
 ATGACAAGAT TGAGAAGCCA AGCCTGCTGA CGATGATGAA GGAGAACTTC CCCAACTTCC 240
 30 TTAGTGCCTG TGACAAAAG GGCACAAAT ACCTCGCCGA TGTCTTTGAG AAAAAGGACA 300
 AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTTGCTGGGA GACATAGCCA 360
 CAGACTACCA CAAGCAGAGC CATGGAGCAG CGCCCTGTTC CGGGGGCAGC CAGTGACCCA 420
 GCCCCACCAA TGGGCCTCCA GAGACCCAG GAACAATAAA ATGTCTTCTC CCACCAGA

35 Seq ID NO: 75 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 40 MSNTQAERSI IGMIDMFHYK TRRDDKIEKP SLLTMMKENF PNFLSACDKK GTNYLADVFE 60
 KDKKNEDKKI DFSEFLSLLG DIAADYHKQS HGAAPCSGGS Q

45 Seq ID NO: 76 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 111-416

1 11 21 31 41 51
 50 GGGAAGAGCC AGGCTGAGCC TTATAAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
 TCATCCTTCT ACTCGTGACA CTCCCAGTT CTGGCTTTT GAAAGCAAAG ATGAGCAACA 120
 CTCGAAGCTGA GAGTCCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCGACGTG 180
 ATGGCAAGAT TGAGAAGCCA AGCCTGCTGA CGATGATGAA GGAGAACTTC CCCAATTTCC 240
 TCAGTGCCTG TGACAAAAG GGCATACATT ACCTCGCCAC TGTCTTTGAG AAAAAGGACA 300
 55 AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTTGCTGGGA GACATAGCCG 360
 CAGACTACCA CAAGCAGAGC CATGGAGCGG CGCCCTGTTC TGGGGGAAGC CAGTGATCCA 420
 GCCCCACCAA GGGCCTCCA GAGACCCAG GAACAATAAG TGTCTCTCC CACCAGA

60 Seq ID NO: 77 Protein sequence:
 Protein Accession #: XP_048124.1

1 11 21 31 41 51
 65 MSNTQAERSI IGMIDMFHYK TGRDGKIEKP SLLTMMKENF PNFLSACDKK GIHYLATVFE 60
 KDKKNEDKKI DFSEFLSLLG DIAADYHKQS HGAAPCSGGS Q

70 Seq ID NO: 78 DNA sequence
 Nucleic Acid Accession #: Z73678.1
 Coding sequence: 253-2433

1 11 21 31 41 51
 75 GGGGTGGTGC AGGGCAGGGG TGGTATATCC TGTCTGACGG AGGGCGGGCC TCGCCAGTGC 60
 CAGAGAGGGA CGAACCAGGG TGAAGCGCC AGGAGCAGCT GCAGGGAGCC CTCACGCGGA 120
 CCTCGCAGTC TATGGCCGTA GGGAGCGGCT GAGAGCGAGA AGAGCAGCT CCTGCCCGCC 180
 CGCTGCACCG CACCTCGCCT CGCTCTCTG CTCTCTTAGG CCGCGGCCG GCGCCACCG 240
 CCTCCCGCCA CCATGAACCA CTGCGCGCTC AAGACCGCCT TGGCGTACGA ATGCTTCCAG 300
 GACCAGGACA ACTCCAGTT GCGTTTGGCG TCGGACCAA AGATGAAAAC AGGCACGTCT 360
 80 GGCAGGCAGC GCGTGCAGGA GCAGGTGATG ATGACCGTCA AGCGGCAGAA GTCCAAGTCT 420
 TCCCAGTCGT CCACCTGAG CCACTCCAAT CGAGGTTCCA TGTATGATGG CTTGGCTGAC 480
 AATTACAAC ATGGGACCAC CAGCAGGAGC AGCTACTACT CCAAGTTCCA GGCAGGGAAT 540
 GGCTCATGGG GATATCCGAT CTACAATGGA ACCCTCAAGC GGGAGCCTGA CAACAGGCGC 600
 TTAGCTCTCT ACAGCCAGT GGAGAACTGG AGCCGCGACT ACCCCCGGG CAGCTGTAAC 660
 85 ACCACCGCG CAGGCAGCGA CATCTGCTTC ATGCAGAAA TCAAGCGCAG CCGCAGTGAG 720
 CCGACCTCT CTTGTGACCC ACGGGGCACC CTGCGCAAGG GCACGCTGGG CAGCAAGGCG 780
 CAGAAGACCA CCTCAGACCG CTACAGCTT TACAGCACT GCAGTGGTCA GAAGGCCATA 840
 AAGAAGTGCC CTGTGCGCCC GCGCTCTTGT GCCTCAAGC AGGACCTGT GTATATCCG 900

	CCCATCTCCT	GCAACAAGGA	CCTGTCTCTT	GGCCACTCTA	GGGCCAGCTC	CAAGATCTGC	960
	AGTGAGGACA	TCGAGTGCAG	TGGGCTGACC	ATCCCCAAGG	CTGTGCAGTA	CCTGAGCTCC	1020
	CAGGATGAGA	AGTACCAAGC	CATTGGGGCC	TATTACATCC	AGCATACCTG	CTTCCAGGAT	1080
5	GAATCTGCCA	AGCAACAGGT	CTATCAGCTG	GGAGGCATCT	GCAAGCTGGT	GGACCTCCTC	1140
	CGCAGCCCCA	ACCAGAACGT	CCAGCAGGCC	CGCGCAGGGG	CCCTCGCGAA	CCTGGTGTTC	1200
	AGGAGCACC	CCAACAAGCT	GGAGACCCGG	AGGCAGAAATG	GGATCCGCGA	GGCAGTCAGC	1260
	CTCCTGAGGA	GAACCGGGAA	CGCCGAGATC	CAGAAGCAGC	TGACTGGGCT	GCTCTGGAAC	1320
	CTGTCTTCCA	CTGACGAGCT	GAAGGAGGAA	CTCATTGCGG	ACGCCCTGCC	TGTTCTGGCC	1380
10	GACCGCGTCA	TCATTCCCTT	CTCTGGCTGG	TGCGATGGCA	ATAGCAACAT	GTCCCGGGAA	1440
	GTGGTGGACC	CTGAGGTCTT	CTTCAATGCC	ACAGGCTGCT	TGAGGAACCT	GAGCTCGGCC	1500
	GATGCAGGCC	GCCAGACCAT	GCGTAACATC	TCAGGGCTCA	TTGATTCCCT	CATGGCCTAT	1560
	GTCCAGAACT	GTGTAGCGGC	CAGCCGCTGT	GACGACAAAT	CTGTGGAAAA	CTGCATGTGT	1620
	GTCTCTGCAC	ACCTCTCCTA	CCGCCCTGGAC	GCCGAGGTGC	CCACCCGCTA	CCGCCAGCTG	1680
15	GAGTATAACG	CCGCTCAAGC	CTACACCGAG	AAGTCCCTCA	CTGGCTGCTT	CAGCAACAAG	1740
	AGCGACAAGA	TGATGAACAA	CAACTATGAC	TGCCCCCTGC	CTGAGGAAGA	GACCAACCCC	1800
	AAGGGCAGCG	GCTGGTTGTA	CCATTCAAGT	GCCATCCGCA	CCTACCTGAA	CCTCATGGGC	1860
	AAGAGCAAGA	AAGATGCTAC	CCTGGAGGCC	TGTGCTGGTG	CCCTGCAGAA	CCTGACAGCC	1920
	AGCAAGGGCG	TGATGTCCAG	TGGCATGAGC	CAGTTGATTT	GGCTGAAGGA	AAAGGGCCTG	1980
20	CCACAAATTG	CCGATCTCCT	CCAACTCTGG	AACTCTGATG	TGGTGGGCTC	CGGAGCCTCT	2040
	CTCCTGAGCA	ACATGTCCCG	CCACCCCTCG	CTGCACAGAG	TGATGGGGAA	CCAGGTGTTC	2100
	CCGGAGGTGA	CCAGGCTCCT	CACCAGCCAC	ACTGGCAATA	CCAGCAATC	CGAAGACATC	2160
	TTGTCTCGGG	CCTGCTACAC	TGTGAGGAAC	CTGATGGCCT	CGCAGCCACA	ACTGGCCAA	2220
	CAGTACTTCT	CCAGCAGCAT	GCTCAACAAC	ATCATCAACC	TGTGCCGAAG	CAGTGCCTCA	2280
25	CCCAAGGGCG	CCGAGAGCTG	CCGGCTTCTC	CTGTCTGACA	TGTGGTCCAG	CAAGGAACCT	2340
	CAGGGTGTCC	TCAGACAGCA	AGGTTTCGAT	AGGAACATGC	TGGGAACCTT	AGCTGGGGCC	2400
	AACAGCCTCA	GGAACTTCAC	CTCCCGATT	TAAGAAGAGA	CTGTCCAAGC	AAGTTAGGCT	2460
	TGCAGGAAGA	TATGACCCAG	CTGAGAAGCC	CTCAGGCCTC	GCTGGATGGG	GTTCCTGTTC	2520
	CATCCTGTGC	AGTATTTTGG	AAAGTTTACA	AGAAACTGAG	AAGAAACCTA	AAAACCTGTG	2580
30	ATAGTGGAAA	GATTTTATGA	TTTTTTTTTT	CCTTGGGGAA	ACTGGCAGGC	AATGGGGGTT	2640
	AGGGAGGTTG	GGGCGGGGGG	GGCTTTCTTG	AGTTAAAGGG	GCTTATATGT	GATGTCAATA	2700
	TTTCTCTCTC	TGAGAAATGG	TATATATATG	TGTCTAATGT	AAGTGTGTGC	ATGCATGTGC	2760
	CGGTGCATGT	GTGTGTGTGT	GAGTGTCTTA	AAGCATAACC	ACAAACTGCA	AAAAGCTAGG	2820
	TAAGCTATT	TGTTGCAGCT	CATAAGGTGG	TGAAAAGGAC	TCTCCTGTGT	TTCTTACTCA	2880
35	TAGGCAAGGA	CAACATGTGC	TTTTTGGTGA	GCTGCTCATA	ATTCCTGAAA	TGTGTGGTGC	2940
	CAGGGCAAGG	GGGCCATCAC	TGCAGTCAGG	CCCTCAGAGG	AGTCTCTGAG	GCTTCTCTACC	3000
	AGTGTCTCC	AAGGGTGCAG	GAGTAACCTG	GGCTGGGCCA	GCCTCCCCCT	TTACAAGGCT	3060
	GCCTTCCACG	AAGGGAGGTC	TGGTGTATCT	CATGGGAGAA	TCTGGGGTGT	CTGTAGTGTG	3120
	ACCCCTCCAG	CAGCGCCACA	AGGACTGAGG	TTGGGTAGGT	GTGAGGTTC	AGAGGACAGC	3180
40	AGGACACTCT	CGCTACTTTT	GCCAAATGAG	GCCTGCTCAG	AGGAGTAGGA	GCTGAAAGAT	3240
	GGTGCTCTCA	ACCTCTCTTG	GCTGTGTGCC	CATCAGAGCA	GGCTCAGCCT	GCAAGGCCCC	3300
	TGCACTCAGA	GGTCTTGTA	TCTACTTGTT	GCAGGAGAAA	GAAGGTAAAA	AATGATTTT	3360
	TTAAGAAAAG	CTATTTTATT	GCAGCTCTTT	CCCAAGAGCT	GTCTCTGGAA	TGGCTGGTCT	3420
	TCATATTTCC	AGTGGAGAGG	GGAAACAGTG	GGGCTGGGCA	TATACCTATT	CCGGCTTCTA	3480
45	GTGGGATGGA	TTGGGGTATG	AGAAATTAAC	CAGGAAGATG	TTTCCACCAA	GCCTGCTGTG	3540
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	CCATGCCCCA	CTTCCCTGGA	CCCCAGCTGT	CTTGCTTCCA	CTCTGTGAAA	CCCACAGGGG	3720
50	ATGTGATAAA	CAGGGCTATT	AGGGGTATCA	GCCAGTTCGA	GCCCCCAGAC	TCTGTGCACT	3780
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	TCTACTCTCA	TGCTAGCATT	GCTGGTGTTA	GAGAGGAATT	AACCTTCTGG	TCTGTGCCCT	3960
	TCTCTAGAAG	AATATAAGAT	GCTCCTCCTC	CTCACCCCTT	CTCAGCCTCC	TCCCAAGTCT	4020
	TCTCTCTCTG	CACCACCCCT	GAGTCCAAAC	CCACCTCTTG	CCCCCAGATT	CAGGCTGGAA	4080
55	AACACTGATG	TGGACTCAGT	ATGACCAACT	AGATGGGGGA	AGCCAGACAT	GTGAGGACGC	4140
	TGTCTCTCGA	GAGGTGTCCC	CGGCTGTTAG	CCAGCTGTGC	TGTGGTGTCT	TGGGTCTGTG	4200
	ATACCTCTCC	TGCTTCTCTG	TCACACTGGG	AGGCCCACTC	CTGGCTCAGC	TCTCCCTCTC	4260
	AGGGACCCAC	GTGGGAGCCT	GGATCCCTGG	ACTGTCTCTG	GCATAGGTTT	CAGGGGCTCT	4320
	CTTTGTGTGC	ATCAGAACCC	AGAGGAATTG	TTCTCTTAAA	AAATACGTAT	GGCATAACCA	4380
60	TCTGTGCGGG	GCAGTGTCTT	AAGCACTTAG	ACTACATCAG	GGAAGAACAC	AGACCACATC	4440
	CCCGTCTCTA	TGCGGCTTAT	GTCTTCTGGA	GGAAGTGGGA	GACACAAGTC	CTTGGCTTTA	4500
	GGGCTCCCCC	GGCTGGGGGC	TGTGAGTCTC	GGTCAGGGCG	GGAGGGGAAA	TGCACCGCTG	4560
	CATGTGAACC	TTACCAGCCC	AGGCGGATGC	CCCTTCCCCC	TAGCACTACC	CTGGCCTCCT	4620
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65	CCCTGCCCTG	GGAAACCAGC	AGCCTTCCAG	ACCTCAGGGG	CTGAGGCAGA	CTATTAGGGC	4740
	AGGGCTGACT	TGGTGAACAC	TGCCCATTCC	CTCTCAGGCC	AGCTCAGGTC	ACCCGGGCCCT	4800
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70	TGAGGAAGGA	CACAGACTCT	TCTGCACTGG	GGACCACTCT	AGCAGCCCTG	ACTCCACACT	5040
	GCTCATGGCC	ACCAGCCACC	TCTGCACTGG	GGACCACTCT	AGCAGCCCTG	ACTCCACACT	5100
	CTCCTCTGGG	ACCCAAGAGG	CAGTGTGTCT	GTCTGCGTGT	CCACCTTGGA	ATCTGGCTGA	5160
	ACTGGCTGGG	AGGACCAAGA	CTGCGGCTGG	GGTGGGCAGG	GAAGGGGAAG	CGGGGGCTGC	5220
	TGTGAGGAT	CTTGGAGCTT	CCCTGTAGCC	CACCTTCCCC	TTGCTTCATG	TTTGTAGAGG	5280
75	AACCTTGTGC	CGGCCAGGCC	CAGTTTCTCT	GTGTGATACA	CTAATGTATT	TGCTTTTTTT	5340
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Seq ID NO: 79 Protein sequence:
Protein Accession #: CAA98022.1

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	SQMNWSRHHY	FRGSCNTTGA	GSDFCFMOKI	KASRSEPDLY	CDPRGTLRKG	TLGSKGQKTT	180
85	QKNRYSFYSTC	SGQKAIKKCP	VRPPSCASKQ	DPVYIPIPI	NKDLSPFGHSR	ASSKICSEDI	240
	ECSGLTIPKA	QVYLSQDEK	YQAIGAYYIQ	HTCFQDESAK	QVYQLGGGIC	KLVDLLRSPN	300
	QNVQQAAGAA	LRNLVFRSTT	NKLETRRQNG	IREAVSLRR	TGNAEIQKQL	TGLLWNLST	360

WO 02/086443

PCT/US02/12476

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 QTMRYNSGLI DSLMAYVQNC VAASRCDDKS VENCMLVHN LSYRLDAEVP TRYRQLEYNA 480
 RNAYTEKSSST GCFPNKSDKM MNMNYDCPLP EBETNPFGSG WLYHSDAIRT YLNLMGKSKK 540
 DATLEACAGA LQNLTAASKGL MSSGMSQLIG LKEKGLPQIA RLQSGNSDV VRSGASLLSN 600
 MSRHLPLHRV MGNQVFPEVT RLLTSHTGNT SNSEDILSSA CYTVRNLMAS QPQLAKQYFS 660
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Seq ID NO: 80 DNA sequence
 Nucleic Acid Accession #: NM_006516.1
 Coding sequence: 180-1658

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 TGCTGATCCT GGGCGGCTTC ATCATCGGTG TGTACTGCGG CCTGACCA CA GGCTTCGTGC 600
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 TACCTTGGAT GTCTATCTG AGCATCGTGG CCATCTTTGG CTTTGTGGCC TTCTTTGAAG 1320
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Seq ID NO: 81 Protein sequence:
 Protein Accession #: NP_006507.1

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 GNKDLWPIIL SIIFIPALLQ CIVLPFCPEP PRFLLINRNE ENRAKSVLKK LRGTADVTHD 240
 LQEMKESBRQ MMREKKTIL ELFRSPAYRQ PILIAVVLQL SQQLSGINAV PYYSTSIKFE 300
 AGVQQPVYAT IGSIVNTAF TVVSLFVVER AGRRTLHLIG LAGMAGCAIL MTIALALLEQ 360
 LPWMSYLSIV AIFGVPAPFE VGGPIPWFI VAEFLFSQGR PAALVAGFS NWTNFIIVGM 420
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 GCCCATGCCC TTCTTTTACC TCAAGTGTG TAAAAATGCG TACTGCAATT TAGAGGGGCC 420
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 GCTGTGGCTG GCCATCTCC TGCTGCTGSC CTCATTGCA GCCGGCTCA GCCTGTCTTG 540
 AGCCACGGGA CTGCCACAGA CTGAGCCTTC CGGAGCATGG ACTCGCTCCA GACCGTTGTC 600
 ACCTGTGCTA TTAACTTGT TTCTGTTGA TTACCTCTTG GTTTGACTTC CCAGGGTCTT 660
 GGGATGGGAG AGTGGGGATC AGGTGCAGTT GGCTCTTAAC CCTCAAGGGT TCCTTAACTC 720
 ACATTACAGG GAAGTCCAGA TCTCCTGAGT AGTGATTTTG GTGACAAGTT TTTCTCTTG 780
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 CCTCTGAGGG CTTCAGTATT GATGGGGAGG GAGGCCCTAAG TACCCTCAT GGAGAGTATG 900
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 GGGTGAAGAC ATCCCTGGAG TGAAGGACTC CTCAGCATGG GGGGCAGTGG GGCACACGTT 1020
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 CTACCAGATT CCAGGAGGCA GAAGATAACT AATTGTGTTG AAGAACTTA GACTTCAACC 1140
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 ACTTAGGCCA AGTAGAGAGC ATCAGGGTAA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC 1260
 CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCACCC AAAAAAAT ACAAGGGGAC 1320
 TTCAAAAGTT CAGCAAAAAA AAAAAAATA AAAAAAATA AAAAAAATA AAA

Seq ID NO: 83 Protein sequence:

Protein Accession #: AAH01291

1 11 21 31 41 51
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 KWTEPYCVIA AVKIPPRFFM VAKQCSAGCA AMERPKPEEK RFLLEPMMPF FYLKCKKIRY 120
 CNLEGPPIINS SVFKEYAGSM GESCGGLWLA ILLLLASIAA GLSL

Seq ID NO: 84 DNA sequence

Nucleic Acid Accession #: NM_022893.1

Coding sequence: 229-2726

1 11 21 31 41 51
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	GGGGAACCTG	ATTTAGGCT	TCCATTGTCT	TGGTGGTGT	ACAAGACTTG	TTATCCATTT	4800
	AAAAATGGTA	GTGGAAATTC	TATGCTTGG	ATACACACCG	CTCTTCAGGT	TGTAAAAAAA	4860
	AAAAACATAC	ATTGGGAAAA	GGTTTAAGAT	TATATAGTAC	TTAAATATAG	GAATAATGCAC	4920
	ACTCATGTTG	ATTCTTATGC	TAAATACAT	TTATGGTCTT	TTTTCTGTAT	TTCTAGAAATG	4980
35	GTATTTGAAT	TAAATGTCTA	TCTAGTGTTA	GGCACTATAG	TATTTATATT	GAAGCTTGTA	5040
	TTTTTAACCTG	TGCTTGTCTC	TCTTAAAGG	TATCAATGTA	CCTTTTTGG	TAGTGGAAAA	5100
	AAAAAAGACA	GGCTGCCACA	GATATTTTT	TTAATTTGGC	AGGATAATAT	AGTGCAAAAT	5160
	ATTTGTATGC	TTCAAAAAA	AAAAAAGAG	AGAAACAAAA	AAGTGTGACA	TTACAGATGA	5220
	GAAGCCATAT	AATGGCGGTT	TGGGGGAGCC	TGCTAGAATG	TCACATGGAT	GGCTGTGATA	5280
40	GGGGTTGTAC	ATATCTTTTT	TTGTTCTTTT	TTCTGTCTGC	CATATGTAT	GCAGTACTGC	5340
	AAGCTAATAA	OGTTGGTTTG	TTATGTAGTG	TGCTTTTGT	CCCTTTCTCT	CTATCACCTT	5400
	ACATTCACAG	CACTTACCTT	CATATGCAGT	AAAAGAAAGA	AAGAAAAAAA	AAGGAAAAAA	5460
	AAAAAAAAC	CAATGTTTTG	CAGTTTTTTT	CATTGCCAAA	AACTAAATGG	TGCTTTATAT	5520
	TTAGATTGGA	AAGAATTTCA	TATGCAAGC	ATATTAAAGA	GAAAGCCCGC	TTTACTCAAT	5580
45	ACTTTTTTGT	AATGTGCAAT	GCAGAAATAT	TTGTTATTGG	CCTTTTCTAT	TCCTGTAAATG	5640
	AAAGCTGTTT	GTGTAACCTT	GAAATTTTAT	CTTTTACTAT	GGGAGTCACT	ATTTATTATT	5700
	GCTTATGTGC	CCTGTTTCAA	ACAGAGGCAC	TTAATTTGAT	CTTTTATTTT	TCTTTGTTTT	5760
	TATTTTTTTT	TTTATTAGTA	TGACCAAAAG	TCATTACAAC	CTGGCTTTTT	ATTGTATTGT	5820
	TTTCTGGTCT	TTGTTAAGTT	CTATTGGAAG	AACCACTGTC	TGTGTTTTTT	TGGCAGTTGT	5880
50	CTGCATTAA	CTGTTACATC	ACCCATTTTG	TCCCTTTATT	GAAAAAATAA	AAAAAATTAA	5940

Seq ID NO: 85 Protein sequence:
Protein Accession #: NP_075044.1

55	1	11	21	31	41	51	
	MSRRKQGRKP	HLKREFSPE	PLEAILTDEE	PDHGFPLGAP	GDHDLTTCGQ	QMNFFPLGDI	60
	LIFIEHKRKQ	CNGSLCLEKA	VDKPPSPSP	EMKKASNPVE	VGIQVTPEDD	DCLSTSSRR	120
60	CPKQEHIAAD	LLHWRGLSSP	RSAGHALIPT	PGMSAEYAPQ	GICKDEPSSY	TCTTCKQPFT	180
	SAWFLQHAQ	NTHGLRIYLE	SEHGSPLTFR	VGIPSGLGAE	CPSPPLPHGI	HIADNNPFNL	240
	LRIPGSVSR	ASGLAEGRFP	PTPPLFSPPP	RHLLDPHRIE	RLGAEMALA	THPSAFDRV	300
	LRLNFMAMEP	PAMDFSRRLR	ELAGNTSSFP	LSPGRPSFMQ	RLLPFPQPGS	KPPFLATPPL	360
	PPLQSAPPPS	QPPVKSKECE	FCGKTFKFQS	NLVVHRRSHT	GEKPYKCNLC	DHACTQASKL	420
65	KRHKMTHMHK	SSPMTVKSD	GLSTASSPEP	GTSDLVGSAS	SALKSVVAKF	KSENDPNLIP	480
	ENGDEEEED	DEEBEED	EEELTESER	VDYGFGLSLE	AARHHENSSR	GAVVGVDDES	540
	RALPDVMQGM	VLSSMQHFSE	AFHQVLGEKH	KRHLABAEG	HRDTCDEDSV	AGESDRIDDG	600
	TVNGRGCSFG	ESASGGLSKK	LLGLSPSSLS	PFSKRIKLEK	EPDLPPATMP	NTENVYSQWL	660
	AGYAAARQLK	DPPLSFQDSR	QSPFSSSEH	SENGSLRPS	TPPGELDGGI	SGRSVTGSGG	720
70	STPHISGPCT	GRPSSKEGRR	SDTCEYCGKV	PKNCSNLTVM	RRSHTGERPY	KCELCNYACA	780
	QSSKLTRHMK	THQVGKDVY	KCEICKMPFS	VYSTLEKHKM	KWHSRVLN	DIKTE	

Seq ID NO: 86 DNA sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53-1576

75	1	11	21	31	41	51	
80	GCTCGCTGGG	CCGCGGCTCC	CGGGTGTCCC	AGGCCCGGCC	GGTGCGCAGA	GCATGGCGGG	60
	TGCGGGCCCG	AAGCGGCGCG	CGCTAGCGGC	GCCGGCGGCC	GAGGAGAAGG	AAGAGGCGCG	120
	GGAGAAGATG	CTGGCGCGCA	AGAGCGCGGA	CGGCTCGGCG	CGGCGAGGCG	AGGGCGAGGG	180
	CGTGACCTCTG	CAGCGGAACA	TCACGCTGCT	CAACGCGGCTG	GCCATCATCG	TGGGGACCAT	240
	TATCGGCTCG	GGCATCTTCG	TGACGCCAC	GGCGTGCCTC	AAGGAGGCAG	GCTCGCGCGG	300
85	GCTGGCGCTG	GTGGTGTGGG	CGCGTGGCG	CGTCTTCTCC	ATCGTGGGCG	CGCTCTGCTA	360
	CGCGGAGCTC	GGCACCACCA	TCTCCAAATC	GGCGGCGGAC	TACGCTACAC	TGCTGGAGGT	420
	CTACGGCTCG	CTCGCGCTCT	TCTCAAGCT	CTGGATCGAG	CTGCTCATCA	TCCGCGCTTC	480
	ATCGCAGTAC	ATCGTGGCCC	TGGTCTTCGC	CACCTACCTG	CTCAAGCCGC	TCTTCCCCAC	540

CTGCCCGGTG CCCGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC 600
 GGCCGTGAAC TGCTACAGCG TGAAGGCCGC CACCCGGGTC CAGGATGCCT TTGCCGCGCG 660
 CAAGCTCCTG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GGAAGGGTGA 720
 TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAAGTGGATG TGGGGAACAT 780
 TGTGCTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGAATTACT TGAATTTCTG 840
 CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTCG GCCATCATCA TCTCCCTGCC 900
 CATCGTGACG CTGGGTGTACG TGCTGACCAA CCTGGCCTAC TTCACCACCC TGTCCACCGA 960
 GCAGATGCTG TCCTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGGCGTCAT 1020
 GTCTCGGTAT ATCCCCGTCT TCCTGGGCGT GTCTGCTTC GGCTCCGTCA ATGGGTCCCT 1080
 GTTCACATCC TCCAGGCTCT TCTTCGTGGG GTCCCGGAA GGCCACCTGC CCTCCATCCT 1140
 CTCATGATC CACCCACAGC TCCTACCCCC CGTGGCGTCC CTCGTGTTCA CGTGTGTGAT 1200
 GACGCTGCTC TACGCTTCT CCAAGGACAT CTTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
 CAACTGGCTC TGGGTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
 TGAGCTTAGG CGGCCCATCA AGGTGAACCT GGCCCTGCCT GTGTTCTTCA TCCTGGCCTG 1380
 CCTCTTCTG ATCGCCGTCT CTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC 1440
 CATCATCTC AGCGGCTGC CGCTCTACTT CTTGGGGTCT TGGTGGAAAA ACAAGCCCAA 1500
 GTGGCTCCTC CAGGGCATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAGGTGGT 1560
 CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

Seq ID NO: 87 Protein sequence:
 Protein Accession #: XP_035292.2

1 11 21 31 41 51
 MAGAGPKRRA LAAPAAEBKE EAREKMLAAK SADGSAPAGE GEGVTILQRNI TLLNGVAIIV 60
 GTIIGSGIFV TPTGLVKEAG SGLALVWMA ACGVFSIVGA LCYAEGLTTI SKSGGDYAYM 120
 LEVYGLSPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL PPTCPVPEEA AKLVACLVL 180
 LLTAVNCYSV KAATRVQDAF AAKLLALAL IILGPFVQIG KGDVSNLDPN FSEFGTKLDV 240
 GNIVLALYSG LFAYGGWNYL NFVTEEMINP YRNPLALIII SLPIVTLVYV LTNLAYPTTL 300
 STEQMLSSAA LAVDFGNHYL GVMWIIIPVF VGLSCFGSVN GSLFTSSRLF FVSGREHGLP 360
 SILSMIHPQL LTPVPSLVFT VMTLLYAFS KDIFSVINFP SPFNWLCVAL AIGMIWLRH 420
 RKPELERPIK VNIALPVFFI LACLFILAVS FWKTFVECGI GPTIILSGLP VYFPGVWKN 480
 KPNLLQGIF STTVLCQKLM QVVPQET

Seq ID NO: 88 DNA sequence
 Nucleic Acid Accession #: NM_005268.1
 Coding sequence: 168-989

1 11 21 31 41 51
 TAAAAAGCAA AAGAAATTCGC GGCCGCGTCG ACACGGGCTT CCCCAGAAAC CTTCCTCCGT 60
 TCTGGATATG AAATTCAGAGC TGCTTGCTGA GTCTATTGCG CGGCTGCTGG GAGCCAGGAG 120
 AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
 TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
 TGTCTCTGGT CTTCATCTTC CGCGTCTGGG TGTACTGGT GACGCGCGAG CGTGTGTGGA 300
 GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGTCTGCT 360
 TTGATGAGTT CTTCCTCTGT TCCCATGTGC GCCTCTGGGG CCTGCAGCTT ATCCTGGTGA 420
 CATGCCCTC ACTGCTCGTG GTCATGCAGG TGGCTACCG GGAGGTTTCA GAGAAGAGGC 480
 ACCGAGAAGC CCAATGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGCG AAGAAGCGGG 540
 GTGGGCTCTG GTGACATAT GTCTGCAGCC TAGTGTCAA GGCGAGCGTG GACATCGCCT 600
 TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCTCTCTGTG GTCAAGTGCC 660
 ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA 720
 TTTTCACCTT CTTCATGGTG GCCACAGCTG CCACTGTCAT CCTGTCTAAC CTCGTGGAGC 780
 TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCCCTGGC AGCAAGGAAA GCTCAAGCCA 840
 TGTGCACAGG TCATACCCCG CACGGTACCA CCTCTCTCTG CAAACAAGAC GACCTCCTTT 900
 CGGGTGACCT CATCTTCTG GGCTCAGACA GTCATCTTCC TCTCTTACCA GACCGCCCCC 960
 GAGACCATGT GAAGAAACC ATCTTGTGAG GGGCTGCTCG GACTGGTCTG GCAGGTGGG 1020
 CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
 CATAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC 1140
 TCAACTCCAG CCACCTGCC CAGCTCGACG GCACTGGGCC AGTTCGCCCT CTGCTCTGCA 1200
 GCTCGGTTTC CTTTCTAGA ATGGAAATAG TGAGGGCCAA TGC

Seq ID NO: 89 Protein sequence:
 Protein Accession #: NP_005259.1

1 11 21 31 41 51
 MNWSIFEGLL SGVKNYSTAF GRWLVLVFI FRVLVYLVT A ERVWSDHDKD PDCNTRQPGC 60
 SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VMHVAYREV QEKRRHREAHG ENSRLYLNP 120
 GKRRGGLWWT YVCSLVFKAS VDIAPLYVPH SFYPKYILPP VVKCHADPCP NIVDCPISKP 180
 SEKNIFTLFM VATAAICILL NLVELIYLV KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ 240
 DDLLSGDLIF LGSDSHPPLL PDRPRDHVKK TIL

Seq ID NO: 90 DNA sequence
 Nucleic Acid Accession #: NM_002391.1
 Coding sequence: 26-457

1 11 21 31 41 51
 CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCTCTCTCC TCACCTCCT 60
 CGCCCTGCTG CGCTCACTC CCGCGGTGCG CAAAAAGAAA GATAAGGTGA AGAAGGGCGG 120
 CCGGGGAGC GAGTGCCTG AGTGGGCTG GGGGCCCTGC ACCCCAGCA GCAAGGATTG 180
 CGCGTGGGT TTCGCGAGG GCACCTGCGG GGCCAGACC CAGCGCATCC GGTGCAGGGT 240
 GCCCTGCAAC TGGGAAGAAG AGTTGGAGC CGACTGCAAG TACAAGTTTG AGAAGTGGG 300
 TCGTGTGAT GGGGGCAGC GCACCAAAAT CCGCAAGGC ACCCTGAAGA AGCGCGCTA 360

CAATGCTCAG TGCACAGGAGA CCATCCGCGT CACCAAGCCC TGACCCCCCA AGACCAAAGC 420
 AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGACTAGACG CCAAGCCTGG ATGCCAAGGA 480
 GCCCTCGTGT TCACATG3GGG CCTGGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC 540
 CACCAGTGCC TTCTGTCTGC TCGTGTAGCTT TAATCAATCA TGCCTGCGCT TGTCCCTCTC 600
 ACTCCCCAGC CCCACCCCTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660
 TGAGCCTCCC CCAAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC 720
 ATTACTAAGA AACACATCAA ATAAACTGAC TTTTCCCTCC CAATAAAAGC TCTTCTTTT 780
 TAATAT

Seq ID NO: 91 Protein sequence:
 Protein Accession #: NP_002382.1

1 11 21 31 41 51
 | | | | |
 MQHRGFLLLT LLALLALTSA VAKKKDKVKK GPGSECAEW AWGPCTPSSK DGVGFREGT 60
 CGAQTRIRRC RVPCNWKKEF GADCKYKFEW WGACDGGTGT KVRQGTLLKA RYNAQCQRTI 120
 RVTKPCTPKT KAKAKARKGK GKD

Seq ID NO: 92 DNA sequence
 Nucleic Acid Accession #: NM_005130.1
 Coding sequence: 98-802

1 11 21 31 41 51
 | | | | |
 CTCTACCTGA CACAGCTGCA GCCTGCAATT CACTCCCACT GCCTGGGATT GCCTGGATC 60
 CGTGTGCTCA GAACAAGGTG AACGCCACG TGACGCCATG AAGATCTGTA GCCTCACCCT 120
 GCTCTCCTTC CTCTACTGCG CTGCTCAGGT GCTCCTGGTG GAGGGGAAAA AAAAAGTGAA 180
 GAAATGACTT CACAGCAAGG TGGTCTCAGA ACAAAGGAC ACTCTGGGCA ACACCCAGAT 240
 TAAGCAGAAA AGCAGGCCCG GGAACAAAGG CAAGTTTGTC ACCAAAGACC AAGCCAACTG 300
 CAGATGGGCT GCTACTGAGC AGGAGGAGGG CATCTCTCTC AAGGTTGAGT GCACTCAATT 360
 GGACCATGAA TTTTCTGTGT TCTTTGCTGG CAATCCAACC TCATGCCTAA AGCTCAAGGA 420
 TGAGAGAGTC TATTGGAAAC AAGTTGCCCG GAATCTGCGC TCACAGAAAG ACATCTGTAG 480
 ATATTCCAAG ACAGCTGTGA AAACCCAGAGT GTGCAGAAAG GATTTTCCAG AATCCAGTCT 540
 TAAGCTAGTC AGCTCCACTC TATTGGGAA CACAAAGCCC AGGAAGGAGA AAACAGAGAT 600
 GTCCCCCAGG GAGCACATCA AGGCAAAAGA GACCACCCCT TCTAGCCTAG CAGTGACCCA 660
 GACCATGGCC ACCAAAGCTC CCGAGTGTGT GGAGGACCCA GATATGCCAA ACCAGAGGAA 720
 GACTGCCCTG GAGTTCTGTG GAGAGACTTG GAGCTCTCTC TGCACATTCT TCCTCAGCAT 780
 AGTGCAGGAC ACCTCATGCT AATGAGGTCA AAAGAGAACG GGTTCCTTTA AGAGATGTCA 840
 TGTCTAAGT CCCTCTGTAT ACTTTAAAGC TCTCTACAGT CCCCCCAAAA TATGAACCTT 900
 TGTGCTTAGT GAGTGCACAC AATATTTTAA ACAAGTTTGT TATTTTGTGC TTTTGTGTTT 960
 TGGAAATTTG CTTATTTTTC TTGGATGCGA TGTTCAGAGG CTGTTTCTGT CAGCATGTAT 1020
 TTCCATGGCC CACACAGCTA TGTGTTTGTG CAGCGAAGAG TCTTTGAGCT GAATGAGCCA 1080
 GAGTGATAAT TTCAGTGCAA CGAACTTTCT GCTGAATTAA TGGTAATAAA ACTCTGGGTG 1140
 TTTTTCAAAA AAAAAAAAAA AAA

Seq ID NO: 93 Protein sequence:
 Protein Accession #: NP_005121.1

1 11 21 31 41 51
 | | | | |
 MKICSLTLLS FLLLAQVLL VEGKKKVKNG LHSKVVSQK DTLGNTQIKQ KSRPKNKGKP 60
 VTKDQANCRW AATEQEEGIS LKVECTQLDH EFSCVFAGNP TSCLKLKDER VYWKQVARNL 120
 RSQKIDICRYS KTAVKTRVCR KDFFESSLLK VSSTLFGNTK PRKEKTEMSF REHKGKETT 180
 PSSLAVTQTM ATKAPECED PDMANQRKTA LEFCGETWSS LCTFFLSIVQ DTSC

Seq ID NO: 94 DNA sequence
 Nucleic Acid Accession #: NM_012101
 Coding sequence: 125-1891

1 11 21 31 41 51
 | | | | |
 CTCCTCACAG GTGTGTCTCT AGTCCTCGTG GTTGCTGCCC CCACTCCCTG CCGAGACGCC 60
 TGCCAGAAAG GTCACCTATC CTGAACCCCA GCAAGCCTGA AACAGCTCAG CCAAGCACCC 120
 TCGGATGGAA GCTGCAGATG CCTCCAGGAG CAACGGGTGG AGCCCAAGAG CCAGGGATGC 180
 CCGGAGCCCG TCGGGCCCCA GTGGCAGCCT GGAGAAATGGC ACCAAGGCTG ACGGCAAGGA 240
 TGCCAAAGAC ACCAACGGGC ACGGCGGGGA GGCAGCTGAG GGCAAGAGCC TGGGCGAGCGC 300
 CCGTGAAGCA GCGGAAGGTA AGAGCGCCCT GTTCGCGGGC AATGAGTGGC GCGGACCCAT 360
 CATCCAGTTT GTCGAGTCCG GGGACGACAA GAACTCCAAC TACTTACGCA TGGACTCTAT 420
 GGAAGGCAAG AGGTGCGCGT ACGCAGGGCT CCAGCTGGGG GCTGCCAAGA AGCCACCCGT 480
 TACCTTTGCC GAAAAGGGCG ACGTGCACAA GTCCATTTTC TCGGAGTCCC GGAAGCCAC 540
 GGTGTCCATC ATGGAGCCCG GGGAGACCCG GCGGAACAGC TACCCCGGGG CCGACACGGG 600
 CCTTTTTCCT CCGTCCAAGT CCGGCTCCGA GGAGGTGCTG TGGGACTCCT GCATCGGCAA 660
 CAAGCAGAAG GCGGTCAAGT CCGCTCTGGT GTGCCAGGCC TCCTTCTGCG AGCTGCATCT 720
 CAAGCCCCAC CTGGAGGGCG CCGCTTCCG AGACCACAG CTGCTCGAGC CCATCCGGGA 780
 CTTTGAGGCC CGCAAGGTGC CCGTGATGG CAAGACGATG GAGCTCTTCT GCCAGACGGA 840
 CCAGACCTGC ATCTGTATAC TTTGATGTTT CCAGGAGCAC AAGAAATCATA GCACCGTGAC 900
 AGTGAAGGAG GCGGAAGGCG AGAAGGAGAC GGAGCTGTCA CTGCAAAAGG AGCAGCTGCA 960
 GCTCAAGATC ATTGAGATTG AGGATGAAGC TGAGAAGTGG CAGAAGGAGA AGGACCGCAT 1020
 CAAGAGCTTC ACCACCAATG AGAAGGCCAT CCTGGAGCAG AACTTCCGGG ACCTGGTGGC 1080
 GGACCTGGAG AAGCAAAAGG AGGAAGTGAG GGCTGCGCTG GAGCAGCGGG AGCAGGATGC 1140
 TGTGGACCAA GTGAAGGTGA TCATGGATGC TCTGGATGAG AGAGCCAAGG TGCTGCATGA 1200
 GGACAAAGCAG ACCCGGAGC AGCTGCATAG CATCAGCGAC TCTGTGTTGT TTCTGCAGGA 1260
 ATTTGGTGCA TTGATGAGCA ATTACTCTCT CCCCCACCC CTGCCCACTT ATCATGTCTT 1320
 GCTGGAGGGG GAGGGCCTGG GACAGTCACT AGGCAACTTC AAGGACGACC TGCTCAATGT 1380
 ATGCATGGCG CACGTTGAGA AGATGTGCAA GGCGGACCTG AGCCGTAAC TCACTGAGAG 1440
 GAACCACATG GAGAACGGTG GTGACCATCG CTATGTGAAC AACTACACGA ACAGCTTCGG 1500

5 GGGTGAGTGG AGTGACCCGG ACACCATGAA GAGATACTCC ATGTACCTGA CACCCAAAGG 1560
 TGGGGTCCCG ACATCATACC AGCCCTCGTC TCCTGGCCGC TTCACCAAGG AGACCAACCA 1620
 GAAGAAATTC AACATCTCT ATGGCACCAG AGGTAACCTAC ACCTCCCGGG TCTGGGAGTA 1680
 CTCCTCCAGC ATTCAGAACT CTGACAAATGA CCTGCCCGTC GTCCAAGGCA GCTCCTCTTT 1740
 CTCCTCGAAA GGCTATCCCT CCCTCATGCG GAGCCAAAGC CCCAAGGCC AGCCCCAGAC 1800
 TTGGAATCT GGCAAGCAGA CTATGCTGTC TCACTACCGG CCATTCTACG TCAACAAAGG 1860
 CAACGGGATT GGGTCCAAAG AAGCCCCATG AGCTCCTGGC GGAAGGAACG AGGCGCCACA 1920
 CCCCTGCTCT TCCTCCTGAC CCTGCTGCTC TTGCCTTCTA AGTACTGTG CTGTCTGSG 1980
 TGGAGGGAG CTGTGCTCTG CACCTGCCCT CTGCAGCCCT CTGCCAGCCT CTGGGGGCA 2040
 GTTCCGGCCT CTCGCACTTC CCCACTGGCC AACTCCATT CAGACTCCTT TCCTGCTTG 2100
 TGACCTCAGA TGCTCACCAT CATTCCTGTG CTCAGAGGCC AACCCATCAC AGGGGTGAGA 2160
 TAGGTTGGGG CTGCGCCATA CCCGCCAGCC TCCTCCTCTC GGGCTGGATC TGGGGGCTAG 2220
 CAGTGAGTAC CGCATCTTAA TCAGCCTGCC TCCTCCGCCC ACGCCTGCT GTCTCCAGGC 2280
 CTATAGACGT TTCTCTCAA GGCCTATCC CCCAATGTTG TCAGCAGATG CCTGGACAGC 2340
 15 ACAGCCACCC ATCTCCATT CACATGGCCC ACCTCCTGCT TCCAGAGGA CTGGCCCTAC 2400
 GTGCTCTCTC TCGTCTTACC TATCAATGCC CAGCATGGCA GAACCTGCAG TGGCCAAAGG 2460
 CTGCAGATGG AAACCTCTCA GTGTCTTGAC ATCACCCTAC CCAGGCGGTG GGTCTCCACC 2520
 ACAGCCACTT TGAGCTGTG GTCCCTGGAG GGTGGCTTCT CTGACTGGC AGGATGACCT 2580
 TAGCCAAGAT ATTCTCTGT TCCCTCTGCT GAGATAAAGA ATTCCTTAA CATGATATA 2640
 20 TCCACCCATG CAAATAGCTA CTGGCCAGC TACCATTAC CATTGCTTA CAGAAATTTCA 2700
 TTCAGTCTAC ACTTTGGCAT TCTCTCTGCG GATGGAGTGT GGCTGGGCTG ACCGCAAAAG 2760
 GTGCTTTACA CACTGCCCCC ACCCTCAGCC GTTGCCCCAT CAGAGGCTGC CTCTCCTTC 2820
 TGATTACCCC CCATGTTGCA TATCAGGGTG CTCAGGATT GGAGAGGAGA CAAACCAGG 2880
 AGCAGCACAG DLRNFIERN TCCGCTCTCA ACAGCCCAAG GCCTATGGGG GCTCTGGAAG 2940
 25 GATGGGCCAG CTTGACGGGG TTGGGGAGGG AGACATCCAG CTTGGGCTTT CCCCTTGA 3000
 ATAAACCATT GGTCTGTC

Seq ID NO: 95 Protein sequence:
 Protein Accession #: NP_036233.1

30
 1 11 21 31 41 51
 MEAADASRSN GSSPEARDAR SPSGSPSGSLE NGTKADGKDA KTTNGHGGEEA AEGKSLGSAL 60
 35 KPGEGRSALP AGNEWRRPII QFVESGDDKN SNYFSMDSME GKRSYPAGLQ LGAARKPPVT 120
 FAEKGDVRKS IFSERKPTV SIMEPGETRR NSYPRADTGL FSRKSGSSEE VLCDSCIGNK 180
 QKAVKSCLVK QASFCLEHLK PHLEGAAPRD HQLEPIRDF EARKCPVHKG TMELFCQTDQ 240
 TCICYLCMFQ EHKHNSHTV EBAKAEKETE LSLQKEQLQL KIIEIEDEAE KWQKEKDRIK 300
 40 SFTTNEKAIL EONFRDLVRD LEKQKEEVRA ALEQRBDQAV DQVKVIMDAL DERAKVLHED 360
 KQTRQLHSI SDVSLFLQEF GALMSNYSLP PPLETYHVL EGEGLGQSLG NFKDDLNLNV 420
 MRHVEKMKCA DLGRNFIERN HMENGDDHRY VNNYTNFSGG ENSAPDTMKR YSMYLPKGG 480
 VRTSYQPSSP GRPTKETTKQ NFNNLYGTKG NYTSRVWEYS SSIQNSDNDL FVVQSSSFS 540
 LKGYPSLMRS QSPKAQPQTW KSGKQTMLSH YRPFYVKNKN GIGSNEAP

Seq ID NO: 96 DNA sequence
 Nucleic Acid Accession #: NM_080668.1
 Coding sequence: 83-841

50 1 11 21 31 41 51
 GGCACGAGGG CAGCGAGTGG CCTTCCCGT TGGCGCGCGC CCGGGGCGGC GGCCTGGAG 60
 GAGCTCGAGA CGGAGCCTAG TTATGTCTGG GAGGCGAACG CGGTCCGGAG GAGCCGCTCA 120
 GCGCTCCGGG CCAAGGGCCC CATCTCCTAC TAAGCCTCTG CGGAGGTCCC AGCGGAAATC 180
 55 AGGCTCTGAA CTCCCGAGCA TCCTCCCTGA AATCTGGCCG AAGACACCCA GTGCGCTGCG 240
 AGTCAGAAAG CCCATCGTCT TAAAGAGGAT CGTGGCCCAT GCTGTAGAGG TCCAGCTGT 300
 CCAATCACT CGCAGGAGCC CTAGGATTTC CTTTTCTTG GAGAAAGAAA ACGAGCCCCC 360
 TGGCAGGGAG CTTACTAAGG AGGACCTTT CAAGACACAC AGCGTCCCTG CCACCCCCAC 420
 CAGCACTCT GTGCCGAACC CTGAGGCCGA GTCCAGCTCC AAGGAAGGAG AGCTGGAAGC 480
 60 CAGAGACTTG GAAATGTCTA AGAAAGTCAG GCGTTCCTAC AGCCGCTGAG AGACCTGGG 540
 CTCTGCTCT ACCTCCACCC CAGGCCCGCG GTCTCTGCTT GGCTTCGAGG GGCTGCTGGG 600
 GGCAGAAAGC TTGTCCGGAG TCTCGCCAGT GGTGTGCTCC AAATCACCAG AGGTCGCCAG 660
 GGTGTGTGCA AAGCCCTGGG CCCAGACAT GACTCTCCCT GGAATCTCCC CACCACCCGA 720
 GAAACAGAAA CGTAAGAAGA AGAAAATGCC AGAGATCTTG AAAACGGAGC TGGATGAGTG 780
 GGCTGCGGCC ATGAATGCCG AGTTTGAAGC TGCTGAGCAG TTTGATCTCC TGGTTGAATG 840
 65 AGATGCAATG GGGGGTGAC CTGGCCAGAC TCTCCCTCCT GTCTGTACA TAGCCACCTC 900
 CTTGTGAGA GGAACCTTAG GGTCCCTCC CTTGTCTTG TTACCTGTGT GTGTGCTGGT 960
 GCTGCGCATG AGGACTGTCT GCCTTTGAGG GCTTGGGCG CAGCGGCAGC CATCTTGTT 1020
 TTAGGAAATG GGGCCGCTG GCCAGCCAC TCACTGGTGT CTTGTCTCT GTCTGCTGT 1080
 CTTCTCTATC TCCCAAAGT ACCATAGCCA GTTCCAGAT GGGCCACAGA CTGGGGAGGA 1140
 70 GAATCAGTGG CCCAGCCAGA AGTTAAAGGG CTGAGGGTTG AGGTGAGAGG CACCTCTGCT 1200
 CTTGTTGGGA GGGGTGCTG CTGGGAAATA GCGCCAGGGG CTCTGCCAGC CTGGCCCTCT 1260
 CCCTCCTGAG TTGCTTCTG TTGGTGGCTT TCTTCTTGA CCCACCTGTG TAAAGAGGTT 1320
 TTCAGTTCCT TGGGTTTCCC CTTTGATTCT GTAAATAGTC CCAGAGAGAA TTCGTGGGCT 1380
 75 GAGGGCAATT CTGCTCTTGA GGAAGAAGCT GGACATTGAG CCGTGGAGT CTGAGTTTGT 1440
 AAGGATGTAG GGAGCCTTAG TTGGGTCTCA GACCATAAGT GTGTACTACA CAGAAGCTGT 1500
 GTTTCTAGT TCTGGTCTGC TTGTGAGAT GTTGTAAAT GCCAGGTGTA TAGGGCGCTG 1560
 GCTGCTTGA GCAAGGGTGC CATTTAGGG GTGTGCCACC AGGTGCTGTG AGTTTCTGTG 1620
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Seq ID NO: 97 Protein sequence:
 Protein Accession #: NP_542399.1

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 KRIVAHAVEV PAVQSPRRSP RISFFLEKEN EPPGRELTKE DLFKTHSVPA TPTSTPVFNP 120
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	TCCCACTTCG	CGCTCTGATA	TGCATCAGCC	ACTGGATCCT	CGGGATGGA	CGGGATGGA	11820
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	TTTGGGCTAG	CGTTTGGATC	CGCTACACAG	TTTCTGCCAG	TCCCTGAGTT	GATGCCTTTT	11940
50	CGGCTAACTC	GCCAGTTTAT	CAATCTGATG	TTACCAATGA	AAGAAACGGG	CCTTATGTAC	12000
	AGCATCATGG	TACACGCACT	CCGGGCTTTC	CGCTCAGACC	CTGGCCTGCT	CACCAACACC	12060
	ATGGATGTGT	TTGTCAAGGA	CGCCTCCTTT	GATTGGAAAA	ATTTTGAACA	GAAAAATGCTG	12120
	AAAAAAGGAG	GGTCATGGAT	TCAAGAAATA	AATGTTGCTG	AAAAAATTG	GTACCCCGGA	12180
	CAGAAATAT	GTTACGCTAA	GAGAAAGTTA	GCAGGTGCCA	ATCCAGCAGT	CATTACTTGT	12240
55	GATGAGCTAC	TCTGGGTCA	TGAGAAAGCC	CCTGCCTTCA	GAGACTATGT	GGCTGTGGCA	12300
	CGAGGAAGCA	AAGATCAAC	CATTCTGTCC	CAAGAACCCG	AGAGTGGGCT	TTCAGAAAGG	12360
	ACTCAAGTGA	AAAGCTCTGAT	GGACCAAGCA	ACATCCTTGG	CAGAACCTGG	GAGAACCTGG	12420
	GAAGGATGGG	AGCCCTGGAT	GTGAGGTCTG	TGGGAGTCTG	CAGATAGAAA	GCATTACATT	12480
	GTTTAAAGAA	TCTACTATAC	TTTGGTTGGC	AGCATTCCAT	GAGCTGATT	TCTGAAACA	12540
60	CTAAAGAGAA	ATGTCCTTTG	TGCTACAGTT	TCGTAGCATG	AGTTTAAATC	AAGATTATGA	12600
	TGAGTAAATG	TGTATGGGTT	AAATCAAGAA	TAAGGTTATA	GTAACATCAA	AGATTAGGTG	12660
	AGGTTTATAG	AAAGATGAGT	ATCCAGGCTT	ACCAAGATAT	TAAGTCAAGA	ATATAATATG	12720
	TGATCAGCTT	TCAAGACATT	TACAAGTGCT	GCAAGTTAGT	GAAACAGCTG	TCTCCGTAAA	12780
	TGGAGGAAAT	GTGGGGAAGC	CTTGGAAATG	CCTTCTGGTT	CTGGCACATT	GGAAGGCACA	12840
65	CTCAGAAGGC	TTCATCACCA	AGATTTTGGG	AGAGTAAAGC	TAAGTATAGT	TGATGTAACA	12900
	TTGTAGAAGC	AGCATAGGAA	CAATAAGAAC	AATAGGTAAG	GCTATAATTA	TGGCTTATAT	12960
	TTAGAAATGA	CTGCATTGTA	TATTTTAGGA	TATTTTCTTA	GGTTTTTTCC	TTTCATTTTA	13020
	TTCTCTTCTA	GTTTTCATAT	TTTATGATAG	ATTTGCTCTC	TAGAAGGAAA	CGTCTTTATT	13080
	TAGGAGGGCA	AAAATTTTGG	TCATAGCATT	CACTTTGTCT	ATTCCTAATC	ACAACTGGAA	13140
70	GATACATAAA	AGTGCTTTGC	ATTGAATTG	GGATAACTTC	AAAAATCCCA	TGGTTGTTGT	13200
	TAGGGATAGT	ACTAAGCATT	TCAGTTCCAG	GAGAATAAAA	GAAATTCCTA	TTTGAAATGA	13260
	ATTCCTCATT	TGGAGGAAAA	AAAGCATGCA	TTCTAGCACA	ACAAGATGAA	ATTATGGAAT	13320
	ACAAAGTGG	CTCCTTCCCA	TGTGCACTCC	CTGTCCCTCC	CCGCCAGTCC	TCCACACCCA	13380
	AACTGTTTCT	GATGGCTTTT	TAGCTTTTGT	TTGTTTTTTT	TTTTCTTCTT	AACACTTGTA	13440
75	TTTGGAGGCT	CTTCTGTGAT	TTTGAGAAAT	ATACTCTTGA	GTGTTTAATA	AAGTTTTTTT	13500
	CCAAAGTA						

Seq ID NO: 99 Protein sequence:
Protein Accession #: NP_008835.5

80	1	11	21	31	41	51	
	MAGSGAGVRC	SLRLQETLS	AADRCGAALA	GHQLIRGLGQ	ECVLSSSPAV	LALQTSLVFS	60
	RDFGLLVFVR	KSLNSIEFRE	CREEILKFLC	IFLEKMGQKI	APYSVEIKNT	CTSVYTKDRA	120
	ARKKIPALDL	LILKLQTFRS	SRLMDEFKIG	ELFSKFYGL	ALKKKIPDVT	LEKVVYELLGL	180
85	LGEVHPSEMI	NNAENLPRAF	LGLKTMQTS	AVREPKLFLV	AGCLKGLSSL	LCNFTKSMEE	240
	DPQTSREIFN	FVLKAIKPIQI	DLKRYAVPSA	GLRLFALHAS	QFSTCLLDNY	VSLFEVLLKW	300
	CAHTNVELKK	AALSALESFL	KQVSNMVAKN	AEHMKNLQY	FMEQFYGIIR	NVDSNNKELS	360

	IAIRGYGLFA	GPCKVINAKD	VDFMYVELIQ	RCKQMPLTQT	DTGDDRVYQM	PSFLQSVASV	420
	LLYLDTVPEV	YTPVLEHLVV	MQIDSFPQYS	PKMQLVCCRA	IVKVPLALAA	KGPVLRNCIS	480
	TVVHGLLRI	CSFPVVLPGK	PESESEDHRA	SGEVRTGKWK	VPTYKDYVDL	FRHLLSSDQM	540
5	MDSILADEAF	FSVNSSSES	NHLLYDEFVK	SVLKIVEKLD	LTLIEIQTVEG	QENGDEAPGV	600
	WMIPTSDFAA	NLHPAKPKDF	SAPINLVEFC	REILPEKQAE	FFEPWVYSFS	YELILQSTRL	660
	PLISGFYKLL	SITVRNAKKI	KYFEGVSPKS	LKHSPEDEPK	YSCFALFVKF	GKEVAVKMKQ	720
	YKDELLASCL	TFLLSLPHNI	IELDVRAVVP	ALQMAFKLGL	SYTPLAEVGL	NALEEWISIYI	780
	DRHVMQPYK	DILPCLDGYL	KTSALSDETK	NNWEVSALSR	AAQKGFNKKV	LKHLKKTKNL	840
10	SSNEAISLEE	IRIRVQMLG	SLGGQINKNL	LTVTSSDEMM	KSYVANDREK	RLSFAVPFRE	900
	MKPVIFLDVF	LPRVTELALT	ASDRQTKVAA	CELLHSMVMF	MLGKATQMP	GGQGAAPPYQ	960
	LYKRTFPVLL	RLACDVQVDT	RQLYEPLVMQ	LIHWFTNNKK	PESQDTVALL	EAILDGIIVDP	1020
	VDSTLRDFCG	RCIREFLKWS	IKQITPQQQE	KSPVNTKSLF	KRLYSALALP	NAFKRLGASL	1080
	AFNNIYREFR	EEESLVEQFV	FEALVIYMES	LALAHADEKS	LGTIQCCDA	IDHLCRITKE	1140
15	KHVSINKAKK	RLPRGFFPFS	ASLCLDLVK	WLLAHCGRPO	TECRHKSIEL	FYKFPVLLPG	1200
	NRSPNLWLKD	VLKEEGVSPL	INTFEGGGCG	QPSGILAQPT	LLYLGRPFSL	QATLCWLDLL	1260
	LAALECYNTF	IGERTVGALQ	VLGTEAQSSL	LKAVAPFLES	IAMHDIIAAE	KCPGTGAAGN	1320
	RTSPQEGERY	NYSKCTVVVR	IMEFTTLLN	TSPEGWKLK	KDLCNTHLMR	VLVQTLCEPA	1380
	SIGFNIQDVQ	VMAHLPDVCV	NLMKALKMSP	YKDILETHLR	EKITAQSIIE	LCAVNLVYGP	1440
20	AQVDRSLAA	VVSACKQHLR	AGLLHNILPS	QSTDHHSVVG	TELLSLVYKG	IAPGDERQCL	1500
	PSLDLSCQQL	ASGLLELAPA	FGGLCERLVS	LLLNPAVLST	ASLGSSQGSV	IHFSGHEYFY	1560
	SLFSETINTE	LLKNLDLAVL	ELMQSSVDNT	KMWSAVLNGM	LQSPFRERAN	QKHQGLKLAT	1620
	TILQHWKKCD	SWWAKDSPLE	TKMAVLALLA	KILQIDSSVS	FNTSHGSPFE	VFTTYISLLA	1680
	DTKLDLHLKG	QAVTLLPFPT	SLTGGSLLEL	RRVLEQLIVA	HFPMQSREFF	PQTFRFNNYV	1740
25	DCMKKFLDAL	ELSGSSPMLL	LMTVELCREQ	QHVMEELFQS	SFRRIARRGS	CVTQVGLLES	1800
	VYEMFRKDDP	RLSFTTRQSFV	DRSLTLTLWH	CSLDALREFF	STIVVDADIV	LKSRTFKLNE	1860
	STFDTOITKK	MGYYKILDVM	YSRLPKDDVH	AKESKINQVF	HGSCITEGNE	LTKTLIKLCY	1920
	DAPTENMAGE	NQLLERRRLY	HCAAYNCATS	VICCVFNLK	FYQGLFSEK	PEKNLLIFEN	1980
	LIDLKRRYNF	FVEVEVEMER	KKKYIEIRKE	AREAANGDS	GPSYMSLSY	LADSTLSEAM	2040
30	SOQDFSTGVQ	SYSYSSQDPR	PATGRFRRRR	QRDPTVHDDV	LELEMDLNR	HECMAPLTAL	2100
	VKHMRRSLGP	PQGEEDSVPR	DLPSPMKPLH	GKLGNIPIVL	NIRLFLAKLV	INTEEVFRPY	2160
	AKHWLSPLLQ	LAASENNGGE	GIHYMVVEIV	ATILSWTGLA	TPTGVPKDEV	LANRLNPLM	2220
	KHVFPKRAV	FRHNLEIKT	LVCEWDCLS	IPYRLIFEKF	SGKDPNSKDN	SVGIQLLGIV	2280
	MANDLPPYDP	QCGIQSSEYP	QALVNNMSFV	RYKEVYAAAA	EVGLGLILRV	MERNKILEES	2340
35	LCELVAQKQL	QHQTQSMEDK	IVCLNKVTKS	FPLADRFPMN	AVFLLPKFPH	GVLKTLCLVE	2400
	VLCRVEGMTE	LYPQLKSKDF	VQVMRHRDDE	RQKVCLDIY	KMPKLPKVE	LRELLNPVVE	2460
	FVSHPSSTCR	BQMYNINLMW	HDNYRDPSE	TDNDSQIFK	LAKDVLIOGL	IDENPGLQLI	2520
	IRNFWSHETR	LPSNTLDRLL	ALNSLYSPKI	SVHFLSLATN	FLLEMTSMSP	DYPNPMFEHP	2580
	LSECFEQEYT	IDSDWRFRST	VLTMPFVETQ	ASQGTQLTRT	QEGSLBARWP	VAGQIRATQQ	2640
40	QHDFTLTQTA	DGSSSPDWLT	GSSTDPLVDH	TSPSSDLSLF	AHKRSERLQR	APLKSVPDPF	2700
	GKKRLGLPGD	EVONKVKGAA	GRTDLLRLRR	RFMRDQEKLS	LMYARKGVAE	QKREKEIKSE	2760
	LKMKQDAQVQ	LYRSYRHGDL	PIQIKHSSL	ITPLQAVAR	DPIIAKQLFS	SLPSGILKEM	2820
	DKPKTLSEKN	NITQKLLQDF	NRFLNTTFSF	PPPFVSCIQD	ISCQHAALLS	LDPAAVSAGC	2880
	LASLQQPVGI	RLLEEALLRL	LPAELPAKRV	RGKARLPDVP	LRWVELAKLY	RSIGEYDVL	2940
45	GIFTSEIGTK	QITQSALLAE	ARSDYSEAAK	QYDEALNKQD	WVDGEPTAE	KDPWELASLD	3000
	CYNHLAEWKS	LEYCSTASID	SENPPDLNKI	WSEPFYQETY	LPYMRSLKLV	LLQGEADQS	3060
	LLTFIDKAMH	GELQKATLEL	HYSQELSLLY	LLQDDVDRAK	YYIQNGIQSF	MQNYSSIDVL	3120
	LHQSRLLTKLQ	SVQALTEIQE	FISFISKQGN	LSSQVPLKRL	LNTWTNRYPD	AKMDPMNIWD	3180
	DIITNRCCFL	SKIEEKLTPL	PEDNSMNVQD	DGDPDSRMEV	QEQUEEISSL	IRSCFKFSMK	3240
50	KMIDSARKQN	NFSLAMKLLK	ELHKESKTRD	DWLVSQVQSY	CRLSHCRSRS	QCSQEVLTV	3300
	LKTVSLLEDN	NVSSYSLKNI	LAFRDQNIL	GTTYRIIANA	LSSEPAACLB	IEEDKARRIL	3360
	ELSGSSSEDS	NYAGIAGYQR	APQHLSEAVQ	AAEEEAQPPS	WSCGPAAGVI	DAYMTLADFC	3420
	DQQLRKEEN	ASVIDSAELQ	AYPALVVERM	LKALKLNSNE	ARKLPRLRLQ	IERYPEETL	3480
	SLMTKEISSV	PCNQFISWIS	HMVALLDKDQ	AVAVQHSVEE	ITDNYPQAI	YPPFISSESY	3540
55	SFKDTSFGHK	NKEEFVARIKS	KLDQGGVQD	FINALDQLSN	PBLLPKDWSN	DVRAELAKTP	3600
	VNKKNIEMKY	ERNYAALGDP	KAPGLGAFRR	KFIQTFGKEF	DKHFGKGGSK	LLRMKLSDFN	3660
	DITNMLLLKM	NKDSKPPGCT	KCCSPWMSDF	KVEFLRNELE	IPQYDGRGK	PLPEYHVRIA	3720
	GFDERTVTMA	SLRRPKRIII	RGHDEREHFF	LVKGGEDLRQ	DQVEQLFQV	MNGILAQDSA	3780
	CSQRALQLRT	YSVVPMTSRL	GLIEWLENTV	TLKDLLLNTM	SQEEKAAVLS	DPRAPPCBYK	3840
60	DWLTKMSGKH	DVGAYMLMYK	GANRTETVTS	FRKRESKVPA	DLKRAFVRM	STSPAEPLAL	3900
	RSHPASSHAL	ICTSHWILGI	GDRHLNFMV	AMETGGVIGI	DFGHPAGSAT	QFLPVPELMP	3960
	FRLTRQFINL	ILPMKGTGLM	YSIMVHALRA	FRSDPGLLTN	TMDVFKVEPS	FDWKNFQEQM	4020
	LKKGGSWIQE	INVAEKNWYP	RQKICYAKRK	LAGANPAVIT	CDELLLGHEK	APAFRDYVAV	4080
	ARGSKDHNR	AQEPESGLSE	ETQVKCLMDQ	ATDPNILGRT	WEGWEPWM		

Seq ID NO: 100 DNA sequence
Nucleic Acid Accession #: NM_000673
Coding sequence: 101-1225

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	GTCATATGTT	GCAGAAATAC	AGATCCAAGA	CAAAGACAGG	ATGGGCACTG	CTGGAAGAAAT	120
	TATTAAATGC	AAAGCAGTCG	TGCTTTGGGA	GCAGAGCAAA	CCCTTCTCCA	TTGAGGAAAT	180
75	AGAAGTTGCC	CCACCAAAGA	CTAAAGAAGT	TCGCATTAA	ATTTTGGCCA	CAGGAATCTG	240
	TCGCACAGAT	GACCTATGTA	TAAAGGAAC	AATGGTGTC	AAGTTTCCAG	TGATTGTGGG	300
	ACATGAGGCA	ACTGGGATGG	TAGAGAGCAT	TGGAGAAGGA	GTGACTACAG	TGAACACAGG	360
	TGACAAAGTG	ATCCCTCTCT	TCTGCCACA	ATGTAGAGAA	TGCAATGCTT	GTCGCAACCC	420
	AGATGGCAAC	CTTTGCATTA	GAGAGGATAT	TACTGTCGT	GGAGTACTGG	CTGATGGCAC	480
80	CACCAGATTT	ACATGCAAGG	GCAAAACAGT	ACACCACTTC	ATGAACACCA	GTACATTTAC	540
	CGAGTACACA	GTGGTGGATG	AATCTTCTGT	TGCTAAGATT	GATGATGCAG	CTCCTCTTGA	600
	GAAAGTCTGT	TAAATCTGCT	GTGGGTTTTC	CACTGGATAT	GGCGCTGCTG	TTAAACTGG	660
	CAAGGTCAAA	CCTGGTTCCT	CTTGGTCTGT	CTTTGGCCTG	GGAGGAGTTG	GCCTGTCACT	720
	CATCATGGCG	TGTAAGTCAG	CTGGTGCATC	TAGGATCATT	GGGATTGACC	TCAACAAAGA	780
	CAAAATTTGAG	AAGGCCATGG	CTGTAGGTGC	CACGTAGTGT	ATCAGTCCCA	AGGACTCTAC	840
85	CAAAACCATC	AGTGAGGTGC	TGTCAGAAAT	GACAGGCAAC	AACGTGGGAT	ACACCTTTGA	900
	AGTTATTGGG	GCATGATGGA	TGCCCTGGCA	TCTCTGCCCA	TGAACATATG		960
	GACCAGCGTG	GTTGTAGGAG	TTCCCTCCATC	AGCCAAGATG	CTCACCTATG	ACCCGATGTT	1020

5
10
15
20

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GCTCTTCACT GGACGCACAT GGAAGGGATG TGTCTTTGGA GGTTTGAAAA GCAGAGATGA 1080
TGTCCCAAAA CTAGTGACTG AGTTCTCTGGC AAAGAAATTT GACCTGGACC AGTTGATAAC 1140
TCATGTTTTA CCATTTTAAAA AAATCAGTGA AGGATTTGAG CTGCTCAATT CAGGACAAAG 1200
CATTGGAACG GTCTCTGACG TTTGAGATCC AAAGTGGCAG GAGGTCTGTG TTGTCATGGT 1260
GAACTGGAGT TTCTCTGTGT AGAGTTCCCT CATCTGAAAT CATGTATCTG TCTCACAAT 1320
ACAAGCATAA GTAGAAGATT TGTGAAGAC ATAGAACCCT TATAAGAAT TATTAACCTT 1380
TATAAACATT TAAAGTCTTG TGAGCACCTG GSAATTAGTA TAATAACAAT GTTAATATTT 1440
TTGATTTACA TTTTGTAAAG CTATAATTGT ATCTTTTAAG AAAACATACA CTGGGATTTC 1500
TATGTTGAAA TGGAGATTTT TAAGAGTTTT AACCAGCTGC TGCAGATATA TAACTCAAAA 1560
CAGATATAGC GTATAAAGAT ATAGTAAATG CATCTCCAG AGTAATATTC ACTTAACACA 1620
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TAACTTGGAT TACATTTTGA AATCAGTTCA TTCCATGATG CATATTACTG GATTAGATTA 1740
AGAAAGACAG AAAAGATTAA GGGACGGGCA CATTTTTCAG CGATTAAAGAA TCATCATTAC 1800
ATAACTTGGT GAAAGTAAAA AAGTATATCA TATGGGTACA CAAGGCTATT TGCCAGCATA 1860
TATTAATATT TTAGAAATA TTCTTTTGT AATACTGAAT ATAAACATAG AGCTAGAGTC 1920
ATATTATCAT ACTTATCATA ATGTTCAATT TGATACAGTA GAATTGCAAG TCCCTAAGTC 1980
CCTATTCACT GTGCTTAGTA GTGACTCCAT TTAATAAAAA GTGTTTTTAG TTTTAAACAA 2040
CTAAACCG

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Seq ID NO: 101 Protein sequence:
Protein Accession #: NP_000664

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1 11 21 31 41 51
MGTAGKVIK KAAVLWEQKQ PFSIEIEIVA PPKTKEVRIK ILATGICRTD DHVIKGTMVS 60
KFPVIVGHEA TGIVSIGEG VTTVKPGDKV IPLFLPQCRE CNACRNPDGN LCIRSDITGR 120
GVLADGTRF TCKGKPVHVF MNTSTPTEYT VDESSVAKI DDAAPPEKVC LIGCGFSTGY 180
GAAVKTKVKV PGSTCVFVGL GGVGLSVIMG CKSAGASRII GIDLNKDKFE KAMAVGATEC 240
ISFKDSTKFI SEVLSEMTGN NVGYTFEIVG HLETMIDALA SCHMNYGTSV VVGVPSSAKM 300
LTYDPMLETF GRTNKGCVFG GLKSRDDVPK LVTFLAKKFF DLDQLITHVL PFKKISEGFE 360
LLNSGQSIRT VLTF

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Seq ID NO: 102 DNA sequence
Nucleic Acid Accession #: NM_006783.1
Coding sequence: 1..786

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1 11 21 31 41 51
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACACTC CACCAGCATC 60
GGGAAGGTGT GGATCACAGT CATCTTTATT TTCCGAGTCA TGATCCTAGT GGTGGCTGCC 120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTGCTCTGCA ACACACTGCA ACCGGGATGC 180
AAAAATGTGT GCTATGACCA CTTTTTCCTG GTGTCCACA TCCGGCTGTG GGCCTCCAG 240
CTGATCTTGG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
GAAACCACTC GCAAGTTTCA GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
ATTAAAAAGC ACAAGGTTTG GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420
TTTTTCCGAA CATCTTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCCT TTACAATGGG 480
TACCACCTGC CTGCGGTGTT GAAATGTGGG ATTGACCCCT GCCCAACCTT TGTGACTGTC 540
TTTATTTCTA GGCCAACAGA GAAGACCGTG TTTACCATT TATGATTTC TCGCTCTGTG 600
ATTTCATGTC TGCTTAACGT GGCAGAGTTG TGCTGAAAGT GTGTTTTAGG 660
AGATCAAGAA GAGCACAAGC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
CAGAATGAAA TGAATGAGCT GATTTTCAGT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
AGCTAA

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Seq ID NO: 103 Protein sequence:
Protein Accession #: NP_006774.1

55
60

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1 11 21 31 41 51
MDWGLTLTFI GGVNKHSTSI GKVVITVIFI FRVMILVVAA QEVWQDEQED FVCNTLQPGC 60
KNVCYDHPFP VSHIRLWALQ LIPVSTPALL VAMHVAYYRH ETTRKFRRGE KRNDPKDIED 120
IKKKHVRIEG SLWWTYTSII FFRIIPEAAF MVVFFLYLNG YHLPWVLKCG IDPCPNLVDC 180
FISRPTKTV FTIFMISASV ICMLLNVAEL CYLLLVKCFR RSKRAQTQKN HPNHALKESK 240
QNEMNELISD SQQNAITGFP S

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Seq ID NO: 104 DNA sequence
Nucleic Acid Accession #: NM_020411
Coding sequence: 86-526

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80

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1 11 21 31 41 51
GGACCTGGGA AGGAGCATAG GACAGGGCAA GGCGGGATAA GGAGGGGCAC CACAGCCCTT 60
AAGGCACGAG GGAACCTCAC TGCGCATGCT CCTTTGGTGC CCACCTCAGT GCGCATGTTC 120
ACTTGGCGTC TTCCCATCGC CCCCTTCGCC AGTGTGGGGA ACGCGGCGGA GCTGTGAGCC 180
GGCGACTCGG GTCCCTGAGG TCTGGAATCT TTCTCCGCTA CTGAGACACG GCGGACACAC 240
ACAAACACAG AACCAACAGC CCAGTCCCAG GAGCCCAGTA ATGGAGAGCC CCAAAAAGAA 300
GAACCAAGTC GTAAAGTCG GGATCCTACA CCTGGGCAGC AGACAGAAGA AGATCAGGAT 360
ACAGCTGAGA TCCAGTGC GGCATGGAA GGTGATCTGC AAGAGCTGCA TCAGTCAAAC 420
ACCGGGGATA AATCTGGAAT TGGGTTCGGG CGTCAAGGTG AAGATAATAC CTAAGAGGGA 480
ACACTGTAAA ATGCCAGAAG CAGGTGAAGA GCAACCACAA GTTTAAATGA AGACAAGCTG 540
AAACAACGCA AGCTGGTTTT ATATTAGATA TTTGACTTAA ACTATCTCAA TAAAGTTTTG 600
CAGCTTTCAC CAAAAA AAAA

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Seq ID NO: 105 Protein sequence:
Protein Accession #: NP_065144.1

85

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1 11 21 31 41 51

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MLLWCPPQCA CSLGVFPSPAP SPVWGTTRSC EPATRVPEVW ILSPLLRRHG HTQTQNHAS 60
PRSPVMESPK KKNQQLKVG I LHLGSRQKKI RIQLRSQCAT WKVICKSCIS QTPGINLIDL 120
SGVKVKIIFK EHKCKMPEAG EEQFPQV

Seq ID NO: 106 DNA sequence
Nucleic Acid Accession #: J04129
Coding sequence: 99-587

1 11 21 31 41 51
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCTCCTGC 60
TCACCCTGGG CGTGGCCCTG GTCGTGTGGT TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
ACATCTCCCT CATGGCGACA CTGAAGGCCC CTCTGAGGGT CCACATCACC TCACTGTTGC 240
CCACCCCGGA GGACAACTTG GAGATCGTTC TGCACAGATG GGAGAACAAC AGCTGTGTTG 300
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
TGGCGAACGA GGCCACGCTG CTCGATACTG ACTACGACAA TTTCCTGTTT CTCTGCCTAC 420
AGGACACCA CACCCCAATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCTGGTGG 480
AGGACGATGA GATCATGCAG GGATTCATCA GGGCTTTCAG GCCCTGCCCC AGGCACCTAT 540
GGTACTTGCT GGACTTGAAA CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCGCCT 600
CCAGGAAGAC CAGACTCCCA CCCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCTGCCCC 660
TTTCAAAGAA TAACCACAGC TCAGAAGACG ATGACGTGGT CATCTGTGTC GCCATCCCCT 720
TCTGTCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAACC CTTGGAGCAT G

Seq ID NO: 107 Protein sequence:
Protein Accession #: AAA60147

1 11 21 31 41 51
MDIPQTKQDL ELPKLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPTE EDNLEIVLHR 60
WENNSCVEKK VLGETGTGNPK KFKINYTVAN EATLLDSTDY NFLFLCLQDT TTPIQSMCMQ 120
YLARVLVEDD EIMQGFIRAP RPLPRHLWYL LDLKQMEEP C RF

Seq ID NO: 108 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 48-794

1 11 21 31 41 51
TCCAGGCGAG CAGTTAGCCC GCCGCCGCC TGTGTGTCCC CAGAGCCATG GAGAGAGCCA 60
GTCTGATCCA GAAGGCCAAG CTGGCAGAGC AGGCCGAACG CTATGAGGAC ATGGCAGCCT 120
TCATGAAAGG CCGCTGGAG AAGGGCGAGG AGCTCTCCTG CGAAGAGCGA AACCTGCTCT 180
CAGTAGCCCTA TAAGAACGTG GTGGGCGGCC AGAGGGCTGC CTGGAGGGTG CTGTCCAGTA 240
TTGAGCAGAA AAGCAACGAG GAGGGCTCGG AGGAGAAGGG GCCCGAGGTG CGTGAGTACC 300
GGGAGAAGGT GGAGATCAG CTCAGGGCG TGTCCGACAC CGTGTCTGGC CTGTGGGACA 360
GCCACCTCAT CAAGGAGGCC GGGGACGCCG AGAGCCGGGT CTTCTACCTG AAGATGAAGG 420
GTGACTACTA CCGCTACCTG GCCGAGGTGG CCACCGGTGA CGACAAGAAG CGCATCATTG 480
ACTCAGCCCG GTACGCTAC CAGGAGGCCA TGGACATCAG CAAGAAGGAG ATGCCGCCCA 540
CCAAACCCAT CCGCTGGGC CTGGCCCTGA ACTTTCCGT CTTCCACTAC GAGATCGCCA 600
ACAGCCCGA GGAGGCCATC TCTCTGGCCA AGACCACTT CGACGAGGCC ATGGCTGATC 660
TGACACCCCT CAGCGAGGAC TCCTACAAAG ACAGCACCTT CATCATGCGA CTGCTGGAG 720
ACAACTGAC ACTGTGGAG GCCGACAACG CCGGGGAAGA GGGGGGCGAG GCTCCCAGG 780
AGCCCGAGAG CTGAGTGTG CCGGCCACCG CCGCCCTCCG CCCCCTCCAG TCCCCACCC 840
TGCCGAGAGG ACTAGTATGG GGTGGGAGGC CCCACCTTC TCCCTAGGCG GCTGTCTCTG 900
CTCCAAAGGT TCCCTGTGAG AGGACTGGC AGAGCTGAGG CCACCTGGGG CTGGGGATCC 960
CACTCTTCTT GCAGCTGTG AGCGACCTA ACCACTGGTC ATGCCCCAC CCCTGCTCTC 1020
CGCACCGCT TCTCTCCGAC CCCAGGACCA GGCTACTTCT CCCCCTCTCT TGCTCCCTC 1080
TGCCCCCTGC TGCCCTGTAT CGTAGGAATT GAGGAGTGTG CCGCTTGTG CTGAGAACT 1140
GGACAGTGGC AGGGGCTGGA GATGGGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG 1200
CGCGCGCGCC AGTGCAAGAC CGAGATTGAG GGAAAGCATG TCTGCTGGGT GTGACCATGT 1260
TTCCTCTCAA TAAAGTTCCC CTGTGACACT C

Seq ID NO: 109 Protein sequence:
Protein Accession #: NF_006133.1

1 11 21 31 41 51
MERASLIQKA KLAQEAEYE DMAAFMKAV EKGEELSCEE RNLLSVAYKN VVGQRAAWR 60
VLSSIEQKSN EEGSEEGPE VREYREKVT ELQGVCDTVL GLDLSHLIKE AGDAESRVFY 120
LKMKGDIYRY LAEVATGDDK KRIIDSARSA YQEAMDISK EMPPTNPRL GLALNFSVPH 180
YEIANSPEEA ISLAKTTTDE AMADLHTLSE DSYKDSLTLM QLLRDLNLTLM TADNAGEEGG 240
EAPQEPQS

Seq ID NO: 110 DNA sequence
Nucleic Acid Accession #: NM_000695
Coding sequence: 407-1564

1 11 21 31 41 51
CAGGAGTTGG TTTGGGAGCT GCCAGTCTCC TGGGAGGATC GCAGTCAGCA GAGCAGGGCT 60
GAGGCCTGGG GGTAGGAGCA GAGCCTGCGC ATCTGGAGGC AGCATGTCCA AGAAAGGGAG 120
TGGAGGTGCA GCGAAGGACC CAGGGGCGA GCGGCGCTG GGGATGGACC CCTTCGAGGA 180
CACACTGCGG CGGCTGCTG AGGCCTTCAA CTGAGGGCGC ACGCGGCCGG CCGAGTTCCG 240
GGCTGCGCAG CTCAGGGGCC TGGGCCACTT CCTTCAAGAA AACAAGCAGC TTCTGCGCGA 300

	CGTGTGGCC	CAGGACCTGC	ATAAGCCAGC	TTTCGAGGCA	GACATATCTG	AGCTCATCCT	360
	TTGCCAGAAC	GAGGTGACT	ACGCTCTCAA	GAACCTTCAG	GCCTGGATGA	AGGATGAACC	420
	ACGGTCCAGC	AACCTGTTC	TGAAGCTGGA	CTCGGTCTTC	ATCTGGAAGG	AACCCCTTGG	480
5	CTGGTCCCTC	ATCATCGCAC	CCTGGAACCT	CCCATTTGAA	CTGACCCCTG	TGCTCCTGGT	540
	GGGACCCCTC	CCCGCAGGAA	ATTGCGTGGT	GCTGAAGCCG	TCAGAAATCA	GCCAGGGCAC	600
	AGAGAAGGTC	CTGGCTGAGG	TGCTGCCCCA	GTACCTGGAC	CAGAGCTGCT	TTGCCGTGGT	660
	GCTGGGCGGA	CCCCAGGAGA	CAGGGCAGCT	GCTAGAGCAC	AAGTTGGACT	ACATCTTCTT	720
	CACAGGAGAG	CCTCGTGTGG	GCAAGATTGT	CATGACTGCT	GCCACCAAGC	ACCTGAAGCC	780
10	TGTCACCTCG	GAGCTGGGGG	GCAAGAACCC	CTGCTACGTG	GACGACAACT	GCGACCCCCA	840
	GACCGTGGCC	AACCGCGTGG	CCTGGTTCTG	CTACTTCAAT	GCCGGCCAGA	CCTGCGTGGC	900
	CCCTGACTAC	TCCTGTGTGA	GCCCCGAGAT	GCAGGAGAGG	CTGCTGCCCG	CCCTGCAGAG	960
	CACCATCACC	CGTTTCTATG	GCGACGACCC	CCAGAGCTCC	CCAAACCTGG	GCCGCATCAT	1020
	CACCCAGAAA	CAGTTCCAGC	GGCTGCGGGC	ATTGCTGGGG	TGCGGCCGCG	TGGCCATTGG	1080
15	GGGCGAGAGC	AACGAGAGCG	ATCGCTACAT	CGCCCCCAGC	GTGCTGGTGG	ACGTGCAGGA	1140
	GACGAGAGCT	GTGATGCAGG	AGGAGATCTT	CGGGCCCATC	CTGCCCATCG	TGAACGTGCA	1200
	GAGCGTGGAC	GAGGCGATCA	AGTTTATCAA	CCGGCAGGAG	AAGCCCCCTG	CCCTGTAAGC	1260
	CTTCTCCAAC	AGCAGACAGG	TTGTGAACCA	GATGCTGGAG	CGGACCAGCA	GCGGCAGCTT	1320
	TGGAGGCAAT	GAGGGCTTCA	CCTACATATC	TCTGCTGTCC	GTGCCATTGG	GGGGAGTCGG	1380
20	CCACAGTGGG	ATGGGCGCGG	ACCACGGCAA	GTTCACCTTC	GACACCTTCT	CCCAACCAAG	1440
	CACCTGCTGG	CTCGCCCCCT	CGGCGCTGGA	GAAATTAAG	GAGATCCGCT	ACCCACCCCTA	1500
	TACCGAGCTG	AACCGACGAG	TGTTACGCTG	GGGCATGGGC	TCCACAGAGT	GCACCTCTCT	1560
	GTGAGCGTCC	CACCCGCTTC	CAACGGGTCA	CACAGAGAAA	CCTGAGTCTA	GCCATGAGGG	1620
	GCTTATGTCT	CCAATCTACA	TTGTTCTCTC	AGACCGCAGG	CTCCCCCAGC	CTCAGGTTGC	1680
25	TGGAGCTGTC	AACATGAGTC	ATCCTGCTCG	CCAGGGCTGC	AAAGCAAGGT	CTTGCTTCTA	1740
	CTTGGGGGAG	GCTGCTGAG	AGAGGCGGAG	AGGCGCCAGA	ACATGCCAGG	TGTCCTCACT	1800
	CACCCACCCC	CTCGGGAATA	CAGCCCTTTG	CCCTCTCGGT	CAGGGTTGGC	CAGGCCCACT	1860
	CACAGGGGCA	GTGTACCCCT	GGAAAATACA	GTGCCCTGCC	TTCTTAGGGG	CATCAGCCCT	1920
	GAACGGTGA	GAGCGTGGAG	CCCTCCAGGC	CTTGTCTCTC	CCCTCTAGGC	ACACGCGCAC	1980
30	TTCCACCTCT	GGCCCATCCC	AACATGACCA	GCACCTGCTC	CCCCAGGGAT	CCTCTCACAT	2040
	CCCACTGCTG	TCTCTGCACC	ACCCCTCTGG	TTCAACCCGC	ACCCCTGACT	CACCCACAGC	2100
	AGCTCATATC	ACTGGGAAAA	CTGGGGTTTG	CATCACTCCA	CTGCACAGTG	TTAGTGGGAC	2160
	CTGGGGGCAA	GTCCCTTGAC	TTCTCTGAGC	CTCAGTTTCC	TTATGTGAAA	GTTGCTGGAA	2220
	CCAAATGGA	GTCACTTATG	CCAAACTCTA	ATAAAATGGA	GTCCGGGGGG	CACATAGAAG	2280
35	CCCTACACCA	CACATGCCCG	TAACAGGATT	TATCACCAAG	ACACGCTCTG	ATGTAAGACC	2340
	AGACACAGGG	CGTATGGAAG	AGCACGTCTT	CAAAGACTGT	AGTATTCAGG	ATGAGCTGCA	2400
	GATGCTTACC	TCCACGGGAA	GTCTCCACCA	GAAAACCATC	GCCAACTCTT	GCGATCAGCT	2460
	TGTGACTTAC	AAACCTTGTG	TAAAAGCTGC	TTACATGGAC	TTCTGTCTCT	TAAAACGTTT	2520
40	CCCTTGGCTG	TGGCCCTCTG	TGTATGCTCG	GGATCCTTCC	AAGCACTCAT	AGCCACAGATA	2580
	GGAATCCTCT	GCTCCTCCCA	AATAAATTCA	TCTGTTTC			

Seq ID NO: 111 Protein sequence:
Protein Accession #: NP_000686

45	1	11	21	31	41	51	
	MDDEPRSTNL	FMKLDVSFVW	KEPFGLVLII	APWNYPLNLT	LVLLVGTLP	GNCVVLKPS	60
	ISQGTKEVLA	EVLPPYLDQS	CPAVVLGGPQ	ETQQLLEHL	DYIFFTGSPP	VGRIVMTAAT	120
50	KHLTPVTLLE	GGKNPCYVDD	NCDPQTVANR	VAWFYCFNAG	QTCVAPDYVL	CSPMEQERLL	180
	PAIQSTITRF	YDDDPQSSEF	LGRIINQKQF	QRLRALLGCG	RVAIGGQSNE	SDRYIAPTVL	240
	VDVQETEPFM	QBEIFGPILL	IVNVQSVDEA	IKPINRQEPK	LALYAFNSNR	QVNVQMLBRT	300
	SSGSFGNGEG	FTYISLLSVP	FGGVGHSGMG	RYHGKFTFDT	FSHHRTCLLA	PSGLEKLKEI	360
	RYPPYTDWNQ	QLLRWGMGSQ	SCTLL				

Seq ID NO: 112 DNA sequence
Nucleic Acid Accession #: NM_004456
Coding sequence: 58-2298

60	1	11	21	31	41	51	
	GAATTCGGGG	CGACGCGCGG	GAACAACGCG	AGTCGGCGCG	CGGGACGAAG	AATAATCATG	60
	GGCCAGACTG	GGAAGAAATC	TGAGAAGGGA	CCAGTTTGTG	GGCGGAAGCG	TGTAAATCA	120
	GAGTACATGC	GACTGAGACA	GCTCAAGAGG	TTCAAGACGAG	CTGATGAAAT	AAAGAGTATG	180
65	TTTAGTTC	ATCGTCAGAA	AATTTTGGAA	AGAACGGAAA	TCTTAAACCA	AGAATGGAAA	240
	CAGCGAAGGA	TACAGCCTGT	GCACATCCTG	ACTTCTGTGA	GCTCATTGCG	CGGGACTAGG	300
	GAGTGTTCGG	TGACCAAGTA	CTTGGATTTT	CCAACACAAG	TCATCCCAT	AAAGACTCTG	360
	AATGCAAGTG	CTTCAGTACC	CATAATGTAT	TCTTGGTCTC	CCCTACAGCA	GAATTTTATG	420
	GTGGAAGATG	AAACTGTTTT	ACATAACATT	CCTTATATGG	GAGATGAAAT	TTTAGATCAG	480
70	GATGGTACTT	TCATTGAAGA	ACTAATAAAA	AATTATGATG	GGAAGTACA	CGGGGATAGA	540
	GAATGTGGGT	TTATAAATGA	TGAAATTTTT	GTGGAGTTGG	TGAATGCCCT	TGGTCAATAT	600
	AATGATGATG	ACGATGATGA	TGATGGAGAC	GATCCTGAAG	AAAGAGAAGA	AAAGCAGAAA	660
	GATCTGGAGG	ATCACCGAGA	TGATAAAGAA	AGCCGCCCCC	CTCGGAAATT	TCCTTCTGAT	720
75	AAAATTTTGG	AGGCCATTTC	CTCAATGTTT	CCAGATAAGG	GCACAGCAGA	AGAACTAAAG	780
	GAAAAATATA	AAGAACTCAC	CGAACAGCAG	CTCCAGGGCG	CACCTCCTCC	TGAATGTACC	840
	CCCAACATAG	ATGGACCAAA	TGCTAAATCT	GTTCAGAGAG	AGCAAAGCTT	ACACTCCTTT	900
	CATACGCTTT	TCTGTAGGCG	ATGTTTAAAA	TATGACTGCT	TCCTACATCC	TTTTTCATGCA	960
	ACACCCACAA	CTTATAAGCG	GAAGAACACA	GAAACAGCTC	TAGACAACAA	ACCTTGTGGA	1020
	CCACAGTGTG	ACCAGCATTT	GGAGGGAGCA	AAGGAGTTTG	CTGCTGCTCT	CACCGCTGAG	1080
80	CGGATAAAGA	CCCCACCAAA	ACGTCCAGGA	GGCCGCGAG	GAGGACGGCT	TCCCAATAAC	1140
	AGTAGCAGGC	CCAGCACCCC	CACCATTAAT	GTGCTGGAAT	CAAAGGATAC	AGACAGTGAT	1200
	AGGGAAGCAG	GGACTGAAR	GGGGGGAGAG	AACAATGATA	AAGAAGAAGA	AGAGAAGAAA	1260
	GATGAACACT	CGAGCTCTCT	TGAAGCAAA	TCTCGGTGTC	AAACACCAAT	AAAGATGAAG	1320
	CCAAATATTG	AACCTCTCTG	GAATGTGGAG	TGGAGTGGTG	CTGAAGCCTC	AATGTTTAGA	1380
85	GTCTCATTTG	GCACCTACTA	TGACAATTTT	TGTGCCATTG	CTAGGTTAAT	TGGGACCAAA	1440
	ACATGTAGAC	AGGTGTATGA	GTTTAGAGTC	AAAGAATCTA	GCATCATAGC	TCCAGCTCCC	1500
	GCTGAGGATG	TGGATACTCC	TCCAAGGAAA	AAGAAGAGGA	AACACCGGTT	GTGCGCTGCA	1560
	CATGACAGAA	AGATACAGCT	GAAAAAGGAC	GGCTCCTCTA	ACCATGTTTA	CAACTATCAA	1620

5
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CCCTGTGATC ATCCACGGCA GCCTTGTGAC AGTTCGTGCC CTTGTGTGAT AGCACAAAAT 1680
TTTTGTGAAA AGTTTTGTCA ATGTAGTTCA GAGTGTCAAA ACCGCTTTCC GGGATGCCGC 1740
TGCAAAAGCAC AGTGCACACAC CAAGCAGTGC CCGTGCTACC TGGCTGTCCG AGAGTGTGAC 1800
CCTGACCTCT GTCTTACTTG TGGAGCCGCT GACCATGGG ACAGTAAAAA TGTGTCTCTG 1860
AAGAACTGCA GTATTACGCG GGGCTCCAAA AAGCATCTAT TGCTGGCACC ATCTGACGTG 1920
GCAGGCTGGG GGATTTTAT CAAAGATCCT GTGCAGAAA ATGAATTCAT CTCAGAATAC 1980
TGTGGAGAGA TTATTCTCA AGATGAAGCT GACAGAAGAG GGAAAGTGTA TGATAAATAC 2040
ATGTGCAGCT TTCTGTTCAA CTGTAACAAAT GATTTTGTGG TGGATGCAAC CCGCAAGGGT 2100
AACAAAAATC GTTTTGCAAA TCATTGCGTA AATCCAAACT GCTATGCAAA AGTTATGATG 2160
GTTAAACGTTG ATCAGAGGAT AGGTATTTT GCCAAGAGAG CCATCCAGAC TGGCGAAGAG 2220
CTGTTTGTG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTCGG CATCGAAAGA 2280
GAAATGGAAA TCCCTTGACA TCTGCTACCT CCTCCCCTC CTCTGAAACA GCTGCCTTAG 2340
CTTCAGGAAC CTCGAGTACT GTGGGCAATT TAGAAAAAGA ACATGCAGTT TGAATTTCTG 2400
AATTGCAAAA GTACTGTAAG AATAATTTAT AGTAATGAGT TTAATAATCA ACTTTTATT 2460
GCCTTCTCAC CAGCTGCAAA GTGTTTGTGA CCAGTGAATT TTTGCAATAA TGCAGTATGG 2520
TACATTTTTC AACTTTGAAT AAAGAATACT TGAACCTGAA AAAAAA AAAAAA

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20 Seq ID NO: 113 Protein sequence:
Protein Accession #: NP_004447

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35

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1 11 21 31 41 51
MGQTGKKSEK GPVCRWRKRVK SEYMRLRLQLK RFRRRADEVKS MFSSNRQKIL ERTEILNQEW 60
KQRRIQPVHI LTVSSSLRGT RECSVTSDDL FFTQVILPKT LNAVASVPIM YSWSPLOQNF 120
MVEDEVVLHN IPYMGDEVL D QGTFIEELI KNYDGKVGHD RECGFINDEI FVELVNALGO 180
YNDDDDDDDG DDPEEREKQ KDLEDHRDDK BSRPFRKFPF DKILEAISSM FPDKGTAEEL 240
KEKYKELTEQ QLPGLAPPEC TPNIDGPNNAK SVQREQSLHS FHTLFCRRCF KYDCFLHPFH 300
ATPNTYKRKN TETALDNKPC GPQCYQHLEG AKEFAAALTA ERIKTPPKRP GRRRRGRLPN 360
NSSRPSTTI NVLESKDTDS DREAGTETGG ENNDKEEEK KDETSSSSSEA NSRCQTPIM 420
KNPIEPPEPV EWSGABASMP RVLIGTYDYN FCAIARLIGT KTCRQVYEFR VKESSIIAPA 480
PAEDVDTPPR KKKRKHRLWA AHCRIQLKK DGSSNHVYNY QPCDHPRQPC DSSCPCVIAQ 540
PFCEKPCQCS SECQNRFPFC RCKAQCNTHQ CFCYLAVREC DPDLCLTCGA ADHWDKSNV 600
CNKNSIQRGS KKHLLALLPSD VAGWGIKID PVQKNFISE YCGEIIISQDE ADRRGKVYDK 660
YMCSEFLNLN NDFVVDATRK GNKIRFANHS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE 720
ELFVDYRYSQ ADALKYVGIE REMEIP

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40 Seq ID NO: 114 DNA sequence
Nucleic Acid Accession #: NM_001827
Coding sequence: 96-335

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50
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1 11 21 31 41 51
AGTCTCCGGC GAGTTGTGTC CTGGGCTGGA CGTGGTTTGG TCTGCTGCGC CGCTCTTCG 60
CGCTCTCGTT TCATTCTCTG CAGCGCGCCA CGAGGATGGC CCACAAGCAG ATCTACTACT 120
CGGACAAAGTA CTTGAGCAAA CACTACGAGT ACCCGCATGT TATGTTACCC AGAGAACTTT 180
CCAAACAAAGT ACCTAAAACT CATCTGATGT CTGAAGAGGA GTGGAGGAGA CTGGTGTCC 240
AACAGAGTCT AGGCTGGGTT CATTACATGA TTCATGAGCC AGAACCATAT ATTCTTCTCT 300
TTAGACGACC TCTTCCAAAA GATCAACAAA AATGAAGTTT ATCTGGGGAT CGTCAAATCT 360
TTTTCAAATT TAATGTATAT GTGTATATAA GGTAGTATTC AGTGAATACT TGAGAAATGT 420
ACAAATCTTT GATCCATACC GTGTCATGAG CTGTATTCTT CACAGCAACA GAGCTCAGTT 480
AAATGCAACT GCAAGTAGGT TACTGTAAAG TGTTTAAGAT AAAAGTCTCT CCAGTCAGTT 540
TTTCTCTTAA GTGCTGTTT GAGTTTACTG AAACAGTTTA CTTTGTGTTCA ATAAAGTTTG 600
TATGTTGCAT TTAATAAAAA AAAAAA

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60 Seq ID NO: 115 Protein sequence:
Protein Accession #: NP_001818

65

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1 11 21 31 41 51
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EPEPHILLFR RPLPKDQK

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70 Seq ID NO: 116 DNA sequence
Nucleic Acid Accession #: CAT cluster

75
80
85

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1 11 21 31 41 51
TCAGACCTCA TGAGTCACTT GGACTCTTGA GCCACCTCTG GGGGTGGAGT CTCTCTCCTG 60
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AGAGGTGTGT TCCAGGGAAA GCCCTATCT CTCTGCAGAG GTCAAGTGAA AGCGACGGCC 180
GCAGCCAACA GAGTTCAAAA TGCAGGCTTG GAAAGTACAG GGGGCTCTGT GGAGGATGGG 240
AAGGACTGAT CCACATCCCC ACCAGGAAGT TTAGCAGAAC CCCCGGTGTC CAACTGGACC 300
CCTTGGAAAG ACCTGGCTCA GGCTGGACCA CCTCTTGAGA GGGAGGAGCT CTGGATTGTA 360
TCAAGAATTC TTTGCTGAGC ATGGTGCCTC ATGCCTATAA TACCAACACT TTGGGAGGCC 420
AGTGTGGGAG GATCTCTTGA GCCCAGGAGT TCAAGACTAG CCTGGGCAAC ACAGAGAGAA 480
CCCATCTCTA AAATAATAAT AATAATAAAA TAAAAAATTA GCAGGGCATG GTGGCATGTG 540
CCTGTAGTTC CAGCTACCCA GGAGGCTGAG GCAAGAGGAT GGCTGGAGCT TGGGATGTTG 600
AGGCTGCAAT GAACGTGTAT TACCCCACTG CACTCCAGCC TGGGCAAAAG AGCGAGAGAA 660
CCTGTCTCAA ATAATAATAA TAATAATAAT CTTATTTTGG AGAATAAGA GACCTCTGGA 720
TTTGAGGTGC CATTTGGGTA GAAAGAAAAG ACGTTTACAC CGAGAAATAG TCTGTGTTGC 780
CCTGAAGGAG CAGAGGGATG CATCGCTGGA GGTGACCTAC AGTTGAAGAA GACTCATTAT 840
GACAGACTTC GTCTTCTTC CTGTGTGAAA GTGTTTCTCT TGCTGCTACT GCTCATGAGA 900
CTCTTCCCCC TCCCTGTCCC AGGGAACCAA AGGGCTTTCT ACCACACCT TCTTGTCCCC 960
CGCCCTCCCA TGTCTGCTGT GCCTTTGTAC TCAGCAATTC TTGTTTGTCT CATTATCTTC 1020
CAGCCGGATA CAGAGTGAAT AGTTAACCACT ACTTAGGTCA AATAGGATCT AAATTTTGT 1080
TCCTGCTCCG TGTAAGAGG CCAGTGTGTT TGTGTGCAA GCAGCCTTG AATAGTAAT 1140

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5 CTTCTCATTT GTTGGGATC TGGCCACCAA GTTCCAGAAT GATACACGGA TCAGTGCAGA 1200
 AGTTCATCAG GCTCTCGGAC CTTAGGGCTG TTGAGAAAGG CTTGAGCAGC AGAACTGATG 1260
 GTGAAGGCTC GTGTTCTCCA TCCTCAACTT TCTTTGCTTC GATCATACAC AAGAATACAT 1320
 TTGGAAGGGC AAAAAATGAA CACTGTCGTT CATTGCAGCC GTGTTTTGTG ACACAGATGC 1380
 ACAGTCTGCT GTGAAGACCT TCTCTCAAGT GGCATTGTTG AGTCCATGCC AGATCATGGT 1440
 GCTTCTAGAG ATGACTGACAG CTATCAGGGG TTGTGGCACT TAGTGAGGAC TCTCTCCCC 1500
 CAGTGTGTGC TGATGACACA ATACACCTCG ACAAATAGCT GAGTCTTCTC TGTTCCTTTT 1560
 ACTCTGTAGC CAACATACAC ATGATTTAAA ACCCTTTCTA AATATCTATC ATGGTTTCATC 1620
 10 CTTGTCCAAA TGCAGAGTCA GAGCTATTTC TACTTCATTA TTATTTCCAA GGCAGAAATAGT 1680
 TGGCTTTCTT TTTGCAAAAA TAATTAAAGT TTTTGTATGT TGCAAAAAAA AAAAAAAA 1740
 AAACAAAAAA

Seq ID NO: 117 DNA sequence
 Nucleic Acid Accession #: BC012178.1
 Coding sequence: 204-2285

1 11 21 31 41 51
 20 CTTCTCTCCC GCGCGCTGG GCGCGCGCT CCGCTGCTGT TGCTCCATTG GCGCGTTTTT 60
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 CCGCGGCTCC GGCCTTGGCC CCGATGGCTC TGTGCAACGG AGACTCCAAG CTGGAGAATG 240
 CTGGAGGAGA CCTTAAGGAT GGCCACCACC ACTATGAAGG AGCTGTTGTC ATTCTGGATG 300
 25 CTGGTGTCTCA GTACGGGAAA GTCATAGACC GAAGAGTGAG GGAAGTGTTC GTGCAGTCTG 360
 AAATTTTCCC CTGGGAAACA CCAGCATTTC CTATAAGGA ACAAGGATTC CGTGTCTATTA 420
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 TATTCACATAT TGGCAAGCCT GTTCTTGGA TTTGCTATGG TATGCAGATG ATGAATAAGG 540
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 30 TGGATAATAC ATGTTCATTA TTCAGGGGCC TTCAGAAGGA AGAAGTGTGT TGTCTTACAC 660
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 TAGTAGCAGG AGAATCTAAA AGTTTATATG AGCACAGTTC CACCCTGAAG 780
 TTGGCCTTAC AGAATATGGA AAGTAATATC TGAAGAATTT CCTTTATGAT ATAGCTGGAT 840
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 35 GAGTAGGCAC GTCAAAAGTT TTGTTTTTAC TCAGTGGTGG AGTAGACTCA ACAGTTTGTA 960
 CAGCTTTGCT AAATCGTGCT TTGAACCAAG AACAAAGTCAT TGCTGTGCAC ATTGATAATG 1020
 GCTTTATGAG AAAACGAGAA AGCCAGTCTG TTGAAGAGGC CCTCAAAAAG CTTGGAATTC 1080
 AGGTCAAAGT GATAATGTCT GCTCATCTCT TCTACAATGG AACAAACAAC CTACCAATAT 1140
 CAGATGAAGA TAGAACCCCA CGGAAAAGAA TTAGCAAAAC GTTAAATATG ACCCAAGTCA 1200
 40 CTGAAGAGAA AAGAAAAATC ATTGGGGATA CTTTGTATA GATTGCCAAT GAAGTAATTTG 1260
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 45 TTTCCAGGCA TCCATTTCCA GGTCTTGGCC TGGCAATCAG AGTAATATGT GCTGAAGAAC 1560
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 50 CCAGTAAAGA TGAACCTGAC TGGGAATCAC TTATTTTCTT GGCTAGGCTT ATACCTCGCA 1860
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 CAGATGTGTAC TCCCACTTTC TTGACACAG GGGTGTCTAG TACTTTACGC CAAGCTGATT 1980
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 55 GATCTGTGGT TATTCGAAAC TTTATTACTA GTGACTTCAT GACTGGTATA CTGCAACAC 2160
 CTGGCAATGA GATCCCTGTA GAGGTGGTAT TAAAGATGGT CACTGAGATT AAGAAGATTC 2220
 CTGGTATTC TCGAATTATG TATGACTTAA CATCAAAGCC CCCAGGAAC ACTGAGTGGG 2280
 AGTAATAAAC TTCTGTCTCT ATTAATA

Seq ID NO: 118 Protein sequence:
 Protein Accession #: AAH12178.1

1 11 21 31 41 51
 65 MALCNGDSKL ENAGGDLKDG HHHYEGAVVI LDAGAQYGVK IDRRVRELTV QSEIFPLETP 60
 AFAIKEQGFRI AIISGGFNS VYAEAPWFD PAIFTIGKPV LGICYGMQMM NKVFGGTVHK 120
 KSVREDGVFN ISVDNTCSLF RGLQKEVVLL LTHGDSVDKV ADGFKVVAR S GNIVAGIANE 180
 SKKLYGAQFH PEVLGTENGK VILKNFLYDI AGCSGTFTVQ NRELECIREI KERVTGTSKVL 240
 70 VLLSGGVNST VCTALLNRAL NQEQVIAVHI DNGPMRKRES QSVESALKKL GIQVKVINAA 300
 HSFYNGTTTL PISDEDRTFR KRISKTLNMT TSPEEKRII GDTFVKIANE VIGEMNLKPE 360
 EVFLAQGTLR PDLIESASLV ASGKAELIKT HHNDTELIRK LREEGKVIEP LKDPHKDEV 420
 ILGRELGLPE ELVSRHPFPG PGLAIRVICA EEPYICKDFP ETNNILKIVA DFSASVKKPH 480
 TLLQRVKACT TEEDQELMQ ITSLSLNAF LLPIKTVGVQ GDGRSYSYVC GISSKDEPDW 540
 75 ESLIFLARLI PRMCHNVNRV VYIFGPPVKE PPTDVTPTFL TTGVLSTLRQ ADPEAHNLR 600
 ESGYAGKISQ MPVILTPLHF DRDPLQKPS QQRSVVIRTF ITSDFMTGIP ATPGNEIPVE 660
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Seq ID NO: 119 DNA sequence
 Nucleic Acid Accession #: NM_006500.1
 Coding sequence: 27..1967

1 11 21 31 41 51
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 CCGCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCTCTCCC 180
 AGTCCCAAGG CAACCTCAGC CATGTCGACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC 240

	TCATCTTCGG	TGTGCGCCAG	GGCCAGGGCC	AGAGCGAACC	TGGGGAGTAC	GAGCAGCGGC	300
	TCAGCCTCCA	GGACAGAGGG	GCTACTCTGG	CCCTGACTCA	AGTCACCCCC	CAAGACGAGC	360
	GCATCTTCTT	GTGCCAGGGC	AAGCGCCCTC	GGTCCCAGGA	GTACCGCATC	CAGCTCCGCG	420
5	TCTACAAAGC	TCCGGAGGAG	CCAAACATCC	AGGTCAACCC	CCTGGGCATC	CCTGTGAACA	480
	GTAAGGAGCC	TGAGGAGGTC	GCTACCTGTG	TAGGGAGGAA	CGGGTACCCC	ATTCTCAAG	540
	TCATCTGGTA	CAAGAAATGGC	CGGCCTCTGA	AGGAGGAGAA	GAACCCGGTC	CACATTCAAGT	600
	CGTCCCAGAC	TGTGGAGTCG	AGTGGTTTGT	ACACCTTGCA	GAGTATTCTG	AAGGCACAGC	660
	TGGTTAAAGA	AGACAAAGAT	GCCCAGTTTT	ACTGTGAGCT	CAACTACCGG	CTGCCAGTGT	720
10	GGAAACCAT	GAAGGAGTCC	AGGGAAGTCA	CCGTCCCTGT	TTTCTACCCG	ACAGAAAAG	780
	TGTGGCTGGA	AGTGGAGCCC	GTGGGAATGC	TGAAGGAAGG	GGACCGCGTG	GAATCAGGT	840
	GTTTGGCTGA	TGGCAACCTT	CCACCACACT	TCAGCATCAG	CAAGCAGAAC	CCCAGCACCA	900
	GGGAGGCAGA	GGAAAGAGACA	ACCAACGACA	ACGGGCTCCT	GGTGTGAGAG	CCTGCCCGGA	960
	AGGAACACAG	TGGGCGCTAT	GAATGTCAGG	CCTGGAACTT	GGACACCATG	ATATCGCTGC	1020
15	TGAGTGAACC	ACAGGAACTA	CTGGTGAAC	ATGTGTCTGA	CGTCCGAGTG	AGTCCGCGAG	1080
	CCCCTGAGAG	ACAGGAAGGC	AGCAGCCTCA	CCCTGACCTG	TGAGGCAGAG	AGTAGCCAGG	1140
	ACCTCGAGTT	CCAGTGCTCG	AGAGAAGAGA	CAGACCAAGT	GCTGGAAAGG	GGGCGTGTGC	1200
	TTCAGTTGCA	TGACCTGAAA	CGGGAGGCAG	GAGGCGGCTA	TGCTGCGTGT	GGCTCTGTGC	1260
	CCAGCATACG	CGGCTGTAAC	CGCACACAGC	TGGTCAAGCT	GGCCATTTTT	GGCCCCCTTT	1320
20	GGATGGCATT	CAAGGAGAGG	AAGGTGTGGG	TGAAAGAGAA	TATGTGTGTG	AATCTGTCTT	1380
	GTGAAGCGTC	AGGGCAGCCC	CGGCCACCA	TCTCTGGAA	CGTCAACGGC	ACGGCAAGTG	1440
	AACAAGAGCA	AGATCCACAG	CGAGTCTCTG	GCAACCTGAA	TGTCTCGTGT	ACCCCGGAGC	1500
	TGTTGGAGCA	AGGTGTTGAA	TGCACGGCCT	CCAACGACCT	GGGCAAAAC	ACCAGCATCC	1560
	TCCTTCTGGA	GGCTCTCAAT	TAAACACCC	TCACACAGA	CTCCAACACA	ACCACTGGCC	1620
25	TCAGCACTTC	CACTGCCAGT	CCTCATACCA	GAGCCAACAG	CACCTCCACA	GAGAGAAAGC	1680
	TGCCGGAGCC	GGAGAGCCGG	GGCGTGGTCA	TCGTGGCTGT	GATTGTGTGC	ATCCTGGTCC	1740
	TGGCGGTGCT	GGGCGTGTCT	CTCTATTTC	TCTATAAGAA	GGGCAAGCTG	CCGTGCAGGC	1800
	GCTCAGGAA	GCAGGAGATC	ACGCTGCCCT	CGTCTCGTAA	GACCGAAGCT	GTAGTTGAAG	1860
	TTAAGTCAGA	TAACTCCCA	GAAGAGATGG	GCCTCTGACA	GGGCAGCAGC	GGTGACAAGA	1920
30	GGGCTCCGGG	AGACCAGGGA	GAGAAATACA	TCGATCTGAG	GCATTAGCCC	CGAATCACTT	1980
	CAGCTCCCTT	CCCTGCTGCG	ACCATTCCCA	GCTCCCTGCT	CACCTCTCTC	TCAGCCAAAG	2040
	CCTCCAAAGG	GACTAGAGAG	AAGCCTCCTG	CTCCCTCAC	CTGCACACCC	CCTTTCAGAG	2100
	GGCCACTGGG	TTAGGACCTG	AGGACCTCAC	TGGGCCCTGC	AAGCCGCTTT	TCAGGGAACA	2160
	GTCCACCACC	ATCTCTCTCA	CGTTGAGTGA	AGCTCATCCC	AAGCAAGGAG	CCCCAGTCTC	2220
35	CCGAGCGGGT	AGGAGAGTTT	CTTGACAGAC	GTGTTTTTTC	TTTACACACA	TTATGGCTGT	2280
	AAATACCTGG	CTCTGTCAG	GAGCTGAGCT	GGGTAGCCTC	TCTGAGCTGG	TTTCTGCCC	2340
	CAAAGGCTGG	CTTCCACCAT	CCAGGTGCAC	CACTGAAATG	AGGACACACC	GGAGCCAGGC	2400
	GGCTGCTCAT	GTTGAAGTGC	GCTGTTTACA	CCCGCTCCGG	AGAGCACCCC	AGCGGCATCC	2460
	AGAAGCAGCT	CGCTGTGTGC	TGCCACCACC	CTCCTGCTCG	CCTCTTCAAA	GTCTCTGTGT	2520
40	ACATTTTTTC	TTTGGTCAGA	AGCCAGGAAC	TGGTGTCTAT	CCTTAAAGA	TACGTGCCGG	2580
	GGCCAGGTGT	GGTGGCTCAC	GCCTGTAATC	CCAGCACTTT	GGGAGGCCGA	GGCGGGCGGA	2640
	TCACAAAGTC	AGTACGAGAC	CATCCTGGCT	AACACGGTGA	AACCTGTCTC	CTACTAAAAA	2700
	TACAAAAAAA	AATAGCTAG	CGGTAGTGGT	TGGCACCTAT	AGTCCCAGCT	ACTCGGAAGG	2760
	CTAAGCGAGG	AAATGTGTAT	GATCCAGGA	GGTGGAGCTT	GCAGTGAGCT	GAGACCGTGC	2820
45	CACTGCATCT	CAGCTGGGCG	AACACAGCGA	GACTCCGTCT	CGAGGAAAAA	AAAAGAAAAA	2880
	ACGCGTACCT	GCGGTGAGGA	AGCTGGGCGC	TGTTTTTCAG	TTGAGGTGAA	TTAGCTCTCA	2940
	TCCCGTGTGT	CACCTGTCTC	CATAGCCCTC	TTGATGGATC	ACGTAAAGCT	GAAGGCAGC	3000
	GGGAGGACGA	CAAGATGTAG	GTCTACACTG	TCCTTCATGG	GGATTAAAGC	TATGGTTATA	3060
	TTAGCACCAA	ACTTCTACAA	ACCAAGCTCA	GGGCCCAAC	CTAGAAAGGG	CCCAATGAG	3120
50	AGAAATGTAC	TTAGGGATGG	AAAACGGGGC	CTGGCTAGAG	CTTCGGGTGT	GTGTGTCTGT	3180
	CTGTGTGTAT	GCATACATAT	ATGTGTATAT	TGTGTATATA	TATATGAAAA	TATATATATA	3240
	TGTTTTCTCT	TATATATGTA	TATATGAAAA	TATATATATA	TATGAAAAAT	TATGAAAAAT	3300
	AAAGCTTAAT	TGTCCCAGAA	AATCATACAT	TGCTTTTTTA	TTCTACATGG	GTACCACAGG	3360
	AACCTGGGGG	CCTGTGAAAC	TACAACCAAA	AGGCACACAA	AACCGTTTCC	AGTTGGCAGC	3420
55	AGAGATCAGG	GGTTACCTCT	GCTTCTGAGC	AAATGGCTCA	AGCTCTACCA	GAGCAGACAG	3480
	CTACCCTACT	TTTCAGCAGC	AAAACGTCCC	GTATGACGCA	GCACGAAGGG	CCTGGCAGGC	3540
	TGTTAGCAGG	AGCTATGTCC	CTTCTATATG	TTTCCGTCCA	CTT		

Seq ID NO: 120 Protein sequence:
Protein Accession #: NP_006491.1

	1	11	21	31	41	51	
65	MGLPRIVCAF	LLAACCCCPR	VAGVPGEAEO	PAPELVEVEV	GSTALLKCOL	SQSQGNLSHV	60
	DWFSVHKEKR	TLIFRVRQGG	QSEPGGEYEQ	RLSLQDRGAT	LALTQVTFQD	ERIFLCQGR	120
	PRSQEYRIQL	RVYKAPBEPN	IQVNPGLGIPV	NSKEPEEVAT	CVGRNGYPIPI	QVIWYKNGRP	180
	LKEEKNRVHI	QSSQTVSSSG	LYTLQSLILKA	QLVKEDKDAQ	FYCELNYRLP	SGNHMKESRE	240
70	VTVPVFYFTE	KVWLEVEFVG	MLKEGDRVEI	RCLADGNPPP	HFSISKQNFPS	TREAEETTN	300
	DNGVLVLEPA	RKEHSGRYEC	QAWNLDTMIS	LLSEPOELLV	NYVSDVRVSP	AAPERQEGSS	360
	LTLTCEABSS	QDLFQWLRE	ETDQVLERGP	VLQLHDLKRE	AGGGYRCVAS	VPSIPGLNRT	420
	QLVKLAIFGP	PWMAFKERKV	WVKENMVLNL	SCBASGHPRP	TISWNVNGTA	SEQDQDPQRV	480
	LSTLNLVLT	ELLETVGECT	ASNDLGKNTS	ILFLELVNLT	TLTPDSNTTT	GLSTSTASPH	540
75	TRANSTSTER	KLPEPESRGV	VIVAVIVCIL	VLAVLGAVLY	FLYKKGKLPC	RRSGRQEITL	600
	PFSRKTELVV	EVKSDKLPPE	MGLLQSSSGD	KRAPGDQGEK	YIDLRH		

Seq ID NO: 121 DNA sequence
Nucleic Acid Accession #: NM_018306
Coding sequence: 60-671

	1	11	21	31	41	51	
80	ATAGTCTACA	CAGAGCTCCC	CTTGCTGCCC	AGACAAGCTG	AAGGACCACA	GGAAAAGCCA	60
	TGGAGACTTC	AGCATCTCTC	TCCAGCCTC	AGGACAACAG	TCAAGTCCAC	AGAGAAACAG	120
85	AAGATGTAGA	CTATGGAGAG	ACAGATTTC	ACAAGCAAGA	CGGGAAGGCT	GGACTCTTTT	180
	CCCAAGAAC	ATATGAGAGA	AACAAGTCTT	CTTCTCTCTC	CTTCTCTTCC	TCCTCATCTC	240
	CCTCATCTTC	TTCATCTCTC	TCCTCTCTCAG	GTCTGGGCA	TGGGAGCCT	GACGTTTTGA	300

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PCT/US02/12476

AGGATGAGCT TCAACTCTAT GGAGATGCTC CTGGAGAGGT GGTACCCTCT GGGGAATCAG 360
 GACTCCGAAG GAGAGGCTCT GACCCAGCAA GTGGAGAAGT GGAGGCCTCT CAGTTAAGAA 420
 GACTGAATAT AAAGAAAGAT GATGAGTTT TCCATTTCGT CCTCCTGTGC TTTGCCATCG 480
 GGGCCTTGCT GGTGTGTTAT CACTATTACG CAGACTGGTT CATGTCTCTT GGGGTCCGCC 540
 TGCTCACCTT CGCTCCCTTG GAAACCGTTG GCATCTACTT CGGACTAGTG TACCGTATCC 600
 ACAGCGTCCT CCAAGGCTTC ATCCCTCTCT TCCAGAAAGT TAGGCTGACA GGGTTCAGGA 660
 AGACTGACTG AGGCCACTTC CAGGTGGGCA GCAGAGGCAG GCCCAGTGT GACCACCACT 720
 GCGACCCCTG AGCCCAAG GGCAGAGCAG CATTCTGAGA GACGCACAGG AGACCAAGCC 780
 AGACCAATAA ACAGAACACT TTTCTTCCA TGTGCTGTA ATGTTGGCAC CAGCCCGGCC 840
 AGGGGCATCT CATTGCGGCA GTACTGCTGT GCAACCCAGC TGCAAGGATG GAAGGCAGAG 900
 GGTGGGTGTG GGGCCTGAGG CTTCACAGTA CCTGGACCAG CAGGAAGATT CTGGGAGGTC 960
 ACTGCTCTCA GAGGACAGCA AGGGACCCCTG AGCTCTGCAA GCTGTGATCT GTCTGGGTTT 1020
 ATGGTTTTTC TCAAATCCCA GGCTATCTGC ATGCGCTCTC AGGTGCTACC GAGCCATCCT 1080
 GGGAGAGATG GATGGTCCAC TGCTTTGAGG CAGGGAGCCA TCGGCTGGG GCCCTTGGT 1140
 GAACTCGATG CAGGTAAAGT GCTGAGGACT AAAACCATTT TTTTGCACC CAAAAAATAA 1200
 GGCAGGAAAA TGATCTCAG AAACCTAAATG GCAGCCAGGC ATGGGGGCTC ACGACTGTAA 1260
 TCCTCGCACT TTGGGAGGCT CAGGCTAAGG GTGCGCTTGA GCTGAGAGTT CAAGACCAAC 1320
 CTGGGCAACA TAGTGAGACC CCGATCTCTA CAATTTTTTT TTAATGACCA AATGTGGCGG 1380
 TACATACCTG TACATACCTG CGGTTCACAG TACTCAAGAG GCTGAGGCAG GAGGACTGCT 1440
 TGAGCCCAAG AGTTCAGGGC TGCACTGAGG TACGATCAAG CCACTGCACT CCAGCCTGGG 1500
 CGACAGAGCA AGATCGTTTC TCTAAAAAT

Seq ID NO: 122 Protein sequence:
 Protein Accession #: NP_060776

1 11 21 31 41 51
 METSASSSQP QDNSQVHRET EDVDYGETDF HKQDGKAGLF SQEQYERNKS SSSSFSSSSS 60
 SSSSSSSSSS PPHGHEPDLV KDELQLYGDA PGEVVPSSGBS GLRRRGSDPA SGEVEASQLR 120
 RLNIKKDEDF FHFVLLCFPI GALLVCYHY ADWFMSLGVG LLTFASLETV GIYFLVYRI 180
 HSVLQGFPL FQKRLTGFR KTD

Seq ID NO: 123 DNA sequence
 Nucleic Acid Accession #: BC022542
 Coding sequence: 243..896

1 11 21 31 41 51
 ACTTGGTCCC AGCCGATAAA TCTGGGGCAG CGCGCGGTAG GAGCTGCGGG CGGCCAGGCC 60
 CCTTCTGCGG TCCGCGACCTG QCCCGCGCGG CCCCTCTCGG GCGTCCGGCT TCCGGCGTCC 120
 TGGCGGCTCG GGTGGCGGCG GTTCCGGCGG CGCGCTGCGT GCTCCTCGGG GCGGCGACGG 180
 GGCTCACGCG CGGCGCGCGG CCGGCTTCA CCGCGCGCGG CTCTGACGCC GGCATAAGGG 240
 CCATGTGTTC TGAATTTATT TTGAGGCAAG AAGTTTTGAA AGATGGTTTC CACAGAGACC 300
 TTTTAATCAA AGTGAAGTTT GGGGAAAGCA TTGAGGACTT GCACACGTGC CGTCTCTTAA 360
 TTAAACAGGA CATTCCTGCA GCACTTTATG TGGATCCGTA TGAGTTGGCT TCATTACGAG 420
 AGAGAAACAT AACAGAGGCA GTGATGGTTT CAGAAAAATT TGATATAGAG GCCCTTAAT 480
 ATTTGTCCAA GGAATCTGAA GTTCTCATTT ATGCCAGACG AGATTACAGG TGCATTGACT 540
 GTTTTCAAGC CTTTTGCGCT GTGCACTGCC GCTATCATCG GCCGCACAGT GAAGATGGAG 600
 AAGCCTCGAT TGTGGTCAAT AACCCAGATT TGTGTATGTT TTGTGACCAA GAGTCCCGA 660
 TTTTGAATG CTGGGCTCAC TCAGAAAGTG CAGCCCTTGG TGTCTTGGAT AATGAGGATA 720
 TAGTCCCAATG GAACAAGATG AAGTATAAAT CAGTATATAA GAATGTGATT CTACAAGTTC 780
 CAGTGGGACT GACTGTACAT ACCTCTCTAG TATGTTCTGT GACTCTGCTC ATTACAATCC 840
 TGTGCTCTAC ATTGATCCTT GTAGCAGTTT TCAAATATGG CCATTTTTCC CTATAAGTTT 900
 TATGTAGTTA AATGCTTCTT AGAAACCTAA ATAAGATCTA TTAATTTCTG ACGAGAGGTG 960
 TTCTTCTAGA ATTAATTACT TTTATCTTTT GTCTTCATTT GTGGCCAAAA TTATGTTTAC 1020
 TAGAGGAAAT TTGGGATCAT TCTCAGCTAA TTCCAAATG TAGTGTCTTA TTGCTGATG 1080
 CCTTGGTAAT CCTCAAGCAT CAGATGCCAT AAGGGGAAAC TTAATTTCTG TAAATTAATG 1140
 TTTATTTTGT GAGAAGTGCA TTTATCTTCA TTTGGGGTAG AAAAATTATT TCTTTATGTA 1200
 GTAGAGACAA ATTATTCTCA TTTTGCAAGT ACITTTCAAT TAAGCTACAA ATTGAGAAAA 1260
 CGTTTATAAA TAAGAATAAA ATAGGCCAGG CACAGTGGCT CACACCTGTA ATCCAGCAC 1320
 TTTGGGAGGC CGAGGTGGGC GGATCACCAG AGGTCAAGAG TTTGAGACCA GCTTGGTGAA 1380
 ACCCTGTCTC TACTAAAAAT ACAAAAGTTA GCTGGGGCTG GTGGTGGGCA TCTGTAGTCC 1440
 CAGCTAATTG GAAGGGTGAG GCGGGAGGAT CGCTTGAACC TGGGAGGCGG AGGTTCCAGA 1500
 GAGCCAAGAT CGCACCACTG CACTACAGCC TGGGCGACAG AACGAGACCC TGTCTCCAAA 1560
 GGAATAACAA AAAAGAAGAA TAAATAATT TGGATGAAAA TCATGTTTAT TTAATAGTA 1620
 ATGTCATGAG ACTATTAAAG ATGTGCCAGA GTTTCAATGA AAATCATTAA AGTAGGACA 1680
 CTAAGAAATT AATATTAATA TAAAAATTAT TGATAATCTT AAATTATGTA TTATTCCTTA 1740
 ACGCACTCCA TTCTCTTTT ACATTTTATC ATGTTTCTTT TGAATATATG AATTGGCAAA 1800
 GGACTTGATG AAACGTAGTA CTAAGATTG GTACAGAGTA TGTGAGGAAG ACAACTCAGA 1860
 TTGCCATTTT AAATAAAGTT GTACATGAAC AAAAAAATAA AAAAAA

Seq ID NO: 124 Protein sequence:
 Protein Accession #: AAH22542

1 11 21 31 41 51
 MCSBIILRQE VLKDGPHRDL LIKVKFGESI EDLHTCRLLI KQDIPAGLYV DPYELASLRE 60
 RNITEAVMVS ENFDIAPNY LSKSEVLIVY ARRSQCIDC FQAFPLVHCR YHRPHSEGE 120
 ASIVVMNPD LMFCDQAGSR RMIRFRFDSF DKTIEFPILK CWAHSEVAAP CALENEDICQ 180
 WNKMKYKSVY KNVILQVPVG LTVHTSLVCS VTLITILCS KKKKK

Seq ID NO: 125 DNA sequence
 Nucleic Acid Accession #: NM_004994.1
 Coding sequence: 20..2143

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1      11      21      31      41      51
|      |      |      |      |      |
AGACACCTCT GCCCTCACCA TGAGCCTCTG GCAGCCCTG GTCTGTGTGC TCCTGGTGCT 60
GGGCTGTGTC TTTGCTGCCC CCAGACAGCG CCAGTCCACC CTGTGTCTCT TCCCTGGAGA 120
CCTGTAGAAC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA 180
CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCCTGCGC TGTCTGTTCT 240
CCAGAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT 300
GCGAACCCCA CGGTGCGGGG TCCCAGACCT GGCAGATTG CAAACCTTTG AGGGCGACCT 360
CAAGTGGCAC CACCACAACA TCACCTATTG GATCCAAAC TACTCGGAAG ACTTGGCCGG 420
GGCGGTGATT GACGACGCCT TTGCGCGCGC CTTCGCACTG TGGAGCGCGG TGACGCCGCT 480
CACCTTCACT CGCGTGATCA GCCGGGAGCG AGACATCGTC ATCCAGTTTG GTGTGCGGGA 540
GCACGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CCTTCTCTCC 600
TGGCCCCGCG ATTACGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCCTGGGCAA 660
GGGCGTGTG GTTCCAATC GGTTTGGAAA CGCAGATGGC GCGGCTGCC ACTTCCCTTT 720
CATCTTGGAG GGCCGCTCCT ACTCTGCTCG CACCACCGAC GGTCTGCTCG ACGGCTTGCC 780
CTGGTGTGAGT ACCACGGGCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCCCAGCGA 840
GAGACTCTAC ACCCGGGAGC GCAATGTCTG TGGGAAACCC TGCCAGTTTC CATTCATCTT 900
CCAAGGCCAA TCCTACTCCG CCTGCACCAC GGACGGTTCG TCCGACGGCT ACCGTGGTG 960
CGCCACCACC GCCAACTAGC ACCGGGACAA GCTCTTCCGC TTCTGCCGA CCCGAGTGTA 1020
CTCGACGGTG ATGGGGGGCA ACTCGCGGGG GGAGCTGTGC GTCTTCCCTT TCACTTTCTT 1080
GGGTAAAGAG TACTCGTACT GTACCAAGCG GGGCCGCGGA GATGGGCGCC TCTGGTGCGB 1140
TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGGCTTC TGCCCGGACC AAGGATACAG 1200
TTTGTCTCTC GTGGCGGCGC ATGAGTTCCG CCACGCGCTG GGCTTAGATC ATTCTCAGT 1260
GCGGAGGCG CTCTGTACC CTATGTACCG CTTCAGTAG GGGCCCCCTT TGCATAAGGA 1320
CGACGTGAAT GGCATCCGGC ACCTCTATGG TCCTCGCCTT GAACCTGAGC CACGGCCTCC 1380
AACCAACACC ACCACGGGCA CACCGGCTCC CCGCAGGTC TGCCCCACCG GACCCCCAC 1440
TGTCCACCCC TCAGAGCGGC CCACAGCTGG CCCCACAGGT CCCCCCTCAG CTGGCCCCAC 1500
AGTCCGCCCC ACTGCTGGCC TTCTACGGC CACTACTGTG CCTTTAGTGC CGGTGGACGA 1560
TGCCTGCAAC GTGAACATCT TCGACGCCAT CGCGGAGATT GGGAAACCAGC TGTATTTGTT 1620
CAAGATGGG AGTACTGGC GATTCTCTGA GGGCAGGGGG AGCGGGCGCG AGGGCCCTTT 1680
CCTTATCGCC GACATGGTGC CCGCGCTGCC CCGCAAGCTG GACTCGGTCT TTGAGGAGCC 1740
GCTCTCAAG AAGCTTTTCT TCTTCTCTGG GCGCCAGGTG TGGGTGTACA CAGGCGCGTC 1800
GGTGTGGGC CCGAGGCGTC TGGACAAGCT GGGCCTGGGA GCCGACGTGG CCCAGGTGAC 1860
CGGGGCCCTC CGGAGTGGCA GGGGGAAGAT GCTGCTGTTT AGCGGGCGGC GCCTCTGAG 1920
GTTGAGCGTG AAGCGGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGGATGTT 1980
CCCCGGGGTG CCTTTGGACA CGCACGACGT CTTCAGTAC CGAGAGAAAG CCTATTTCTG 2040
CCAGGACCGC TTCTACTGGC GCGTGAGTTC CCGGAGTGAG TTGAACCAGG TGGACCAAGT 2100
GGGCTACGTG ACCATGACA TCTGCAATG CCTGAGGAC TAGGGCTCCC GTCTGCTTT 2160
GCAGTGCCAT GTAAATCCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCGGATA 2220
CAAACTGGTA TTCTGTCTG GAGGAAAGGG AGGAGTGGAG GTGGGCTGGG CCTCTCTTCT 2280
TCACCTTTGT TTTTGTGG AGTGTCTTA ATAAACTTGG ATTTCTAAC CTTT

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Seq ID NO: 126 Protein sequence:
Protein Accession #: NP_004985.1

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1      11      21      31      41      51
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MSLWQPLVLV LVLVLCFFAA PRQRQSTLVL FPGDLRLNLT DRQLAEYLY RYGYTRVAEM 60
RGESKSLQPA LLLQLQLSL PETGELDSAT LKAMRTPRCG VPDLGRFQTF EGDLLKWHHN 120
ITYWIQYSE DLPRVIDDA FARAFALWSA VTPLTPTRVY SRDADIVIOF GVAEHGDCYP 180
FDGKDGLLAH AFPFGPIQG DAHPDDDELW SLGKGVVPT RFGNADGAAC HFPFIFEGRS 240
YSACTTGRS DGLFWCSTTA NYDTRDRFPG CPSERLYTRD GNADGKPCQF PFIFQGGSYS 300
ACTTDRSDG YRWCAATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP PTFLGKEYST 360
CTSEGRDGR LWCATTSNFD SDKWKGFPCD QGYSLFLVAA HEFGHALGLD HSSVPEALMY 420
PMYRFTGPP LHKDDVNGIR HLYGPRPEPE PRPFTTTTPQ PTAPPTVCPT GPPTVHPSER 480
PTAGPTGPPS AGPTGPPTAG PSTATTVPLS PVDDACNVNI FDAIAEIGNQ LYLFPKDGKYW 540
RFSEGRGSRP QGFPLIADKW PALPRKLDV FEEPLSKLFP FFSGRQVWVY TGA SVLGP RR 600
LDKLGLGADV AVQTGALRSR RGMMLFSGR RLWRFDVKAQ MVDPRSASEV DRMPFPGVPLD 660
THDVFQYREK AYPQDRFYW RVSSRSELNQ VDQGVVYTD ILQCPED

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Seq ID NO: 127 DNA sequence
Nucleic Acid Accession #: NM_004181
Coding sequence: 32-670

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1      11      21      31      41      51
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GCAGAAATAG CCTAGGGAGA TCAACCCCGA GATGCTGAAC AAAGTGCTGT CCCGCTGGG 60
GGTGC CGCGC CAGTGGCGCT TCGTGGACGT GCTGGGGCTG GAAGAGGAGT CTCTGGGCTC 120
GGTGCCAGCG CTGCTGCTGC CGCTGCTGCT GCTGTTTCCC CTCACGCGCC AGCATAGAGAA 180
CTTCAGGAAA AAGCAGATTG AAGAGCTGAA GGGACAAGAA GTTAGTCTTA AAGTGTACTT 240
CATGAAGCAG ACCATTGGGA ATTCCTGTGG CACAATCGGA CTATTTCAGC CAGTGGCCAA 300
TAATCAAGAC AAATCGGGAT TTGAGGATGG ATCAGTTCTG AAACAGTTTC TTTCTGAAAC 360
AGAGAAAATG TCCCTGAAG ACAGAGCAAA ATGCTTTGAA AAGAATGAGG CCATACAGGC 420
AGCCCATGAT GCCGTGGCAC AGGAAGGCCA ATGTCGGGTA GATGACAAGG TGAATTTCCA 480
TTTTATTCTG TTTAACCAAG TGGATGGCCA CCTCTATGAA CTTGATGGAC GAATGCCTTT 540
TCCGGTGAAC CATGGGCCCA GTTCAGAGGA CACCCTGCTG AAGGACGCTG CCAAGGTGTG 600
CAGAGAATTG ACCGAGCGTG AGCAAGGAGA AGTCCGCTTC TCTGCCGTGG CTCTCTGCAA 660
GGCAGCCTAA TGCTCTGTGG GAGGACTTT GCTGATTTC CCTCTTCCCT TCAACATGAA 720
AATATATACC CCCCATGCAG TCTAAAATGC TTCAGTACT GTGAAACACA GCTGTTCTTC 780
TGTCTGCAG AACCGCTTC CCTCAGCCA CACCAGGCA CTTAAGCACA AGCAGAGTGC 840
ACAGCTGTCC ACTGGGCCAT TGTGGTGTGA GCTTCAGATG GTGAAGCATT CTCGCCAGTG 900
TATGTCTTGT ATCCGATATC TAACGCTTTA AATGGCTACT TTGGTTTCTG TCTGTAAAGT 960
AAGACCTTGG ATGTGGTTAT GTTGTCTTAA AGAATAAATT TTGCTGATAG TAGC

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Seq ID NO: 128 Protein sequence:
Protein Accession #: NP_004172

1	11	21	31	41	51	
MLNKVLSRLG	VAGQWRFVDV	LGLEEESLGS	VPAPACALLL	LFPLTAQHEN	FRKKQIEELK	60
GQEVSPKVYF	MKQITIGNSCG	TIGLIHAVAN	NQDKLGFEDG	SVLKKQLFSET	EKMSPEDRAK	120
CFEKNEAIIQA	AHDAVAQEGG	CRVDDKVNPH	FILFNNVDGH	LYELDGRMPF	PVNHGASSED	180
TLLKDAAKVC	REFTEREQGS	VRFSVALCK	AA			

Seq ID NO: 129 DNA sequence
Nucleic Acid Accession #: NM_000213
Coding sequence: 127-5385

1	11	21	31	41	51	
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CCCCGAGGTA	GGTCCAGGAC	GGGCGCACAG	CAGCAGCCGA	GGCTGGCCGG	GAGAGGGAGG	120
AAGAGGATGG	CAGGGGCCAG	CCCCAGCCCA	TGGGCCAGGC	TGCTCCTGGC	AGCCTTGATC	180
AGCGTCAGCC	TCTCTGGGAC	CTTGGCAAAC	CGCTGCAAGA	AGGCCCCAGT	GAAGAGCTGC	240
ACGAGGTGTG	TCCGTGTGGA	TAAGGACTGC	GCCTACTGCA	CAGACGAGAT	GTTCAGGGAC	300
CGCGCGTGCA	ACACCCAGGC	GGAGCTGCTG	GCCGCGGGCT	GCCAGCGGGA	GAGCATCGTG	360
GTCAATGGAGA	GCAGCTTCCA	AATCACAGAG	GAGACCCAGA	TTGACACCAC	CCTGGCGGCG	420
AGCCAGATGT	CCCCCAAGG	CCTGCGGGTC	CGTCTGCGGC	CCGGTGAGGA	GCGGCATTTC	480
GAGCTGGAGG	TGTTTGAAGC	ACTGGAGAGC	CCCCTGGACC	TGTACATCCT	CATGGACTTC	540
TCCAATCCCA	TGTCGGATGA	TCTGGACAAC	CTCAAGAAGA	TGGGCGAGAA	CCTGGCTCGG	600
GTCTTGAGCC	AGCTCACCAG	CGACTACACT	ATTGGATTGG	GCAAGTTTGT	GGACAAAGTC	660
AGCGTCCGCG	AGACGGACAT	GAGGCGCTGAG	AAGCTGAAGG	AGCCCTGGCC	CAACAGTGAC	720
CCCCCTTCT	CCTTCAAGAA	CGTCATCAGC	CTGACAGAAG	ATGTGGATGA	GTTCGGGAAT	780
AAACTGCAGG	GAGAGCGGAT	CTCAGGCAAC	CTGGATGCTC	CTGAGGGCGG	CTTCGATGCC	840
ATCCTGCAGA	CAGCTGTGTG	CACGAGGGAC	ATTGGCTGGC	GCCGCGCAGC	CACCCACCTG	900
CTGGTCTTCT	CCACCGAGTC	AGCCTTCCAC	TATGAGGCTG	ATGGCGCCAA	CGTGCTGGCT	960
GGCATCATGA	GCGCAACGA	TGAACGGTGC	CACCTGGACA	CCACGGGCAC	CTACACCCAG	1020
TACAGGACAC	AGGAATCAAC	GTCCGTGCCC	ACCCCTGGTG	GCCTGTCTGC	CAAGCACAAAC	1080
ATCATCCCCA	TCTTTGCTGT	CACCAACTAC	TCCTATAGCT	ACTACAGAGAA	GCTTCACACC	1140
TATTTCCCTG	TCTCTCACT	GGGGGTGCTG	CAGGAGGACT	CGTCCAAACAT	CGTGAGCTG	1200
CTGGAGGAGG	CCTTCAATCG	GATCCGCTCC	AACCTGGACA	TCCGGGCCCT	AGACAGCCCC	1260
CGAGGCCTTC	GGACAGAGGT	CACCTCCAAG	ATGTTCCAGA	AGACGAGGAC	TGGGTCTTTT	1320
CACATCCGGC	AGGGGGAGCT	GGGTATATAC	CAGGTGCAGC	TGCGGGCCCT	TGAGCACGTG	1380
GATGGGACGC	CGGTGTGCCA	GCTGCGGGAG	GACCAGAAAG	GCAACATCCA	TCTGAAACCT	1440
TCCTTCTCCG	ACGGCCTCAA	GATGGACGCG	GGCATCATCT	GTGATGTGTG	CACCTGCGAG	1500
CTGCAAAAG	AGGTGCGGTC	AGCTCGCTGC	AGCTTCAACG	GAGACTTCGT	GTGCGGACAG	1560
TGTGTGTGCA	GCGAGGGCTG	GAGTGGCCAG	ACCTGCAACT	GCTCCACCGG	CTCTCTGAGT	1620
GACATTTCAGC	CCTGCTTGCG	GGAGGGCGAG	GACAAGCCGT	GCTCCGCGCG	TGGGGAGTGC	1680
CAGTGCGGGC	ACTGTGTGTG	TACGGCGGAA	GGCCGCTACG	AGGTCAGATT	CTGCGAGTAT	1740
GACAACTTCC	AGTGTCCCCG	CACCTCCGGG	TTCTCTGCA	ATGACCGAGG	ACGCTGCTCC	1800
ATGGGCCAGT	GTGTGTGTGA	GCCTGGTTGG	ACAGGCCCAA	GCTGTGACTG	TCCCTCAGC	1860
AATGCCACCT	GCATCGACAG	CAATGGGGGC	ATCTGTAATG	GACGTGGCCA	CTGTGAGTGT	1920
GGCGGCTGCC	ACTGCCACCA	GCAGTGCCTC	TACACGGACA	CCATCTGCGA	GATCAACTAC	1980
TGGCGATCC	ACCGGGGCGT	CTCGAGGAC	CTACGCTCCT	CGGTGCAATG	CCAGGCGTGG	2040
GGCACCGGCG	AGAGAAGAGG	GCGCAAGTGT	GAGGAATGCA	ACTTCAAGGT	CAAGATGGTG	2100
GACGAGCTTA	AGGAGCGCGA	GAGGTGGTGG	GTGCGCTGCT	CCTTCCGGGA	CGAGGATGAC	2160
GACTGCACCT	ACAGCTACAC	CATGGAAGGT	GACGGCGCCC	CTGGGCCCAA	CAGCACTGTC	2220
CTGGTGACCA	AGAAGAAGGA	CTGCCCTCCG	GGCTCCTTCT	GGTGGCTCAT	CCCCCTGCTC	2280
CTCCTCCTCC	TGCGCTGCTC	GGCCCTGCTA	CTGCTGCTAT	GTGGAAGTA	CTGTGCTGTC	2340
TGCAAGGCGT	GCCTGGCACT	TCTCCCGTGC	TGCAACCGAG	GTCAATGGT	GGGCTTTAAG	2400
GAAGACCAT	ACATGTCTGG	GGAGAACCTG	ATGGCCTCTG	ACCACTTGGG	CACGCCCATG	2460
CTGCGCAGCG	GGAACTCAA	GGGCGGTGAC	GTGGTCCGCT	GGAGGTTCAC	CAACAACATG	2520
CAGCGGCGCT	GCTTTGGCAC	TCATGCCCGC	AGCATCAACC	CCACAGAGCT	GGTGCCTTAC	2580
GGCTGTGCTC	TGCGCCTGGC	CCGCTTTTGC	ACCGAGAACC	TGCTGAAGCC	TGACACTCGG	2640
GAGTGCGCCG	AGCTGCGCCA	GGAGGTGGAG	GAGAACCTGA	ACGAGGTCTA	CAGGCAGATC	2700
TCCGGGTGAC	ACAACTCTCA	CGAGACCAAG	TTCCGGCAGC	AGCCCAATGC	CGGGAAGGAG	2760
CAAGACCAAC	CCATTGTGGA	CACAGTGTCT	ATGGCGCCCC	GCTCGGCCAA	GCCGGCCCTG	2820
CTGAAGCTTA	CADAGAAGCA	GGTGAACACG	AGGGCCTTCC	ACGACCTCAA	GGTGGCCCCC	2880
GGCTACTACA	CCCTCACTGC	AGACCAGGAC	GCCCCGGGCA	TGGTGGAGTT	CCAGGAGGGC	2940
GTGGAGCTGG	TGGAGCTAGC	GGTGCCCTTC	TTTATCCGGC	CTGAGGATGA	CGACGAGAAG	3000
CAGCTGCTGG	TGGAGGCCAT	CGACGTGCCC	GCAGGCACTG	CCACCTCCGG	CCGCGCGCTG	3060
GTAAACATCA	CCATCATCAA	GGAGCAAGCC	AGAGACGTGG	TGTCTTGTGA	GCAGCCTGAG	3120
TTCTCGGTCA	GCGCGGGGGA	CCAGGTGGCC	CGCATCCCTG	TCATCCGGCG	TGTCTGGAC	3180
GGCGGGAAGT	CCCAGGTCTC	CTACCGCACA	CAGGATGGCA	CCGCGCAGGG	CAACCGGGAC	3240
TACATCCCGG	TGGAGGGTGA	GCTGTGTTTC	CAGCCTGGGG	AGGCCTGGAA	AGAGCTGCAG	3300
GTGAAGCTCC	TGGAGCTGCA	AGAAGTTGAC	TCCCTCCTGC	GGGGCCGCCA	GGTCCGCGCT	3360
TTCCAGCTCC	AGCTCAGCAA	CCCTAAGTTT	GGGGCCCAAC	TGGGCCAGCC	CCACTCCACC	3420
ACCATCATCA	TCAGGGACCC	AGATGAACCTG	GACCGGAGCT	TCACGAGTCA	GATGTTGTCA	3480
TCACAGCCAC	CCCCTCACGG	CGACCTGGGC	GCCCCGCGAG	ACCCCAATGC	TAAGGCCGCT	3540
GGGTCCAGGA	AGATCCATTT	CAACTGGCTG	CCCCCTTCTG	GCAAGCCAAAT	GGGGTACAGG	3600
GTAAAGTACT	GGATTCAAGG	TGACTCCGAA	TCCGAAGCCC	ACCTGCTCGA	CAGCAAGGTG	3660
CCCTCAGTGG	AGCTCACCAA	CCTGTACCCG	TATTGCGACT	ATGAGATGAA	GGTGTGCGCC	3720
TACGGGGCTC	AGGGCGAGGG	ACCTTACAGC	TCCCTGGTGT	CCTGCGGCAC	CCACAGGAGG	3780
GTGCCACGCG	AGCCAGGGCG	TCTGGCCTTC	AATGTGCTCT	CCTCCACGGT	GACCCAGCTG	3840
AGCTGGGCTG	AGCCGGCTGA	GACCAACGGT	GAGATCACAG	CCTACGAGGT	CTGCTATGGC	3900
CTGGTCAACG	ATGACCAACG	ACCTATTGGG	CCCATGAAGA	AAGTGTCTGG	TGACAAACCT	3960
AAGAACCGGA	TGCTGTATAT	TGAGAACCTT	CGGGAGTCCC	AGCCCTACCG	CTACACGGTG	4020
AAGGCGCGCA	ACGGCGGGCG	CTGGGGGCTC	GAGCGGGAGG	CCATCATCAA	CCTGGCCACC	4080
CAGCCCAAGA	GGCCCATGTC	CATCCCATC	ATCCCTGACA	TCCTATCGT	GGACGCCACG	4140
AGCGGGGAGG	ACTACGACAG	CTTCCTTATG	TACAGCGATG	ACGTTCTACG	CTCTCCATCG	4200
GGCACCAGGA	CTCCGATGAC	CTCCGATGAC	ACTGAGCACC	TGGTGAATGG	CCGGATGGAC	4260
TTTGCTTCC	CGGCGAGCAC	CAACTCCCTG	CACAGGATGA	CCACGACGAG	TGCTGCTGCC	4320
TATGGCACCC	ACCTGAGCCC	ACACGTGCCC	CACCGCGTGC	TAAGCACATC	CTCCACCTTC	4380

	ACACGGGACT	ACAACCTCACT	GACCCGCTCA	GAACACTCAC	ACTCGACCAC	ACTGCCGAGG	4440
	GACTACTCCA	CCCTCACTCTC	CGTCTCTCTCC	CACGACTCTC	GCCTGACTGC	TGGTGTGCCC	4500
	GACACGCCCA	CCCGCCTGGT	GTCTCTTGCC	CTGGGGCCCA	CATCTCTCAG	AGTGAGCTGG	4560
5	CAGGAGCCGC	GGTGCAGGCG	GCCGCTGCAG	GGCTACAGTG	TGGAGTACCA	GCTGCTGAAC	4620
	GGCGGTGAGC	TGCATCCGCT	CAACATCCCC	AACCTCGCCC	AGACCTCGGT	GGTGTGGAA	4680
	GACCTCTGCG	CCAACCACTC	CTACGTGTTT	CGCGTGCGGG	CCCAGAGCCA	GGAAGGCTGG	4740
	GGCCGAGAGC	GTGAGGGTGT	CATCACCATT	GAATCCCAGG	TGACCCCGCA	GAGCCCACTG	4800
	TGTCCCTTGC	CAGGCTCCGC	CTTCACTTTG	AGCACTCCCA	GTGCCCCAGG	CCCGCTGGTG	4860
10	TTCATGCCCC	TGAGCCCAAG	CTCGCTGCAG	CTGAGCTGGG	AGCGGCCACG	GAGGCCCAAT	4920
	GGGGATATCG	TGGGTACCTT	GGTGACCTGT	GAGATGGCCC	AAGGAGGAGG	GCCAGCCACC	4980
	GCATTCCGGG	TGGATGGAGA	CAGCCCCGAG	AGCCGGCTGA	CCGTGCCGGG	CCTCAGCGAG	5040
	AACGTGCCCT	ACAAGTTCAA	GGTGCAAGCC	AGGACCACTG	AGGGCTTCGG	GCCAGAGCGC	5100
	GAGGGCATCA	TCACCATAGA	GTCCCAAGAT	GGAGGACCCT	TCCCGCAGCT	GGGCAGCCGT	5160
15	GCCGGGCTCT	TCCAGCACCC	GCTGCAAAAG	GAGTACAGCA	GCATCACACC	CACCCACACC	5220
	AGCGCCACCG	AGCCCTTCTT	AGTGGATGGG	CCGACCCCTG	GGGCCACGCA	CCTGGAGGCA	5280
	GGCGGCTCCC	TCACCCGCGA	TGTGACCCAG	GAGTTTGTGA	GCCGGACACT	GACCCACGCA	5340
	GGAAACCTTA	GCACCCACAT	GGACCAACAG	TTCTTCCAAA	CTTGACCGCA	CCCTGCCCCA	5400
	CCCCCGCCAT	GTCACCATAG	GGCTCTCTCC	GACTCTCTCT	CCGGAGCCTC	CTCAGTACT	5460
20	CCATCCTTGC	ACCCCTGGGG	GCCAGCCCA	CCCGCATGCA	CAGAGCAGGG	GCTAGGTGTC	5520
	TCTTGGGAGG	CATGAAGGGG	GCAAGGTCCG	TCTCTGTGG	GCCCAACCT	ATTGTAAACC	5580
	AAAGAGCTGG	GAGCAGCAC	AGGACCCAGC	CTTTGTTCTG	CACCTAATAA	ATGGTTTTCG	5640
	ACTG						

Seq ID NO: 130 Protein sequence:
Protein Accession #: NP_000204

	1	11	21	31	41	51	
30	MAGPRPSPNA	RLLLAALISV	SLSGTLANRC	KKAPVKSCTE	CVRVDKDCAY	CTDEMFRDRR	60
	CNTQAEELAA	GQGRESIVVM	ESSFQITEET	QIDTTLRRSQ	MSPQGLRVRL	RPGEERHFEL	120
	EVFEPLSEFV	DLVILMDFSN	SMDDLDNLK	KMGQNLARVL	SQLTSDYTTG	FGKFVDKVSU	180
	PQTDMPREKL	KEPWNSDDPP	FSFKNVISLT	EDVDEFRNKL	QGERISGNLD	APEGGFDAIL	240
35	QTAVCTRDIG	WRPDSTHLLV	FSTESAFHYE	ADGANVLAGE	MSRNDERCHL	DTTGTYYTQYR	300
	TQDYPSVPTL	VRLLAKHNII	PIPAVTNYSY	SYYEKLHTYF	PVSSLGVLQE	DSSNIVELLE	360
	EAFNRIRSNL	DIRALDSPRG	LRTETVSKMF	QKTRTGSFHI	RRGEVGIYQV	QLRALEHVDG	420
	THVQQLPEDQ	KGNHKLKPSF	SDGLKWDAGI	ICDVCTCSLQ	KEVRSARCSF	NGDFVCGQCV	480
	CSEGWSGQTC	NLCSTGSLSDI	QPCLRGEGDK	PCSGRGECQC	GHCVCYGEGR	YEQFCEYDN	540
40	FQCPRTSGFL	CNDRGRCSMG	QCVCEPGWTG	PSCDCPLSNA	TCIDSNNGIC	NGRGHCECGR	600
	CHCHQQLSLT	DTICEINYS	IHPGLCEDLR	SCVQCQAWGT	GEKKGRTCEE	CNFKVKMVDL	660
	LKRAEVEVVR	CSPRDEDDDC	TYSYTMEDGD	APGPNSTVLV	HKKDCPPGS	FWHLIPLLLL	720
	LLPLALLLLL	LWKYCACCK	ACLLALLPCCN	RGHMVGFKE	HYMLRENLM	SDHLDTPLML	780
	SGNLGRNDVV	RCWVNTNMQR	PGFATHAASI	NPTLVPYGL	SLRLARLCTE	NLLKPDTRER	840
45	AQLRQVEEEN	LNEVYRQISG	VHKLQQTFR	QQPNAGKKQD	HTIVDTVLMA	PRSAKPALLK	900
	LTEKQVEQRA	FHDLKVAPGY	YTLTADQDAR	GMVEFQEGVE	LVDVRVPLFI	RPEDDDEKQL	960
	LVEAIDVPAG	TATLGRRLVN	ITIIKEQARD	VVSFEQPEFS	VSRGDQVARI	PVIRRVLDGG	1020
	KSQVSYRTQD	GTAGQNRDVI	PVEGELLFPQ	GEAWKELQVK	LLELQBVDSL	LRGRQVRRFH	1080
	VQLSNPKFGA	HLGQPHSTTI	IIRDPELDR	SFTSQMLSSQ	PPPHGLDLAG	QNPNAKAAGS	1140
50	RKIHFNMWLP	SGKPMGYRVK	YNIQGDSESE	AHLDSKVPSS	VELTNLYPYC	DYEMKVCAYG	1200
	AQGEQPYSSL	VSCRTHQVEP	SEPGRLAFNV	VSTVTQLSW	AEPAETNGEI	TAYEVCYGLV	1260
	NDDNRPIGPM	KKVLVDNPKN	RMLLIENLRE	SQPYRYTVKA	RNGAGWGPFR	EAIINLATQP	1320
	KRPMISIPPI	DIPIVDAQSG	EYDYSFLMYS	DDVLRSPSGS	QRPVSDDTE	HLVNGRMDFA	1380
	FFGSTNSLHR	MTTISAAAYG	THLSPHVPHR	VLSTSSLTTR	DYNSLRSESH	SHSTTLPRDY	1440
55	STLTSVSSH	SRLTAGVPDT	PTRLVFSALG	PTSLRVSWQE	PRCERPLQGY	SVEYQLLNGG	1500
	ELHRLNIPNP	AQTSVVVEDL	LPNHYSVFRV	RAQSQEGWGR	EREGVITIES	QVHPQSPLCP	1560
	LPGSAFTLST	PSAPGPLVFT	ALSPDSLQLS	WERFRPNPND	IVGYLVTCME	AQGGGPATAF	1620
	RVDGDSPESR	LTPVGLSENV	PYKFKVQART	TEGFGPEREG	IITIESQDGG	PPFQLGSRAG	1680
60	LFQHPLQSEY	SSITTTHTSA	TEPFLVDGPT	LGAQHLEAGG	SLTRHVTTQEF	VSRTLTTSST	1740
	LSTHMDQQFF	QT					

Seq ID NO: 131 DNA sequence
Nucleic Acid Accession #: BC004372
Coding sequence: 132..2231

	1	11	21	31	41	51	
65	CCTCGTGCCG	CGGACCCCG	CCTCTGCCAG	GTTCCGGTCCG	CCATCCTCGT	CCCGTCTCTC	60
	GCCGGCCCTT	GCCCCCGGCC	CAGGGATCCT	CCAGCTCCTT	TGCGCCGCGC	CCTCCGTTGG	120
	CTCCGGACAC	CATGGACAAG	TTTTGGTGGC	ACGCAGCCTG	GGGACTCTGC	CTCGTGCCGC	180
70	TGAGCCTGGC	GCAGATCGAT	TGAAATATAA	CCTGCCGCTT	TGCAGGTGTA	TTCCACGTGG	240
	AGAAAAATGG	TCGCTACAGC	ATCTCTCGGA	CGGAGGCGCG	TGACCTCTGC	AAGGCTTTCA	300
	ATAGCACCTT	GCCCACAATG	GCCCAAGATG	AGAAAGCTCT	GAGCATCGGA	TTTGAGACCT	360
	GCAGGTATGG	GTTCATAGAA	GGGCATGTGG	TGATTCCTCG	GATCCACCCC	AATCTCATCT	420
75	GTGCAGCAAA	CAACACAGGG	GTGTACATCC	TCACATCCAA	CACCTCCCAG	TATGACACAT	480
	ATTGCTTCAA	TGCTTCAGCT	CCACCTGAAG	AAGATTGTAC	ATCAGTCACA	GACCTGCCCA	540
	ATGCTCTTGA	TGGACCAATT	ACCATAACTA	TTGTAAACCG	TGATGGCACC	CGCTATGTCC	600
	AGAAAGGAGA	ATACAGAAGC	AATCCTGAAG	ACATCTACCC	CAGCAACCCCT	ACTGATGATG	660
	ACGTGAGCAG	CGGCTCTCC	AGTGAAAGGA	GCAGCACTTC	AGGAGGTTAC	ATCTTTTACA	720
	CCTTTTCTAC	TGTACACCCC	ATCCAGACCG	AAGACAGTCC	CTGGATCACC	GACAGCACAG	780
80	ACAGAATCCC	TGCTACCCAG	ACGTCTTCAA	ATACCATCTC	AGCAGGCTGG	GAGCCAAATG	840
	AAGAAAATGA	AGATGAAGA	GACAGACACC	TCAGTTTTC	TGGATCAGGC	ATTGATGATG	900
	ATGAAGATTT	TATCTCCAGC	ACCATTTCAA	CCACACCAAG	GGCTTTTGAC	CACACAAAAC	960
	AGAACCAGGA	CTGGACCCAG	TGGAACCCAA	GCCATTCAAA	TCGGGAAGTG	CTACTTCAGA	1020
	CAACCACAAG	GTAGCATGAT	GTAGACAGAA	ATGGCACCA	TGCTTATGAA	GGAAACTGGA	1080
85	ACCCAGAACG	ACACCTCTCC	CTCATTCACC	ATGAGCATCA	TGAGGAAGAA	GAGACCCACA	1140
	ATTCTACAAG	CACAATCCAG	GCAACTCCTA	GTAGTACAAC	GGAAGAAACA	GCTACCCAGA	1200
	AGGAACAGTG	GTTTGGCAAC	AGATGGCATG	AGGGATATCG	CCAAACACCC	AGAGAAGACT	1260

CCCATTCCGAC AACAGGGACA GCTGCAGCCT CAGCTCATAC CAGCCATCCA ATGCAAGGAA 1320
 GGACAACACC AAGCCCAGAG GACAGTTTCT GGACTGATTT CTTCACCCCA ATCTCACACC 1380
 CCATGGGACG AGGTCAATCAA GCAGGAAGAA GGATGGATAT GGACTCCAGT CATAGTACAA 1440
 CGCTTCAGCC TACTGCAAT CCAACACAG GTTTGGTGA AGATTGGAC AGGACAGGAC 1500
 CTCTTTCAAT GACAAACGAG CAGAGTAATT CTCAGAGCTT CTCTACATCA CATGAAGGCT 1560
 TGGAAAGAAG TAAAGACCAT CCAACAACCT CTACTCTGAC ATCAAGCAAT AGGAATGATG 1620
 TCACAGGTGG AAGAAGAGAC CCAATCATTT CTGAAGGCTC AACTACTTTA CTGGAAGGTT 1680
 ATACCTCTCA TTACCCACAC ACGAAGGAAA GCAGGACCTT CATCCAGTG ACCTCAGCTA 1740
 AGACTGGGTC CTTTGGAGTT ACTGCAGTTA CTGTTGGAGA TTCCAATCTT AATGTCAATC 1800
 GTTCCTTATC AGGAGACCAA GACACATTCC ACCCCAGTGG GGGGTCCCAT ACCACTCATG 1860
 GATCTGAATC AGATGGACAC TCACATGGGA GTCAAGAAGG TGGAGCAAAC ACAACCTCTG 1920
 GTCCTATAAG GACACCCCAA ATTCCAGAAT GGCTGATCAT CTGGGCATCC CTCTTGGCCT 1980
 TGGCTTTGAT TCTTGCAATT TGCAATTGCA TCAACAGTCG AAGAAGGTGT GGGCAGAAGA 2040
 AAAAGCTAGT GATCAACAGT GGCAATGGAG CTCTGGAGGA CAGAAAGCCA AGTGGACTCA 2100
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 CTCAGAGACA GTTTATGACA CTGATGGAGA CAAGGAACCT GCAGAAATGT GACATGAAGA 2220
 TTGGGGTGTA ACACCTACAC CATATCTTTG GAAAGAAACA ACCGTTGGAA ACATAACCAT 2280
 TACAGGGAGC TGGGACACTT AACAGATGCA ATGTGCTACT GATTGTTTCA TTGCGAATCT 2340
 TTTTTCAGCAT AAAATTTTCT ACTCTTAAAA AAAAAAAAAA AAAAAA

Seq ID NO: 132 Protein sequence:
 Protein Accession #: AAH04372

1 11 21 31 41 51
 MDKFWHAAW GLCLVPLSLA QIDLNITCRF AGVPHVEKNG RYISIRTEAA DLCKAFNSTL 60
 PTMAQMEKAL SIGPETCRYG PIEGHVVIPR IHPNSICAAN NTGVYILTSN TSQYDTCYFN 120
 ASAPPEEDCT SVTDLPNAFD GPITITIVNR DGTRVYVQKE YRTNPEDIYP SNPTDDVSS 180
 GSSSERSSTS GGYIFYYFST VHPIDEDSP WITDSTDRIIP ATSTSSNTIS AGWEPNEENE 240
 DERDRHLSFS GSGIDDDDFD ISSTISSTPR AFDHTKQND WTQWNPFSHN PEVLQTTTR 300
 MTDVDRNGTT AYEONWNPFA HPLIHHEHH EEEETPHSTS TIQATPSSTT EBTATQKEQW 360
 FGNRNHEGYR QTPREDSHST TGTAAASAHT SHPMQGRITP SPEDSSWTD FNPISHPMGR 420
 GHQAGRRMDM DSSHSTTLQP TANPNTGLVE DLDRTGPLSM TTQSSNSQSP STSHEGLEED 480
 KDHPPTTLT SENRNDVTGG RRDPNHSEGS TTLLEGYTSY YPHTKESRTF LPVTSKATGS 540
 FGVTAVTVGD SNSNVNLSLS GDQDTFHPSS GSHTTHGSES DGHSHGSEQE GANTTSGPIR 600
 TPQIPFWLLI LASLALALI LAVCIAVNSR RRCGQKKLV INSGNGAVED RKPSSGLNGEA 660
 SKSQEMVHLV NKSESSETDQ FMTADETRNL QNVDMKIGV

Seq ID NO: 133 DNA sequence
 Nucleic Acid Accession #: NM_002882
 Coding sequence: 150-755

1 11 21 31 41 51
 CGAGGTTCCG GTCGTGGGGC GGAGGGAAGA GCGGGCGGGC GGGAGGCGCC GCGCCAGAC 60
 GCGGAGGAA GGAGCTACGA GTAGCCGCGG AGAGGCCGCG GAGCCAGCGA CGACCCAGCC 120
 AGCCGAGCCG CCGCCGCGCG CGCGCCCCCA TGGCGGCGCG CAAGGACACT CATGAGGACC 180
 ATGATACTTC CACTGAGAAT ACAGACGAGT CCAACCATGA CCTCAGTTT GAGCCAATAG 240
 TTTCTCTTCC TGAGCAAGAA ATTAAACAC TGGAAGAAGA TGAAGAGGAA CTTTTTAAAA 300
 TCGGGGCAAA GTTTTCCGA TTTGCCTCTG AGAACGATCT CCCAGATGG AAGGAGCGAG 360
 GCACCTGGTA CGTCAAGCTC CTGAAGCACA AGGAGAAAGG GGGCATCCG CTCTCATGCG 420
 GGAGGGACAA GACCTGAAG ATCTGTGCCA ACCACTACAT CAGCCGATG ATGGAGCTGA 480
 AGCCCAACGC AGGTAGCGAC CGTGCCCTGG TCTGGAACAC CCACGCTGAC TTCGCCGACG 540
 AGTGCCCCAA GCCAGAGCTG CTGGCCATCC GCTTCTGAA TGCTGAGAA GCACAGAAAT 600
 TCAAAACAAA GTTTGAAGAA TGCAAGAAAG AGATCGAAGA GAGAGAAAAG AAAGCAGGAT 660
 CAGGCAAAAA TGATCATGCC GAAAAAGTGG CGGAAAAGCT AGAAGCTCTC TCGGTGAAGG 720
 AGGAGACCAA GGAGGATGCT GAGGAGAAGC AATAAATCGT CTTATTTTAT TTTCTTTTCC 780
 TCTCTTCTCT TTCCTTTTTT TAAAAAATTT TACCCTGCCC CTCTTTTTCG GTTTGTTTTT 840
 ATTCTTTCAT TTTTACAGG GACGTTATAT AAAGAACTGA ACTC

Seq ID NO: 134 Protein sequence:
 Protein Accession #: NP_002873

1 11 21 31 41 51
 MAAAKDTHED HDTSTENTDE SNHDPQFEPI VSLPEQEIKT LEEDEEELPK MRKLFRFAS 60
 ENDLPEWKER GTGDVKLLKH KEKGAIKLLM RRDKTLKICA NHYITPMEL KPNAGSDRAW 120
 VVNTHADPAD ECPKPELLAI RFLNAENAQK PKTKPEECRK EIEEREKKAG SKNDHAEKV 180
 AEKLEALSVK EETKEDAEK Q

Seq ID NO: 135 DNA sequence
 Nucleic Acid Accession #: NM_000077.2
 Coding sequence: 277-742

1 11 21 31 41 51
 CCAACCTGG GCGCACTTCA GGTGTGCCAC ATTGCTAAG TGCTCGGAGT TAATAGCACC 60
 TCCTCCGAGC ACTCGCTCAC GCGGTCCCCT TGCCGTGAAA GATACCGCGG TCCTCCAGA 120
 GGATTTGAGG GACAGGGTCC GAGGGGGCTC TTCCGCCAGC ACCGAGGAA GAAAGAGGAG 180
 GGGCTGGCTG GTACCCAGAG GGTGGGGCGG ACCCGGTGCG CTGCGGCGCT GCGGAGAGGG 240
 GGAGACAGG CAGCGGGCGG CGGGGAGCAG CATGAGGCGG GCGGCGGGGA GCAGCATGGA 300
 GCCTTCGGCT GACTGGCTGG CCACGGCCCG CCGCCGGGGT CGGGTAGAGG AGGTGCGGGG 360
 GCTGCTGGAG GCGGGGGCGC TGCCCAACGC ACCGAATAGT TACGGTCGGA GGCCGATCCA 420
 GGTATGATG ATGGGCAGCG CCCGAGTGGC GGAGCTGCTG CTGCTCCACG GCGCGGAGCC 480

CAACTGCGCC GACCCCGCCA CTCTCACCG ACCCGTGCAC GACGCTGCCC GGGAGGGCTT 540
 CCTGGACACG CTGGTGGTGC TGCACCGGGC CGGGGCGCGG CTGGACGTGC GCGATGCTCG 600
 GGGCGGTCTG CCGGTGGACC TGGCTGAGGA GCTGGGCCAT CGGATGTGCG CACGGTACCT 660
 GCGCGCGGCT GCGGGGGGCA CCAGAGGCAG TAACCATGCC CGCATAGATG CCGCGGAAGG 720
 TCCCTCAGAG ATCCCGGATT GAAAGAACCA GAGAGGCTCT GAGAAACCTC GGGAAACTTA 780
 GATCATCAGT CACCGAAGGT CCTACAGGGC CACAACCTGC CCGGCCACAA CCCACCCGCG 840
 TTTGCTAGTT TTCAATTAGA AATAGAGCT TTTAAAAATG TCCTGCCTTT TAACGTAGAT 900
 ATATGCTTTC CCCCACTACC GTAAATGTCC ATTTATATCA TTTTATATAT ATTCTTATAA 960
 AAATGTAAAA AAGAAAAACA CCGCTTCTGC CTTTCTACTG TGTGGAGTT TTCTGGAGTG 1020
 AGCACTACAG CCTTAAGCGC ACATTCATGT GGGCATTTC TGGAGCCTC GCAGCCTCCG 1080
 GAAGCTGTG ACTTCATGAC AAGCATTTTG TGAACTAGGG AAGCTCAGGG GGGTTACTGG 1140
 CTTCTCTGA GTCACTGTC TAGCAAATGG CAGAACCAAA GCTCAATAA AAATAAAATA 1200
 ATTTTCATTC ATTCATTC

Seq ID NO: 136 Protein sequence:
 Protein Accession #: NP_000068.1

1 11 21 31 41 51
 MEPAAGSSME PSADWLATAA ARGVEEVRA LLEAGALPNA PNSYGRRIQ VMMGSRVA 60
 ELLLLHGAEP NCADPATLTR VHDAAAREGF LDTLVVLHRA GARLDVRDWA GRIPVDLAE 120
 LGHRDVARYL RAAAGGTRGS NHARIDAAEG PSDIPD

Seq ID NO: 137 DNA sequence
 Nucleic Acid Accession #: NM_058196.1
 Coding sequence: 104-421

1 11 21 31 41 51
 TGTGTGGGG TCTGCTTGGC GGTGAGGGGG CTCTACACAA GCTTCTTTC CGTCATGCGG 60
 GCCCCACCCC TGGCTCTGAC CATTCTGTTT TCTCTGGCAG GTCATGTAGA TGGGCAGCGC 120
 CCGAGTGGCG GAGCTGCTGC TGCTCCACGG CCGGAGCCCC AACTGCGCGG ACCCGCCAC 180
 TCTCACCCGA CCGGTGCACG ACGCTGCCCG GGAGGGCTTC CTGGACACGC TGGTGGTGCT 240
 GCACCGGGCC GGGGCGGGC TGGACGTGCG CGATGCTTGG GGCCTGTGCG CCGTGGACCT 300
 GGCTGAGGAG CTGGGCCATC GCGATGTCGC ACGGTACCTG CCGCGGGCTG CCGGGGGCAC 360
 CAGAGGCACT AACCATGCC CATAGATGCG CCGGAAGGT CCCTCAGACA TCCCGGATTG 420
 AAAGAACCAG AGAGGCTCTG AGAAACCTCG GGAACCTTAG ATCATCAGTC ACCGAAGGTC 480
 CTACAGGGCC ACAACTGCCC CCGCCACAC CCACCCGCT TCGTAGTTT TCATTAGAA 540
 AATAGAGCTT TTAATAATGT CCTGCCTTTT AACGTAGATA TAAGCCTTCC CCCACTACCG 600
 TAAATGTCCA TTTATATCAT TTTTATATA TTCTTATAAA AATGTAAAAA AGAAAAACAC 660
 CGCTTCTGCG TTTTCTGCT GTTGGAGTTT TCTGGAGTGA GCACTCACGC CTAAGCGCA 720
 CATTATGTCG GGCATTTCCT GCGAGCCTCG CAGCCTCCGG AAGCTGTGCA CTTATGACA 780
 AGCATTTTGT GAACTAGGGA AGCTCAGGGG GGTACTGGC TTCTCTTGG TCACTATGCT 840
 AGCAATGGC AGAACCAAG CTCAAATAAA AATAAAATAA TTTTCATTCA TTCATC

Seq ID NO: 138 Protein sequence:
 Protein Accession #: NP_478103.1

1 11 21 31 41 51
 MVMGSRVAE LLLHGAEPN CADPATLTRP VHDAAAREGF DTLVLHRAH ARLDVRDANG 60
 RLPVDLAEEL GHRDVARYLR AAAGGTRGSN HARIDAAEGP SDIPD

Seq ID NO: 139 DNA sequence
 Nucleic Acid Accession #: NM_058197.1
 Coding sequence: 272-684

1 11 21 31 41 51
 CCCAACCTGG GGGCACTTCA GGTGTGCCAC ATTGCTAAG TGCTCGGAGT TAATAGCACC 60
 TCCTCCGAGC ACTCGCTCAC GCGGTCCCT TGCCTGGAAG GATACCGCGG TCCCTCCAGA 120
 GGAATTTAGG GACAGGGTGC GAGGGGGCTC TTCGCGCAGC ACCGGAGGAA GAAAGAGGAG 180
 GGGCTGGCTG GTCACAGAG GGTGGGGCGG ACCGCTGCGC CTGGCGGGCT GCGGAGAGGG 240
 GGAGAGCAGG CAGCGGGCGG CCGGGAGCAG CATGGAGCGG CGCGCGGGGA GCAGCATGGA 300
 GCCGCGGGCG GGGAGCAGCA TGGAGCCTTC GGCTGACTGG CTGGCCACGG CCGCGGCCCG 360
 GGGTGGGTA GAGGAGGTGC GGGCGCTGCT GGAGGCGGGG GCGCTGCCCA ACGCACCGAA 420
 TAGTTACGGT CGGAGGCCGA TCCAGTGGG TAGAAGTCT GCAGCGGGAG CAGGGGATGG 480
 CGGGCGACTC TGGAGGACGA AGTTTGACAG GGAATTGGAA TCAGGTAGCG CTTGATTCT 540
 CCGGAAAAAG GGGAGGCTTC CTGGGGAGTT TTCAGAGGGG GTTTGTAATC ACAGACCTCC 600
 TCCTGGCGAC GCCCTGGGGG CTTGGGAAC CAAGGAAGAG GAATGAGGAG CCACGCGCGT 660
 ACAGATCTCT CGAATGCTGA GAAGATCTGA AGGGGGGAAC ATATTGTAT TAGATGGAAG 720
 TCATGATGAT GGGCAGCGCC CGAGTGGCGG AGCTGCTGCT GCTCCACGGC GCGGAGCCCA 780
 ACTGCGCGCA CCCCGCCACT CTCACCCGAC CCGTGCACGA CGCTGCCCGG GAGGGCTTCC 840
 TGGACACGCT GGTGGTGCTG CACCGGGCGG GGGCGCGGCT GGAAGTGGC GATGCTGGG 900
 GCGCTCTGCC CGTGGACCTG GCTGAGGAGC TGGGCCATCG CGATGTGCA CGGTACCTGC 960
 GCGCGGCTGC GGGGGGCACC AGAGGCAGTA ACCATGCCCG CATAGATGCC GCGGAAGGTC 1020
 CCTCAGACAT CCCCAGTTGA AAGAACCCAG GAGGCTCTGA GAAACCTCGG GAACCTAGAT 1080
 CATCAGTCAC CGAAGGTCTT ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCGCTTT 1140
 CGTAGTTTTC ATTTAGAAAA TAGAGCTTTT AAAAAATGCC TGCCTTTTAA CGTAGATATA 1200
 TGCCTTCCCC CACTACCGTA AATGTCCATT TATATCATT TTTATATAT CTTATAAAAA 1260
 TGTAAAAAAG AAAAACACCG TTCTGCTCTT TCTACTGTGT TGGAGTTTTC TGGAGTGAGC 1320
 ACTACGCGCC TAAGCGCACA CTTATGTGGG CATTCTTTCG GAGCCTCGCA GCCTCCGGA 1380
 GCTGTGACT TCATGACAAG CATTTTGTGA ACTAGGGAAG CTCAGGGGGG TTACTGGCTT 1440
 CTCTTGAGTC AACTGCTAG CAAATGGCAG AACCAGAGCT CAAATAAAAA TAAAAAATT 1500

Seq ID NO: 140 Protein sequence:
Protein Accession #: NP_478104.1

1 11 21 31 41 51
MEPAAGSSME PAAGSSMEPS ADWLATAAAR GRVEEVALL EAGALPNAPN SYGRRPIQVG 60
RRSAAGAGDG GRLWRTKFCAG ELESQSASIL RKKGRLPGEF SEGVCNHRPP PGDALGAWET 120
KEEE

Seq ID NO: 141 DNA sequence
Nucleic Acid Accession #: NM_058195.1
Coding sequence: 163-684

1 11 21 31 41 51
CCTCCCTACG GCGCGCTCCG GCAGCCCTTC CCGCGTGGCG AGGGCTCAGA GCCGTCCGA 60
GATCTTGGAG GTCCGGGTGG GAGTGGGGGT GGGGTGGGGG TGGGGGTGAA GGTGGGGGGC 120
GGGCGCGCTC AGGGAGGCGG GGTGCGCGCC TGCGGGGCGG AGATGGGCAG GGGCGGTGC 180
GTGGGTCCCA GTCTGCAGTT AAGGGGGCAG GAGTGGCGCT GCTCACCTCT GGTGCCAAAG 240
GGCGGGCGAG CGGCTGCCGA GCTCGGCCCT GGAGGCGCGG AGAACATGGT GCGCAGGTTT 300
TTGGTGACCC TCCGATTTCG GCGCGCTGCG GGCCCGCGCG GAGTGAGGGT TTTCGTGGTT 360
CACATCCCGC GGCTCACGGG GAGTGGGCA GCGCCAGGGG CGCCCGCCCG TGTGGCCCTC 420
GTGCTGATGC TACTAGGAG CCAGCGTCTA GGGCAGCAGC CGCTTCCTAG AAGACCAAGT 480
CATGATGATG GCGAGCGCGC GAGTGGCGGA GCTGCTGCTG CTCACCGCGC CGGAGCCCAA 540
CTGCGCGGAC CCCGCCACTC TCACCCGACC CGTGACGAC GCTGCCCGGG AGGGCTTCCT 600
GGACACGCTG GTGGTGTGCG ACCGGGCGCG GCGCGGCTG GACGTGCGCG ATGCTTGGGG 660
CCGTCTGCCC GTGGACCTGG CTGAGGAGCT GGGCCATCGC GATGTGCGAC GGTACCTGCG 720
CGCGGCTGGC GGGGGCAGCA GAGGCAGTAA CCATGCCCGC ATAGATGCCG CGGAAGGTCC 780
CTCAGACATC CCCGATTGAA AGAACCCAGG AGGCTCTGAG AAACCTCGGG AAACCTTAGAT 840
CATCAGTCACT CGAAGGTCTT ACAGGGCCAC AACTGCCCCC GCCCAACCCC ACCCCGCTTT 900
CGTAGTTTTT CTTAGAAAAA TAGAGCTTTT AAAAATGTCC TGCCTTTTAA CGTAGATATA 960
TGCTTCCCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA 1020
TGTAATAAAG AAAACACCGC TTCTGCTGCT TTCACTGTGT TGGAGTTTTC TGGAGTGAGC 1080
ACTCAGCCCC TAAGCGCACA TTCACTGTGGG CATTTCTTGC GAGCCTCGCA GCCTCCGGAA 1140
GCTGTGAGCT TCATGACAAG CATTTTGTGA ACTAGGGAAG CTCAGGGGGG TTAAGTGGCT 1200
CTCTTGAGTC ACACGTGTAG CAAATGGCAG AACCAAGCT CAAATAAAAA TAAATAAATT 1260
TTCATTCAAT CACTC

Seq ID NO: 142 Protein sequence:
Protein Accession #: NP_478102.1

1 11 21 31 41 51
MGRGRCVGPS LQLRQEWRC SPLVPKGGAA AAEELGPGGGE NMVRRFLVTL RIRACGPPR 60
VRVFVHHIR LTGEWAAAGA PAAVALVLM LRSQRLGQQP LPRRPBGHDDG QRPSSGAAAA 120
PRRGAQLRRP RHSHPTARR CPGLPLGHAG GAAPGRGAAG RARCLGPSAR GPG

Seq ID NO: 143 DNA sequence
Nucleic Acid Accession #: NM_018131
Coding sequence: 412..1107

1 11 21 31 41 51
GAAATGTCAC ACTTAAAGAC ATCAGTGGAT GAAATCACAA GTGGGAAAGG AAAGCTGACT 60
GATAAAGAGA GACAGAGACT TTTGGAGAAA ATTGAGTCC TTGAGGCTGA GAAGGAGAAG 120
AATGCTTATC AACTCACAGA GAAGGACAAA GAAATACAGC GACTGAGAGA CCAACTGAAG 180
GCCAGATATA GTACTACCGC ATTGCTTGAA CAGCTGGAAG AGACAACGAG AGAAGGAGAA 240
AGGAGGGAGC AGGTGTTGAA AGCCTTATCT GAAGAGAAAG ACGTATTGAA ACAACAGTTG 300
TCTGCTGCAA CCTCAGCAAT TGCTGAACTT GAAAGCAAAA CCAATACACT CCGTTTATCA 360
CAGACTGTGG CTCCAACCTG CTTCAACTCA TCAATAATAA ATATTATGTA AATGGAAAATA 420
CAGCTGAAAG ATGCTCTGGA GAAAAATCAG CAGTGGCTCG TGTATGATCA GCAGCGGGAA 480
GTCTATGTAA AAGGACTTTT AGCAAAAGATC TTTGAGTTGG AAAAGAAAAC GGAACAGACT 540
GCTCATTCAC TCCACAGCA GACAAAAAAG CCTGAATCAG AAGGTTATCT TCAAGAAAGG 600
AAGCAGAAAT GTTACAACGA TCTCTTGGCA AGTGCAAAAA AAGATCTTGA GGTGAAACGA 660
CAAAACATAA CTCAGCTGAG TTTTGAACCT AGTGAATTC GAAGAAAATA TGAAGAAACC 720
CAAAAAGAAG TTCACAAATT AAATCAGCTG TTGTATTAC AAAGAAGGGC AGATGTGCAA 780
CATCTGGAAG ATGATAGGCA TAAACAGAG AAGATACAAA AACTCAGGGA AGAGAATGAT 840
ATTGCTAGGG GAAAACCTGA AGAAGAGAAG AAGAGATCCG AAGAGCTCTT ATCTCAGGTC 900
CAGTCTCTTT ACACATCTCT GCTAAAGCAG CAAGAAGAAC AAACAAGGGT AGCTCTGTTG 960
GAACACAGA TGCAGGCATG TACTTTAGAC TTTGAAATG AAAAAGCTCG CCGTCAACAT 1020
GTGAGCATC AATTGCATGT AATTCTTAAG GAGCTCCGAA AAGCAAGAAA AAATAACACA 1080
GTTGGAATCC TTGAACAGC TTCAATGAGT TGCCATCACA GAGCCATTAG TCACTTTCCA 1140
AGGAGAGACT GAAAACAGAG AAAAAGTTGC CGCCTACCA AAAAGTCCCA CTGCTGCACT 1200
CAATGGAAGC CTGGTGGAAAT GTCCCAAGTG CAATATACAG TATCCAGCCA CTGAGCATCG 1260
CGATCTGCTT GTCCATGTGG AATACTGTTT AAAGTAGCAA AATAAGTATT TGTTTGTATA 1320
TTAAAAGATT CAATACTGTA TTTTCTGTTA GCTTGTGGGC ATTTTGAATT ATATATTTC 1380
CATTTTGCAT AAAACTGCTT ATCTACCTTT GACACTCCAG CATGCTAGTG AATCATGTAT 1440
CTTTTAGGCT GCTGTGCATT TCTCTTGGCA GTGATACCTC CCTGACATGG TTCATCATCA 1500
GGCTGCAATG ACAGAATGTG GTGAGCAGCG TCTACTGAGA TACTAACATT TTGCACTGTC 1560
AAAAACTTGG GTGAGGAAAA GATAGCTCAG GTTATTGCTA ATGGGTTAAT GCACCAGCAA 1620
GCAAAATATT TTATGTTTCG GGGGTTTGA AAAATCAAAG ATAATTAAAC AAGGATCTTA 1680
ACTGTGTTGG CATTTTATAT CCAAGCACTT AGAAAACCTA CAATCCTAAT TTTGATGTCC 1740
ATTGTTAAGA GGTGGTGATA GATACTATTT TTTTTCATA TTGTATAGCG GTTATTAGAA 1800

AAGTTGGGGA TTTCTTGAT CTTTATGCT GCTTACCATT GAACTTAAC CCAGCTGTGT 1860
 TCCCCAATCT TGTCTGCGC ACGAAACAGT ATCTGTTTGA GGCATAATCT TAAGTGGCCA 1920
 CACACAATGT TTTCTCTAT GTTATCTGGC AGTAACTGTA ACTTGAATTA CATTAGCACA 1980
 TTCTGCTTAG CTAAATTTGT TAAATAAAC CCAATGTAGCC CTCTCATTGT 2040
 ATTGACAGTA TTTTAGTTAT TTTTGGCATT CTAAAGCTG GGCATGTAA TGATCAGATC 2100
 TTTGTTTGTG TGAACAGTA TTTTATACA TGCTTTTGT AAACCAAAA CTTTAAATT 2160
 TCTCAGGTT TTCTAACATG CTTACCACTG GGCTACTGTA AATGAGAAAA GAATAAAATT 2220
 ATTTAATGTT TT

Seq ID NO: 144 Protein sequence:
 Protein Accession #: NP_060601

1 11 21 31 41 51
 | | | | |
 MBIQLKDALE KNQQLVVDQ QREVVVKGLL AKIPELEKKT EAAHSLPQQ TKKPESEGYL 60
 QEEKQKCYND LLASAKKDL ESRQTITQLS FELSEFRKRY EETQKEVHNL NQLLYSQRRA 120
 DVQHLEDDRH KTEKIQLRE ENDIARGKLE EEKGRSEELL SQVQSLYTSL LKQSEBQTRV 180
 ALLEQQMQAC TLDPENEXLD RQHVQHLHV ILKELRKARK NNTVGILETA S

Seq ID NO: 145 DNA sequence
 Nucleic Acid Accession #: NM_001168
 Coding sequence: 50..478

1 11 21 31 41 51
 | | | | |
 CCGCCAGATT TGAATCGCGG GACCCGTGCG CAGAGGTGGC GCGCGCGGCA TGGGTGCCCC 60
 GACGTTGCCC CCTGCGCTGGC AGCCCTTTCT CAAGGACCAC CGCATCTCTA CATTCAAGAA 120
 TGGGCCCTTC TTGGAGCTGC CGCGCTGCAC CCGGAGCGG ATGGCCGAGG CTGGCTTCAT 180
 CCACTGCCCC ACTGAGAACG AGCCAGACTT GGCCAGTGT TCTTCTGCT TCAAGGAGCT 240
 GGAAGGCTGG GAGCCAGATG ACGACCCCAT AGAGGAACAT AAAAAGCATT CGTCCGGTTG 300
 CGCTTTCCTT TCTGTCAAGA AGCAGTTTGA AGAATTAACC CTTGGTGAAT TTTTGAAGCT 360
 GGAACAGAGA AGAGCCAAAG ACAAATTTGC AAAGGAAACC AACAATAAGA AGAAAGAAAT 420
 TGAGGAAACT GCGAAGAAAG TGCGCCGTGC CATCGAGCAG CTGGCTGCCA TGGATTGAGG 480
 CCTCTGGCCG GAGCTGCGTG GTCCAGAGT GGCTGCACCA CTTCCAGGGT TTATTCCCTG 540
 GTGCCACCAAG CCTTCTCTGT GGCCTTCTAG CAATGTCTTA GGAAAGGAGA TCAACATTTT 600
 CAAATTAGAT GTTCAACTG TGCTCCTGTT TTGTCTTGAA AGTGGCACA GAGGTGCTTC 660
 TGCTGTGCA GCGGTGCTG CTGGTAACAG TGGCTGCTTC TCTCTCTCTC TCTCTTTTTT 720
 GGGGGCTCAT TTTTGTCTTT TTGATTCCCG GGCTTACCAG GTGAGAAGTG AGGGAGGAAG 780
 AAGGCAGTGT CCTTTTGTCT AGAGCTGACA GCTTTGTTCG CGTGGGCGAGA GCCTTCCACA 840
 GTGAATGTGT CTGGAACCTCA TGTGTGTGAG GCTGTACAG TCCTGAGTGT GGACTTGGCA 900
 GGTGCTGTT GAATCTGAGC TGCAGGTTCC TTATCTGTCA CACCTGTGCC TCCTCAGAGG 960
 ACAGTTTTTT TGTGTGTGTG TTTTGTGTG TTTTGTGTG GGTAGATGCA TGACTTGTGT 1020
 GTGATGAGAG AATGGAGACA GAGTCCCTGG CTCCTCTACT GTTTAACAAC ATGGCTTTCT 1080
 TATTTTGTGT GAATGTGTAA TTCACAGAAT AGCACAACCT ACAATTAATA CTAAGCACAA 1140
 AGCCATTCTA AGTATTGTTG GAAACGGGGT GAACTTCAGG TGATGAGGA GACAGAATAG 1200
 AGTGATAGGA AGCGTCTGGC AGATCTCTCT TTTGCCACTG CTGTGTGATT AGACAGGCCC 1260
 AGTGAGCGCG GGGGCACATG CTGGCCGCTC CTCCTCAGA AAAAGGCGAGT GGCCTAAATC 1320
 CTTTTTAAT GACTTGGCTC GATGCTGTGG GGGACTGGCT GGGCTGCTGC AGGCGGTGTG 1380
 TCTGTGAGCG CAACCTTTCAC ATCTGTACAG TTCTCCACAC GGGGAGAGA CGCAGTCCCG 1440
 CAGGTTCCCG GCTTCTCTTG GAGGCGAGG CTCCGCGAGG GCTGAAGTCT GGCCTAAGAT 1500
 GATGGATTGT ATTGCGCTCT CTCCCTGTCA TAGAGCTGCA GGGTGGATTG TTACAGCTTC 1560
 GCTGGAACCC TCTGGAGGTC ATCTCGGCTG TTCTGAGAA ATAAAGGCC TGTCAATTC

Seq ID NO: 146 Protein sequence:
 Protein Accession #: NP_001159

1 11 21 31 41 51
 | | | | |
 MGAPTLPFAW QPFLKDHRI TFIKNWPFLE CACTPERMAE AGFIHCPTEN EPDLAQCFPC 60
 FKELEGWEED DDPIEEHKKH SSGCAPLSVK KQFEBELTGE FLKLDREERAK NKIAKETNNK 120
 KKEFEETAKK VRAIEQLAA MD

Seq ID NO: 147 DNA sequence
 Nucleic Acid Accession #: NM_014176.1
 Coding sequence: 127-720

1 11 21 31 41 51
 | | | | |
 GCGCGCAGCG CTGGTACCCC GTTGGTCCGC GCGTTGCTGC GTTGTGAGGG GTGTCAGCTC 60
 AGTGATCCCC AGGCAGCTCT TAGTGTGGAG CAGTGAACTG TGTGTGGTTC CTCTACTTGT 120
 GGGATCATGC AGAGAGCTTC ACGTCTGAAG AGAGAGCTGC ACATGTTAGC CACAGAGCCA 180
 CCCCCAGGCA TCACATGTTG GCAAGATAAA GACCAATGG ATGACCTGCG AGCTCAAATA 240
 TTAGGTGGAG CCAACACACC TTATGAGAAA GGTGTTTTTA AGCTAGAAGT TATCATTCCT 300
 GAGAGGTACC CATTGTGAAC TCCTCAGATC CGATTCTCA CTCCAATTTA TCATCCAAAC 360
 ATTGATTCTG CTGGAAGGAT TTGTCTGGAT GTTCTCAAT TGCCACCAAA AGGTGCTTGG 420
 AGACCATCCC TCAACATGCG AACTGTGTTG ACCTCTATT AGCTGCTCAT GTCAGAACCC 480
 AACCTGATG ACCCGCTCAT GGCTGACATA TCCTCAGAA TTAATATAA TAAGCCAGCC 540
 TTCCTCAAGA ATGCCAGACA GTGGACAGAG AAGCATGCAA CACAGAAACA AAAGGCTGAT 600
 GAGGAAGAGA TGCTTGATAA TCTACCAGAG GCTGGTGACT CCAGAGTACA CAACTCAACA 660
 CAGAAAGAGA AGGCCAGTCA GCTAGTAGGC ATAGAAAAGA AATTTCATCC TGATGTTTAG 720
 GGGACTTGTG CTGTTTATGC TTAGTTAATG TGTCTTTTGC CAAGGTGATC TAAGTTGCTC 780
 ACCTGGAATT TTTTGTAAAT TATATTGAT GACATAATT TTGTGTAGTT TATTTATCTT 840
 GTACATATGT ATTTTGAAT CTTTTAAACC TGAAAAATA ATAGTCATT AATGTTGAAA 900

Seq ID NO: 148 Protein sequence:
 Protein Accession #: NP_054895.1

1	11	21	31	41	51	
MQRASRLKRE	LHMLATEPPP	GITCWQDKDQ	MDDLRAQILG	GANTPYEKGV	FKLEVIIPER	60
YFPEPPQIRF	LTPIYHPNID	SAGRICLDVL	KLPPKGAWRP	SLNIATVLTS	IQLLMSEPNP	120
DDPLMADISS	EFKYNKPAFL	KNARQWTEKH	ARQKQRADEE	EMLDNLPEAG	DSRVHNSTQK	180
RKASQLVGIE	KKFHPDV					

Seq ID NO: 149 DNA sequence
 Nucleic Acid Accession #: NM_003812
 Coding sequence: 224-2722

1	11	21	31	41	51	
TCCTCTGCGT	CCCCCCCCCG	GAGTGGCTGC	GAGGCTAGGC	GAGCCGGGAA	AGGGGGCGCC	60
GCCCCAGCCC	GAGCCCCGCG	CCCCGTGCCC	CGAGCCCGGA	GCCCCCTGCC	CGCGGCGGCA	120
CCATGCGCGC	CGAGCCGCGC	TGACCGGCTC	CGCCCGCGGC	CGCCCCGAGC	CTAGCCCGGC	180
GCCTCTGCGC	GCCACACGGA	GCGCGCGCCG	GGAGCTATGA	GCCATGAAGC	CGCCCGGCAG	240
CAGCTGCGCG	CAGCCGCCCC	TGGCGGGCTG	CAGCCTTGCC	GGCGCTTCCT	CGGCCCCCCA	300
ACGCGGCCCC	GCCGGCTCGG	TGCCTGCCAG	CGCCCCGGCC	CGCAGCGCCG	CCTCGCGCCT	360
GGCTTCTCGC	CTTCTCTGCG	TGCCTCCGCT	CGCCCGCTCG	TCCCGGCCCC	GCGCCTGGGG	420
GGCTGCTGCG	AATGGTTTGT	CGCATTGGAA	TGAAACTGCA	GAAAAAATT	TGGGAGTCCT	480
GGCAGATGAA	GACATACAT	TGCAACAGAA	TAGCAGCAGT	AATATCAGTT	ACAGCAATGC	540
AATGCAGAAA	GAAATCACAC	TGCCTTCAAG	ACTCATATAT	TACATCAACC	AAGACTCGGA	600
AAGCCCTTAT	CACGTTCTTG	ACACAAAGGC	AAGACACCAG	CAAAAACATA	ATAAGGCTGT	660
CCATCTGGCC	CAGGCAAGCT	TCCAGATTGA	AGCCTTCGGC	TCCAAATTC	TTCTTGACCT	720
CATACTGAA	ATGGGTTTGT	TGTCTTCTGA	TTATGTGGAG	ATTCACTACG	AAAATGGGAA	780
ACCACAGTAC	TCTAAGGGTG	GAGAGCACTG	TTACTACCAT	GGAAGCATCA	GAGGCGTCAA	840
AGACTCCAA	GTCGCTCTGT	CAACCTGCAA	TGGACTTCAT	GGCATGTTTG	AAGATGATAC	900
CTTCGTGTAT	ATGATAGAGC	CACTAGAGCT	GGTTCATGAT	GAGAAAAGCA	CAGGTCGACC	960
ACATATAATC	GAGAAAACCT	TGGCAGGACA	GTATTCTAAG	CAATGAAGA	ATCTCACTAT	1020
GGAAAGAGGT	CACCAAGTGG	CCTTCTCTCT	TGAAATTACAG	TGGTTGAAAA	GAAGGAAGAG	1080
AGCAGTGAAT	CAATCAGGTG	GTATATTGTA	AGAAATGAAA	TATTTGGAAC	TTATGATTGT	1140
TAATGATACA	AAACGCTATA	AGAAGCATCG	CTCTTCTCAT	GCACATACCA	ACAACTTTGC	1200
AAAGTCCGTG	GTCAACCTTG	TGGATTCTAT	TTACAAGGAG	CAGCTCAACA	CCAGGGTTGT	1260
CTGTGTGGCT	TAGTAGACCT	GGACTGAGAA	GGATCAGATT	GACATCACCA	CCAACCTGT	1320
GCAGATGCTC	CATGAGTTCT	CAAAATACCG	GCAGCGCATT	AAGCAGCATG	CTGATGCTGT	1380
GCACCTCATC	TGCGGGGTGA	CATTCTACTA	TAAGAGAAGC	AGTCTGAGTT	ACTTTGGAGG	1440
TGTCTGTTCT	CGCACAGAGG	GAGTTGGTGT	GAATGAGTAT	GGTCTTCCAA	TGGCAGTGGC	1500
ACAAGTATTA	TGCGAGAGCC	TGGCTCAAAA	CCTTGGAAATC	CAATGGGAAC	CTTCTAGCAG	1560
AAAGCCAAAA	TGTGACTGCA	CAGAATCCTG	GGGTGGCTGC	ATCATGGAGG	AAACAGGGGT	1620
GTCCCACTCT	CGAAAATTTT	CAAAATGCGA	CATTTTGGAG	TATAGAGACT	TTTTACAGAG	1680
AGGAGGTGGA	GCCTGCCTTT	TCAACAGGCC	AACAAAGCTA	TTTGAGCCCA	CGGAATGTGG	1740
AAATGGATAC	GTGGAGAGCTG	GGGAGGAGTG	TGATTGTGGT	TTTCATGTGG	AATGCTATGG	1800
ATTATGCTGT	AAGAAATGTT	CCCTCTCCAA	CGGGGCTCAC	TGCAGCGAAG	GGCCCTGCTG	1860
TAACAATACC	TCATGTCTTT	TTCAAGCCAG	AGGGTATGAA	TGCCGGGATG	CTGTGAACGA	1920
GTGTGATATT	ACTGAATATT	GTACTGGAGA	CTCTGGTCAG	TGCCCACCAA	ATCTTCATAA	1980
GCAAGACGGA	TATGATGCA	ATCAAAATCA	GGGCGCTGCG	TACAATGGCG	AGTGCAAGAC	2040
CAGAGACAA	CAGTGTGAGT	ACATCTGGGG	AACAAAGGCT	GCAGGGTCTG	ACAAGTTCTG	2100
CTATGAAAG	CTGAATACAG	AAGGCACTGA	GAAGGGAAGC	TGCGGGAAGG	ATGGAGACCG	2160
GTGGATTGAG	TGCAGCAAC	ATGATGTGTT	CTGTGGATTG	TTACTCTGTA	CCAATCTTAC	2220
TGAGGCTCCA	CGTATTGGTC	AACCTCAGGG	TGAGATCATT	CCAACTTCCT	TCTACCATCA	2280
AGGCCGGGTG	ATTGACTGCA	GTGGTGCCCA	TGTAGTTTAT	GATGATGATA	CGGATGTGGG	2340
CTATGTAGAA	CAATGGAACG	CATGTGGCCC	GTCTATGATG	TGTTTAGATG	GGAAAGTCCG	2400
ACAAATTCAA	GCCCTAAATA	TGAGCAGCTG	TCCACTCGAT	TCCAAGGGTA	AAGTCTGTTC	2460
GGGCCATGGG	GTGTGTAGTA	ATGAAGCCAC	CTGCATTGTT	GATTTACCT	GGGCAGGGAC	2520
AGATTGAGT	ATCCGGGATC	CAGTTAGGAA	CCTTCACCCC	CCCAAGGATG	AAGGACCCAA	2580
GGGTCTTAGT	GCCACCAATC	TCATAATAGG	CTCCATCGCT	GGTGCCATCC	TGGTAGCAGC	2640
TATTGTCTCT	GGGGGACACG	GCTGGGGATT	TAAAAATGTC	AAGAAGAGAA	GGTTGATGCC	2700
TACTCAGCAA	GGCCCCATCT	GAATCAGCTG	CGCTGGATGG	ACACCGCCTT	GCACTGTTGG	2760
ATTCTGGGTA	TGACATACCT	CGAGCAGTGT	TACTGGAAT	ATTAAGTTTG	TAAACAAAAC	2820
CTTTGGGTGG	TAATGACTAC	GGAGCTAAAG	TTGGGGTGAC	AAGGATGGGG	TAAAGAAAAA	2880
CTGTCTCTTT	TGGAATAAAT	GTCAAAGAAC	ACCTTTTACC	ACCTGTGAGT	AAACGGGGGA	2940
GGGGGCAAAA	GACCATGCTA	TAAAAAGAAC	TGTTCCAGAA	TCTTTTTTTT	TCCCTAATGG	3000
ACGAAGGAAC	AACACACACA	CAAAAATTAA	ATGCAATAAA	GGAATCATT	AAAA	

Seq ID NO: 150 Protein sequence:
 Protein Accession #: NP_003803

1	11	21	31	41	51	
MKPPGSSSRQ	PPLAGCSLAG	ASCGPQRGPA	GSVPASAPAR	TPPCRLLLV	LLLPLLAASS	60
RPRAWGAAAP	SAPHWNETA	KNLGVLADE	NTLQONSSSN	ISYSNAMQKE	ITLPSRLIYY	120
INQDESSEPH	VLDTKARHQ	KHNKAVHLAQ	ASFQIEAFGS	KFILDLLNN	GLLSSDYVEI	180
HYENGKPYYS	KGGHPCYH	SIRGVKDSKV	ALSTCNLHG	MFEDDTFVYM	IEPLBLVHDE	240
KSTGRPHIIQ	KTLAQVYSKQ	MKNLTMERGD	QNPFLSELQW	LKRRKRAVNP	SRGIFPEEMKY	300
LELMIVNDHK	TYKKHRSSEA	HTNNFAKSVV	NLVDSIYKEQ	LNTRVVLVAV	ETWTEKDQID	360
ITINPVQMLH	EFKRYRRIK	QHADAHLIS	RVTFFHYKRSS	LSYFEGGVCSR	TRGVGVNEYG	420
LPMAVAQVLS	QSLAQNLGIQ	WEPSSRKPKC	DCTESWGGCI	MEETGVSHSR	KPSKCSILEY	480
RDPLQRRGGA	CLFNRPTKLF	EPTCCNGYV	EAGEECDCGP	HVECYGLCKC	KCSLSNGAHC	540
SDGFCQNTS	CLFQPRGYEC	RDVNECDIT	EYCTGDSGQC	FPNLHKQDGY	ACNQNGRCY	600
NGECKTRDNQ	QQYINGTKAA	GSDKFCYEKL	NTEGTEKGNC	GKGDWRVIQC	SKBDVFCGFL	660

LCTNLTRAPR	IQQLQGEIIP	TSFYHQGRVI	DCSGAHVVL	DDTDVGYVED	GTPCGPSMMC	720
LDRKCLQIQ	LNMSCLPLD	KGKVCSGHV	CSNEATCIC	FTWAGTDCS	RDPVRNLHP	780
KDEGPKGPS	TNLIIGSIAG	AILVAAIVLG	GTGWGPKNV	KRRFDPTQQ	PI	

5 Seq ID NO: 151 DNA sequence
Nucleic Acid Accession #: NM_023915
Coding sequence: 250-1326

10	1	11	21	31	41	51	
	GGCACGAGGG	TTTCGTTTTTC	ATGCTTTACC	AGAAAAATCCA	CTTCCCTGCC	GACCTTAGTT	60
	TCAAAGGCTTA	TGCTTAATTA	GAGACAAGAA	ACCTGTTTCA	ACTTGAAGAC	ACCGTATAGG	120
	GTGAATTGGAC	AGCCAGCCAC	CACAATGAAA	AGAAATCAAC	CAGGAATAAC	CTATGCTGAA	180
	CCCCACGCCCT	AATCGTCCCC	AAGTGTTCCT	TGACACGCAT	CTTTGTGCTC	AGTGTCATGA	240
15	AACCTGAAGAA	TGGGGTTCAA	CTTGCAGCTT	GCAAAAATTAC	CAAAATAACGA	GCTGCACCGC	300
	CAGAAGAGTC	ACAATTCAAG	CACACAGAGC	GCAGCGGCAG	GAGAAGAACAC	CACCCCTCAC	360
	AATGAATTGT	ACACAATTGT	CTTGCGGGTG	CTTTATCTCA	TTATATTGTT	GGCAAGCATC	420
	TTGCTGAATT	GTTTAGCATT	GTGGATCTTC	TTCCACATTA	GGATAAATAAC	CAGCTTCATA	480
20	TTCTATCTCA	AAAACATAGT	GGTTGCAGAC	CTCATAATGA	CGCTGCACAT	TCCATTTCGA	540
	ATAGTCCATG	ATGCAGGATT	TGGACCTTTG	TACTTCCATG	TTAATTCTCTG	CAGATACACT	600
	TCAGTTTGTG	TTTATGCAAA	CATGTATACT	TCCATCGTGT	TCCTTGGGGT	GATAAGCACT	660
	GATCGCTATC	TGAAGGTGGT	CAAGCCATT	GGGGAATCTC	GGATGTACAG	CATAACCTTC	720
	ACGAAGGTTT	TATCTGTTGT	TGTTTGGGTG	ATCATGGCTG	TTTTGTCTCT	GCCAAACATC	780
25	ATCCTGACAA	ATGGTCAGCC	AACAGAGGAC	AATATCCATG	ACTGCTCAAA	ACTTAAAGT	840
	CCTTTGGGGG	TCAAATGGCA	TACGCGCATC	ACCATATGTA	ACAGCTGCTT	GTTTGTGGCC	900
	GTGCTGGTGA	TTCTGATCGG	ATTGTACATA	GCCATATCCA	GGTACATCCA	CAAAATCCAG	960
	AGGCAATTCA	TAAGTCACTC	AAGCCGAAG	CGAAACACATA	ACAGAGCATC	CAGGGTGTGT	1020
	AGGCTGTGTG	TTTTTACCTG	CTTCTACCA	TATCACTTGT	GCAGAAATTC	TTTTACTTCT	1080
	GTGCACTTAG	CACAGGCTTT	CGATGAATCT	GCACAAAAAA	TCCTATATTA	CTGCAAGAAA	1140
30	ATTACACTTT	TCCTGTCTGC	GTGTAATGTT	TGCGTGGATC	CAATAATTTT	CTTTTTCATG	1200
	TGTAGGTCAT	TTTCAAGAAG	GCTGTTCAAA	AAATACAAATA	TCGAAACCCG	GAGTGAAAGC	1260
	GTGCAATCAT	TGCAAAAGTT	GAGAAGATCG	GAAATTCCGA	TATATTATGA	TTACACTAGT	1320
	CTGTAGGCC	TTTTATTGTT	TGTGGAATCG	ATATGTACAA	AGTGTAATAA	AATGTTTCTT	1380
35	TTCAATTATC	TTAAAAAAA	AA				

Seq ID NO: 152 Protein sequence:
Protein Accession #: NP_076404

40	1	11	21	31	41	51	
	MGFNLTLAKL	PNNELHGQES	HNSGNGRSDGP	GKNTTLHNEF	DTIVLPVLYL	IIFVASILLN	60
	GLAVVIFPHI	RNKTSFIPLY	KNIVVADLIS	TLTFFFRIVH	DAGEGWPYFK	FILCYRTSVL	120
	FYANMYTSIV	FLGLISIDRY	LKVVKPPGDM	RNYSITFTVK	LSVCVWVIMA	VLSLPNIILT	180
45	NGQPTEDNI	DCSKLKSPLG	VKWHATAVTV	NSCLFVAVLV	ILIGCYAIAI	RYIHKSSRQF	240
	ISQSSRRKRK	NQISIRVVVA	FFTCFLPYHL	CRIPPTFSHL	DRLLDDESAK	LIYKCKEITL	300
	FLSACNVCLD	PIIYFFMCRS	FSTRFLFKSN	IKTRSESIRS	LQSVRSBAVR	IYDYDVTDV	

Seq ID NO: 153 DNA sequence
Nucleic Acid Accession #: D80008.1
Coding sequence: 149-739

	1	11	21	31	41	51	
55	GTTCGCGGCC	AAAGCGCGGA	GCGGAGGCCG	AGCGGAGAGC	CTGCGCGCTGT	AGGACTAGAA	60
	CGAAAGGAGT	GAGGCGGCCG	GAGCGCCAGAT	ACCATTTTGG	CGTGAGAGCT	GGTGGTGGCC	120
	AAGCGCCGCG	GAGTGGGAGT	CGTCCGCAT	GTCTCGGAA	AAAGCCATGG	AACTGATCCG	180
	CGAGCTGCAT	CGCGCGCCCG	AAGGCGCACT	GCCCTCGCTC	AACGAGGATG	GACTCAGACA	240
60	AGTTCTGGAG	GAGATGAAAG	CTTTGTATGA	ACAAAACCG	TCGTGATTGA	ATGAAGCAAA	300
	GTCAAGTGGA	CGAAGTGATT	TGATAACCAAC	TATCAAATT	CGACACTGTT	CTCTGTTAAG	360
	AAATCGACGC	TGCATCTGTG	CATACCTGTA	TAGACCGTTG	CTTCGGATAT	GAGACTCATG	420
	ATGGGAATAT	GGTAGCGCTG	TGCGAAATGC	ATTACGATTT	CACATGGCTG	CTGAAGAAAT	480
	GGAGTGGTTT	AATAATTATA	AAAGATCTCT	TGCTACTTAT	ATGAGGTGAC	TGGGAGGAGA	540
65	TGAAGGTTTG	GACATTACAC	AGGATATGAA	ACACCAAAA	AGCCTATATA	TTGAAGTCGG	600
	GTAGCTTAAA	GACTATTGAG	AATTTGAAGT	TGATGATGGC	ACCTTCAGTC	TATTAaaaaa	660
	GAATAGCCAG	CACTTTTCAC	CTCGATGGAA	ATGTGAGCAG	CTGATCAGAC	AGGAGGTCTT	720
	GGAGCAGCAT	CTGTCTAGAC	CATGCGGCCG	GGCATTCTCA	GGCTTCACTC	AACTCATGGA	780
	CTCCTCTGTA	CTCACTCTCT	CCACCACCTC	CTTCACCTCC	CTCTTTGATT	TTAGAGCTTA	840
70	TAGACATTGT	TTAAGATAAC	TAAAGAATACT	TGGCTAAGAA	TATAAATTGT	CTACATTTTA	900
	AGGACTTTCT	TTTTTAAATG	TTGTACACTA	TTCTTCTTAC	GTATTTTTGG	TTTTGGTTTT	960
	GTTTTGTAGA	GACTGTCTCA	CTAAGTGGCC	CGAGCTGGTC	TCAAAGCTCC	GGCCTCAAGC	1020
	AGTCTCTCCA	CCTTAGCTTC	CTAAGGTGTT	GAGATCAGAG	CGGTGAGCTG	CTGCACCCGG	1080
	CCCCTACTCC	TTTTTCTAAT	AAGCTGTATC	TGTAATCACA	GCATCTCTCA	AGTTTGTACA	1140
75	GTGTGTTTTT	TAAATGAAAG	TAAACATGGT	TACATTTGAA	TCTCTTAAAT	AACAGTCATG	1200
	TTGGCTGGAC	AGGAAGAAGG	TAGATCCTGT	GTGCTGTGTT	TTCTGGTCAT	GTGTATTGTA	1260
	CACAGTCATG	AGCTGAAATT	CTGAGATACA	CATTTTCAA	TCACATGCAA	GTGAAGATGA	1320
	TGGTCTGTAG	AAATTTTCAG	TATATAATA	GTTTAATGAC	ATACATAATT	ATTCATCTGG	1380
	TATTTGGGAA	GGAAGGACAC	ACATGGAAAT	TGCACATTTT	CACCATGGTG	GCTGGTGTGG	1440
80	CTTGCTGGTA	GGGCTGTATC	ACCGATATCA	CCACATTTGA	AGGGACAGT	GAAATGGGG	1500
	CTAGAGAAGG	AACTTTGTAC	AGGTTTCCCT	GAGATTTCAG	TTGACTGAAA	AGTCACATGA	1560
	AGAGTTGATT	GTCTTTTAAT	GGTATGTTTT	AAACAGCTGA	CATTTTAAAT	TTTTGATGAAA	1620
	TCCAGTTTAT	TGTTTGTGCT	TTTTATGCTT	TGGGTTGTGC	ATCCGAGAAA	TCCTTTCCCA	1680
	TCCCAAGATC	ACAATTTTTT	TTCCTTTTAA	CTTCTAGAAG	TGTTATAATT	TTAAGCTTTA	1740
85	TACTTTGGTC	TATGACCCGT	TTTTTTTTTT	GTTTTGTGTT	GTTTTCGTGT	TGTTTCTTTT	1800
	GTTTTGAGAT	GGAAGTCTGT	TCTGTCACCC	AGGCTGGGTT	GCAGTGGCGT	GATCTTGGCT	1860
	CACGTCAATG	TCTATCCCCC	GGGTTCAAGT	GATTTCTGTG	TCTCAGCCTC	CCCAAGTAGCT	1920
	GGGATACAC	GCACAGGCGC	CACGCGCTGG	CTAAATTTTG	TATTTTATAG	AGAGACAGAG	1980

5	TTTTACCATG	TTGGCCAGGC	TGGTTTCAAA	CTCCTGACCT	CAAGTGACCC	ACCTTGGCCT	2040
	CCCAAAGTTT	TGGGATTACA	AGTGTGGGCC	ACCGCGGCCA	GCCTATGATC	CATTTTGAAT	2100
	GAATTTTSTA	TATGGTGCNA	GGTGTCAATC	CACCTTCACT	TTTCTTGGG	AATATAGATA	2160
	TCCAGCTGTT	TCACTACCAT	TTTTTGAAAG	GACTGCCCTT	TGCTCTATCA	CCTTTGCATT	2220
	TTTGTAAAA	AGTAGTTGTC	AATGTATATG	TGGGTTTATT	TCAGGACTCT	GTTTTGTGCC	2280
	ATTGACCTGT	TTTTCTCTCC	TGAATGCCAA	TACCATATTT	GTATGTAGTG	TATGTAATTT	2340
	TCTAATAATT	CTTGAAACAG	ATAGTATTAA	TGTGTCTAT	TTTTGTCTGT	GTTTGTATTT	2400
	TTGTAGAGA	TGGGTTTCA	CCGTGTTGGC	CAGGCTGTGT	TGAACTCCTG	AGCTAAAGCA	2460
10	ATACACTTGC	CTCGTCTCTC	CCATGTGCTG	GGATTACAGG	CGTGAGCCTT	GGTGCTGGCC	2520
	CAGTGTACCA	CATTTCTTTT	TGAGATTGTG	TTTGGCTATG	TTAAGTCCTT	TGCTTTTGAT	2580
	GTGAAATTG	GGAACAGGCA	GGGTGTGGTG	GCTTATGCCT	GTAATCCTAG	AACCTTGGGA	2640
	GGCTTAGATG	GGTGGATCAC	TTGAGCTCAG	GAGTTCCAGA	CCAGCCCGGG	CCTATGGCAA	2700
	AACTCCGTCT	CTACAAAAAA	TAGAAAAAAT	TAGCCAGGTG	TGGTGGTGCA	TGCTGTAGT	2760
15	CACAGTTACA	CGGCAGGCTG	AGGTGGGAGG	ATCACTTGAA	CCCCAGAGGT	CAAGACTGCA	2820
	GTGAGCTGAG	ATCACACAC	TGTACTCCAG	CCTGGGTGAC	AAAGTGAGAC	TCTATCTCAA	2880
	AAAGAAATTA	GGATCAATTT	TGCAATTTCT	ACAAACAACA	CAACAAAAAC	CCCTGTTGGG	2940
	CACCTTGATT	GAGATTGCAT	TGAATTTATA	TAAACTGTT	GGGAGAAATT	ACATCTTAAT	3000
	AATATTGAGT	TTCTGCGCCT	ATAACAAGG	TCTGTCTTCC	TAGGTATTAA	TGTTTGTCT	3060
20	TCTATTTCTC	TTAATAATCT	TTTGTAGTTT	TCAGTGATCA	GGTCTACCAT	GTGAGCATTT	3120
	CATAGTTTGG	ATGCTAAATG	GTATTTTAAA	ATTTCAAATT	CTAACCACTT	GTGCTAGTA	3180
	AATAGAAATA	CAATTGATGT	TGAACCTGTA	TCCTTCAGCC	TTGCTAAACT	GTGAGTTCTC	3240
	ATGGTGTTTT	TGTAAATTAC	ATCAACAGTC	ATGTGTTCTA	TGAATAAAGA	GTTTTACTCC	3300
	TTCT						

Seq ID NO: 154 Protein sequence:
Protein Accession #: BAA11503.1

30	1	11	21	31	41	51	
	MFCEKAMELI	RELHRAPEQG	LPAFNEEDGLR	QVLEEMKALY	EQNQSDVNEA	KSGGRSDLIP	60
	TIKPRHCSLL	RNRRTCTVAYL	YDRLLRIRAL	RWEYGSVLPN	ALRFHMAAEE	MEWFNNYKRS	120
	LATYMRSLGG	DEGLDITQDM	KPKKSLYIEV	RCLKDYGEFE	VDDGTSVLLK	KNSQHFLPRW	180
	KCEQLIRQGV	LEHILS					

Seq ID NO: 155 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 149-709

40	1	11	21	31	41	51	
	GTTCGGCGCC	AAAGCGCGGA	GCGGAGGCCG	AGGCGAGAGC	CTGGCGCTGT	AGGACTAGAA	60
	CGAAAGGAGT	GAGGCGCCGA	GAGCCCAGAT	ACCATTTTGG	CGTGAGAGCT	GGTGGTTGGC	120
	AAGGCCGCGG	GAGTGGGAAG	CGTCCGCCAT	GTTCGCGGAA	AAAGCCATGG	AACGTATCCG	180
45	CGAGCTGCAT	CGCGCGCCCG	AAGGGCAACT	GCCTGCCTTC	AACGAGGATG	GACTCAGACA	240
	AGTTCGAGG	GAGATGAAG	CTTTGTATGA	ACAAAACCA	TCTGTATGTA	ATGAAGCAAA	300
	GTCAAGTGGG	CGAAGTGATT	TGATACCAAC	TATCAAATTT	CGACACTGTT	CTCTGTTAAG	360
	AAATCGACGC	TGCACGTGAG	CATACCTGTA	TGACCGCTTG	CTTCGGATCA	GAGCACTCAG	420
	ATGGGAATAT	GGTAGCGTCT	TGCCAATATG	ATTACGATTT	CACATGGCTG	CTGAAGAAAT	480
50	GGAGTGGTTT	AATAATTATA	AAGATCTCT	TGCTACTTAT	ATGAGGTGAC	TGGGAGGAGA	540
	TGAAGGTTTG	GACATTACAC	AGGATATGAA	ACCACCAAAA	AGCCTATATA	TTGAAGCTGG	600
	ATGCAGTGGC	GCGATCTCGG	CTCAACCTGC	AACCTCCACC	TCCCAGGTTT	ACCTCAACTG	660
	CACCTCCAC	CTCCAGGTG	CGGTGTCTAA	AAGACTATGG	AGAATTTGAA	GTGTATGATG	720
	GCACCTTCAG	CCTATTAAAA	AAAAATAGCC	AGCACTTTTT	ACCTCGATGG	AAATGTGAGC	780
55	AGCTGATCAG	ACAAGGAGTC	CTGGAGCACA	TCTGTCTATG	ACCATGCGCC	GAGGCACTTC	840
	CAGGCTTCAC	TCAACTCATG	GACTCCTCTG	TACTCACTCT	CTCCACCACT	CCCTTCACCT	900
	CCCTCTTTGA	TTTTAGAAGC	TATAGACATT	GTTTAAGATA	ACTAAGAATA	CTTGGCTAAG	960
	AAGTATAATT	TGCTAACTAT	TAAGGACTTT	CTTTTITTA	TGTTGTACAC	TATTCTTCTT	1020
	ACTCTTTTTT	GGTTTGGTTT	TGTTTITGTA	GAGACTGTCT	CACATATGTT	CCCAAGCTGG	1080
60	TCTCAAATCT	CTGGCCTCAA	GCACTCCTCC	CACCTTAGCT	TCTCAAAGTG	TTGAGATCAC	1140
	AGGCGTGAAG	CACGTGACCC	CGCCCTTACT	CTTTTITCTA	ATAAGCTGTA	TCTGTAATCA	1200
	CAGCATTCCT	ACAGTTGTTA	CAGTGTGTTT	TTTAAATGAA	AGTAAACATG	GTTCACATTG	1260
	AATCTCTTAA	ATAAGCAGTC	ACTTGGCTGG	ACAGGAAGAA	GGTAGATCCT	GTGTGTCTTG	1320
	TTTTCTGGTC	ATGTGTATTG	TACAAGCTAG	AGAGCTGAAT	TTCTGAGATA	CACATTTTCA	1380
65	AATCAGATGC	AAGTGAAGAT	GAGGTCTGT	AGAAATTTTC	AGTATATATA	ATGTTTAAATG	1440
	ACATACATAAT	TTATCATCTG	GCTATTTGGG	AAGGAAGGAC	ACACATGGAT	TTTGACATT	1500
	TCCACCATGG	TGGCTGTGTG	GGCTTGTGGC	TATGGGGTGA	TCACCAGTAT	CACCACTTTG	1560
	GAAGGGGACA	GTGAAATTGG	GGCTAGAGAA	GGAACTTTGT	ACAGTTTTC	CTGAGATTCA	1620
	GATTGACTGA	AAAGTCACAT	GAAGAGTTGA	TTGTCTTTTA	ATGGTATGTT	TTAAACAGCT	1680
70	GACATTTTAA	ATTTTGTATGA	AATCCAGTTT	ATTCTGTTGT	TCTTTTATGC	TTTGGGTGTT	1740
	GCATCCGAGA	AATCTTTTCC	CATCCCAAGA	TCACAATTTT	TTTTCTTTT	TACTTCTAGA	1800
	AGTGTATATA	TTTTAAGCTT	TATACITTTG	TCTATGACCC	GTTTTITTTT	TTGTTTGTGT	1860
	TTGTTTTTTC	GTTTGTTTCT	TTGTTTTGAG	ATGGAGTCTT	GTTCGTTCAC	CCAGGCTGGG	1920
	GTGCACTGGC	GTGATCTTGG	CTCACTGCAA	TCTCTATCCC	CTGGGTTCAA	GTGATTCTCT	1980
75	TGTCTCAGCC	TCCCAAGTAG	CTGGGATTAC	AGGCACAGGC	CGCCACGCC	GGCTAATTTT	2040
	TGTATTTTAA	GTAGAGACAG	AGTTTACCA	TGTTGGCCAG	GCTGGTTTCA	AACTCCTGAC	2100
	CTCAAGTGAC	CCACTTGGC	CTCCCAAAGT	TTTGGGATTA	CAAGTGTGGG	CCACCGCGGC	2160
	CAGCCTATGA	TCCATTTTGA	ATGAATTTT	TATATGTTGC	AAGGTGTCAA	TCCACCTTCA	2220
	CTTTTCTTGG	GGAATATAGA	TATCCAGCTG	TTTCACTACC	ATTTTITGAA	AGGACTGCCC	2280
80	TTTGCTCTACT	CACCTTTGCA	TTTTTGTATA	AAAGTAGTTG	TCAATGTATA	TGTGGGTTTA	2340
	TTTCAAGACT	CTGTGTTTGG	CCATTGACCT	GTTTTCTCT	CCTGAATGCC	AATACCATAT	2400
	TTGTATGTAG	TGTATGTAAT	TTTCTAATAA	TTCTTGAAAC	AGATAGTATT	AATGTGTCAT	2460
	ATTTTGTCTG	TTGTTGTAT	TTTTTGTAGA	GATGGGGTTT	CACCGTGTG	GCCAGGCTGT	2520
	GTGAACTCC	TGAGCTAAAG	CAATACACTT	GCCTCGTCT	CCCCATGTGC	TGGGATTACA	2580
85	GGCGTGAGCC	TTGTTGCTGG	CCCAAGTGAC	CACATTTCTT	TTTGAGATTT	GTTTTGGCTA	2640
	TGTTAAGTCC	TTTGTCTTGG	ATGTGAAAT	TGGGAACAGG	CAGGGGTGTT	TGGCTTATGC	2700
	CTGTAATCCT	AGAACTTTGG	GAGGCCTAGA	TGGGTGGATC	ACTTGAGCTC	AGGAGTTCCA	2760
	GACCAGCCCG	GGCCTATGGC	AAAACCTCCG	CTCTACAAAA	AATAGAAAAA	ATTAGCCAGG	2820

TGTGGTGGTG CATGCCCTGTA GTCACAGTTA CACGGCAGGC TGAGGTGGGA GGATCACTTG 2880
 AACCCAGAG GTCAGAGCTG CAGTGAGCTG AGATCACACC ACTGTACTCC AGCCTGGGTG 2940
 ACAAGTGGAG ACTCTATCTC AAAAAGAAAT TAGGATCAAT TTGTCAATTT CTACAACAAC 3000
 AACACAAAA ACCCTGTTG GGCACCTTGA TTGAGATTGC ATTGAATTTA TATAAACTG 3060
 5 TGGGAGAAAT TGACATCTTA ATAATATTGA GTCTTCTGGC CTATAACAA GGTCTGTCTT 3120
 CCTAGGTATT AATGTTTGT CTCTATTTC TCTTAATAAT CTTTTGTAGT TTTCAGTGA 3180
 CAGGTCTACC ATGTCAGCAT TTCATAGTTT TGATGCTAAA TGGTATTTTA AAATTTCAA 3240
 TTCTAACAC TTGTGCTAG TAAATAGAAA TACAATTGAT GTTGAACCTG TATCCTTCAG 3300
 10 CCTGTCTAAA CTGTGAGTTC TCATGGTGT TTTGTAAATT ACATCAACAG TCATGTGTTC 3360
 TATGAATAAA GAGTTTACT CCTTC

Seq ID NO: 156 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
 MFCEKAMELI RELHRAPEQG LPAPNEDGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP 60
 TIKFRHCSLL RNRCTVAYL YDRLLRIRAL RWEYGSVLEN ALRFHMAAEE MEWFNNYKRS 120
 20 LATYMRSLLGG DEGLDITQDM KPKKSLYIEA GCSGAISAQP ATSTSQVHLN CNLHLPGPVS 180
 KRLWRI

Seq ID NO: 157 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-621

1 11 21 31 41 51
 TTCCGGCCCA AAGCGCGGAG CGGAGGCCGA GCGGAGAGCC TGGCGCTGTA GGACTAGAAC 60
 GAAAGGAGTG AGGCGCGGAG AGCCAGATA CCATTTTGGC GTGAGAGCTG GTGGTTGGCA 120
 30 AGGCGCGGAG AGTGGGAGAG GTCCGCCATG TTCTGCGAAA AAGCCATGGA ACTGATCCGC 180
 GAGCTGCATC GCGCGCCCGA AGGCAACTG CCTGCCCTCA ACGAGGATGG ACTCAGACAA 240
 GTTCTGGAGG AGATGAAGAG TTTGTATGAA CAAAACCACT CTGATGTGAA TGAAGCAAG 300
 TCAGGTGACG GAAGTGATTT GATACCAACT ATCAAATTTT GACACTGTTT TCTGTTAAGA 360
 AATCGACGCT GCACTGTAGC ATACCTGTAT GACCGCTTGC TTGCGATCAG AGCACTCAGA 420
 35 TGGGAATATG GTAGCGTCTT GCCAAATGCA TTACGATTTC ACATGGCTGC TGAAGAAGTC 480
 CGGTGTCTAA AAGACTATGG AGAATTGAA GTTGATGATG GCACCTCAGT CCTATTAAAA 540
 AAAAAAGCC AGCACTTTT ACCTCGATGG AAATGTGAGC AGCTGATCAG ACAAGGAGTC 600
 CTGGAGCACA TCCGTGTCAT ACCATGCGCC GAGGCACTTC CAGGCTTCAC TCAACTCATG 660
 GACTCCTCTG TACTCACTCT CTCCACCACCT CCCTTCACCT CCCTCTTTGA TTTTAGAAGC 720
 40 TATAGACATT GTTTAAGATA ACTAAGAATA CTGGCTAAG AAGTATAATT TGCTAACTAT 780
 TAAGGACTTT CTTTTTTTAA TGTGTACAC TATCTCTCCT ACTCTTTTTT GGTTTTGGTT 840
 TTGTTTTGTA GAGACTGTCT CACTATGTTG CCCAAGCTGG TCTCAAACCT CTGGCCTCAA 900
 GCAGTCTCC CACCTTGATC TCTCAAAGTG TTGAGATCAC AGGCGTGAGC CACTGCACCC 960
 45 GCGCCCTACT CTTTTTTCTA ATAAGCTGTA TCTGTAATCA CAGCATTCCT ACAGTTGTTA 1020
 CAGTGTGTTT TTTAAATGAA AGTAAACATG GTTACATTTC AATCTCTTAA ATAAGCAGTC 1080
 ACTTGCGTGG ACAGGAAGAA GGTAGATCCT GTGTGCTTGT TTTCTGCTG ATGTGTATTG 1140
 TACAAGTATG AGAGCTGAAT TTCTGAGATA CACATTTTCA AATCAGATGC AAGTGAAGAT 1200
 GATGTCTGT AGAATTATTC AGTATATATA ATGTTTAATG ACATACTAAT TTATCATCTG 1260
 GCTATTTGGG AAGGAAGGAC ACACATGGAT TTGTCACATT TCCACCATGG TGGCTGGTGT 1320
 50 GGCTTGTGGC TATGGGGTGA TCACCAGTAT CACCACCTTG GAAGGGGACA GTGAATTGG 1380
 GGCTAGAGAA GGAACCTTGT ACAGTTTTC CTGAGATTCA GATTGACTGA AAAGTCACAT 1440
 GAAGAGTTGA TTGTCTTTTA ATGGTATGTT TTAACACAGT GACATTTTAA ATTTTGATGA 1500
 AATCCAGTTT ATTCGTTTGT TCTTTTATGC TTTGGGTGTT GCATCCGAGA AATCTTTTCC 1560
 55 CATCCCAAGA TCACAAATTT TTTTCTTTT TACTCTAGA AGTGTATATA TTTTAAGCTT 1620
 TATACTTTGG TCTATGACCC GTTTTCTTGT TTGTTTGTGT TTGTTTCTT GTTTGTTTCT 1680
 TTGTTTGGAG ATGGAGTCTT GTTCTGTGAC CCAGGCTGGG GTGCGATGGC GTGATCTTGG 1740
 CTCACGTCAA TCTCTATCCC CTGGGTCAA GTGATCTCTT TGTCTCAGCC TCCCAGTAG 1800
 CTGGGATTAC AGGCACAGGC CGCCACGCTT GGCTAATTTT TGATTTTATA GTAGAGACAG 1860
 60 AGTTTACCA TGTGGGCCAG GCTGGTTTCA AACTCCTGAC CTCAGTGAC CCACCTTGGC 1920
 CTCCAAAGT TTTGGGATTA CAAGTGTGGG CCACCGCGGC CAGCCTATGA TCCATTTTGA 1980
 ATGAATTTT TATATGGTGC AAGGTGTCAA TCCACCTTCA CTTTTTCTTG GGAATATAGA 2040
 TATCCAGCTG TTCTACTACC ATTTTTTGAA AGGACTGCCC TTTGCTCTAT CACCTTTCGA 2100
 TTTTGTAA AAAGTAGTGT TCAATGTATA TGTGGGTTTA TTTCAGGACT CTGTTTGTGT 2160
 CCATTGACCT GTTTTCTCT CTGAAATGCC AATACCATAT TTGTATGTAG TGTATGTAAT 2220
 65 TTTCTAATAA TTCTTGAAAC AGATAGTATT AATGTGTAT ATTTTGTCTG TTGTTGTAT 2280
 TTTTGTAGA GATGGGTTT CACCGTGTG GCCAGGCTGT GTTGAATCC TGAGCTAAG 2340
 CAATACACTT GCCTGCTCT CCCCATGTGC TGGGATTACA GCGGTGAGCC TTGGTGTCTG 2400
 CCCAGTGTAC CACATTTCTT TTTGAGATT GTTTTGGCTA TGTAAAGTCC TTTGCTTTG 2460
 70 ATGTGAAATT TGGGAACAGG CAGGGTGTGG TGGCTTATGC CTGTAATCCT AGAAGCTTGG 2520
 GAGGCTAGA TGGGTGGATC ACTTGAGCTC AGGAGTTCCA GACCAGCCCG GGCCTATGGC 2580
 AAACTCCGT CTCTACAAAA AATAGAAAAA ATTAGCCAGG TGTGGTGGTG CATGCCTGTA 2640
 GTCACAGTTA CACGGCAGGC TGAGGTGGGA GGTACACTTG AACCCAGAG GTCAAGACTG 2700
 CAGTGAGCTG AGATCACACC ACTGTACTCC AGCCTGGGTG ACRAAGTGAG ACTCTATCTC 2760
 75 AAAAAAGAAAT TAGGATCAAT TTGTCAATTT CTACAACAAC AACAAACAAA ACCCTGTTG 2820
 GGCACCTTGA TTGAGATTGC ATTGAATTTA TATAAACTG TTGGGAGAAAT TGACATCTTA 2880
 ATAATATTGA GTCTCTGGC CTATAACAA GGTCTGTCTT CCTAGGTATT AATGTTTGT 2940
 CTCTATTTC TCTTAATAAT CTTTGTAGT TTTCACTGTA CAGTCTACC ATGTGAGCAT 3000
 TTCTATGTTT TGATGCTAAA TGGTATTTTA AAATTTCAA TTCTAACACC TTTGTGCTAG 3060
 80 TAAATAGAAA TACAATTGAT GTTGAACCTG TATCCTTCAG CCTGTCTAAA CTGTGAGTTC 3120
 TCATGGTGT TTTGTAAATT ACATCAACAG TCATGTGTTC TATGAATAAA GAGTTTACT 3180
 CCTTC

Seq ID NO: 158 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |

MFCEKAMELI RELHRAPEQG LPAFNEGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP 60
 TIKFRHCSLL RNRRTVAYL YDRLLRIRAL RWEYGSVLPN ALRFHMAAEE VRCLKDYGEF 120
 EVDDGTSVLL KKNISQHFLLPR WKCEQLIRQG VLEHILS

5

Seq ID NO: 159 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 149-229

10 1 11 21 31 41 51
 GTTCGGCGCC AAAGCGCGGA GCGGAGGCCG AGGCGAGAGC CTGGCGCTGT AGGACTAGAA 60
 CGAAAGGAGT GAGGCGCCGA GAGCCAGAT ACCATTTTGG CGTGAGAGCT GGTGGTTGGC 120
 AAGGCCGCGG GAGTGGGAAG CGTCCGCCAT GTTCTGCGAA AAAGCCATGG AACTGATCCG 180
 CGAGCTGCAT CGCGCGCCCG AAGGGCAACT GCCTGCCTTC AACAATTAGC TGGGTGTGGT 240
 15 GGCACACACC TGTAAGTCCCA GCAACTTAGG AGGCTGAAGT GAGAGGATTG CATGGCTCCA 300
 GGAAGTTGAA ACTGCAGTGA ACTGTGGTCA CGCTATTACA CTCCAGCCTG GGTGACAGAC 360
 TGAATCCCTG TCTCAAAAAG GAAAAGGAGG ATGGACTCAG ACAAGTCTCTG GAGGAGATGA 420
 AAGCTTTGTA TGAACAAAAC CAGTCTGATG TGTTCTCTGT TAAGAAATCG ACGCTGCACT 480
 GTAGCATACC TGATATGACC CTTGCTTCGG ATCAGAGCAC TCAGATGG

20

Seq ID NO: 160 Protein sequence:
 Protein Accession #: Eos sequence

25 1 11 21 31 41 51
 ATGTTCTGCG AAAAAGCCAT GGAAGTATC CGCGAGCTGC ATCGCGCGCC CGAAGGGCAA 60
 CTGCCTGCCT TCAACAATTA G

30

Seq ID NO: 161 DNA sequence
 Nucleic Acid Accession #: U10694
 Coding sequence: 1333-2280

35 1 11 21 31 41 51
 GGATCCGGCC GGATCTCAGG GAGGTGAGGA CTTTGTCTC AGAGGGTGTG TGTGGACAAA 60
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 AGGAACCTAA GGGAGGATCG AGGGTACCTC CAGGCCAGAG AAATCTCTAG ATCAAGAGAG 180
 TTTGCCCTGC CCTACTGTTC ACCCCAGAGA GCCCGGGCAG GGCTGTCTGC TGAGGTCCCT 240
 40 CTTTATCTC GGGATCACTG GTGTGCGGGA GGGCTGGCCT TGGTCTGAGG GGGCTGCACT 300
 CACGTGAGCA GAGGAGGGGT CCCAGGCCCT GCCAGGAGTC CAGGTGAGAG CTGAGGGGAC 360
 CCCACTCAC AAACACAGAG GACCTAGCCC CACCCTGCC CTTGTGTGAG CTGAGGGGAA 420
 CCGCTGGGTG GATGGACTCC CTTCACTTCC TCTTCAGGTG TCTCTGGAG ATAGGGCCTC 480
 AGGTCAACAG AGGGAGGGTT CCAGACCCTG CAGGCATCAA GATCAGGACC AGGCAGTATC 540
 CTCACCCAG GACACATGGA CCCCATGTGA TTTAGACATC TCTTACTGTA CTTCCGAGGA 600
 45 AACCTCTGGC AGGTGTGGGC AGATGTTGGT TGGGGCATGT CCTTCTGTTC CATATCAGGG 660
 ATGTGAGTCT CTGATCTGAG AGACTCTCAG GCAAGTAGAG GAGTAGAGTC CAGTCCCTGC 720
 CAGGAGAAAG GTCAGGGCCC TGAGTGAGCG CAGAGGGGAC CATCCACCCC AAAAGTGTGT 780
 AGAATCAAG AGTGTCCAGC CCGCCCTCTT GACAGCACTG AGGACCCGGG GCTCTGCCTG 840
 CAGTCTGAG CCTAAGGGCC CCTCGATTCC TCTTCCAGGA GCTCCAGGAA GCAGGCAGGC 900
 50 CTTGTCTGTA GACAGTGTCC TCAGGTGCGA GAGCAGAGGA GACCCAGGCA GTGTGAGCAG 960
 TGAAGGTGAA GTGTTCACCC TGAATGTGCA CCAAGGGGCC CACCTGCCCC AGCACACATG 1020
 GGACCCATA GCACCTGGCC CCATTCCCC TACTGTCACT CATAGAGCCT TGATCTCTGC 1080
 AGGCTAGCTG CACGCTGAGT AGCCCTCTCA CTTCTCCCT CAGGTTCTCG GGACAGGCTA 1140
 ACCAGGAGGA CAGGAGCCCC AAGAGGCCCC AGAGCAGCAC TGACGAAGAC CTGTAAGTCA 1200
 55 GCCTTTGTTA GAACCTCCAA GGTTCGGTTC TCAGCTGAAG TCTCTCACAC ACTCCCTCTC 1260
 TCCCAGGCC TGTGGGTCTC CATCGCCAG CTTCTGCCCA CGTCTCTGAG TGCTGCCCTG 1320
 ACCAGAGTCA TCAATGTCTC CGAGCAGAGG AGTCCGCACT GCAAGCCTGA TGAAGACCTT 1380
 GAAGCCCAAG GAGAGGACTT GGGCCTGATG GGTGCACAGG AACCACAGG CGAGGAGGAG 1440
 60 GAGACTACCT CCTCTCTGTA CAGCAAGGAG GAGGAGGTGT CTGCTGTGCG GTCATCAAGT 1500
 CCTCCCCAG GTCTCTAGGG AGGCGCTTCC TCCTCCATTT CCGTCTACTA CACTTTATGG 1560
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 CCAGCTCAGC TGGAGTTCAT GTTCCAAGAA GCACTGAAAT TGAAGGTGGC TGAGTTGGTT 1680
 CATTTCCCTG TCCCAAATA TCGAGTCAAG GAGCCGCTCA CAAAGGCAGA AATGCTGGAG 1740
 65 AGCGTCATCA AAAATTACAA GCGCTACTTT CTTGTGATCT TCGGCAAGGC CTCGAGTTTC 1800
 ATGCAGGTGA TCTTTGGCAC TGATGTGAAG GAGGTGGACC CCGCCGGCCA CTCCTACATC 1860
 CTTGTCACTG CTCTTGGCCT CTCGTGCGAT AGCATGCTGG GTGATGGTCA TAGCATGCCC 1920
 AAGGCCGCCC TCCTGATCAT TGTCTGGGT GTGATCCTAA CCAAGACAA CTGCGCCCTC 1980
 GAAGAGTTTA TCTGGGAAGC GTTGAAGTGT ATGGGGGTGT ATGTTGGGAA GGAGCACATG 2040
 70 TTCTACGGGG AGCCAGGAA GCTGCTCACC CAAGATTGGG TGCAAGAAA CTACCTGGAG 2100
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 CACGCTGAAA CCAGCTATGA GAAGGTCATA AATTATTTGG TCATGCTCAA TGCAAGAGAG 2220
 CCCATCTGCT ACCCATCCCT TTATGAAGAG GTTTTGGGAG AGGAGCAAGA GGGAGTCTGA 2280
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 75 GCCCATGTG ACATGAGGCC CATTCCTGCG TCTGTGTTTG AAGAGGCAA TCAGTGTCT 2400
 CAGTGGCAGT GGGTGGAAAT GAGCACACTG TATGTATCT CTGGGTTCCT TGCTATTGG 2460
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 AGTTTAATGA ACTTCACCAT CGAAGTTAAT GAATGACAGT AGTCACACAT ATGTCTGTTT 2580
 ATGTTATTTA GAGTAAGAT TCTTGCTTTT GAGTCACATG GGGAAATCCC TGTATTATTG 2640
 TGAATGGGA CAAGATAACA TAGCAGAGGA ATTAATAATT TTTTGAAC TTGAACCTTAG 2700
 80 CAGCAAAATA GAGCTCATAA AGAATAGTG AAATGAAAT GTAGTTAATT CTGCCTTAT 2760
 ACCTCTTTCT CTCTCTGTA AAATTAAAC ATATACATGT ATACCTGGAT TTGCTTGGCT 2820
 TCTTTGAGCA TGTAAAGAA ATAAAAATTG AAAGAATAAT TTTTCTGTT CACTGGCTCA 2880
 TTTTCTTTC AGACACGCAC TGAACATCTG TTATTCGGAA CACCTGGGT T

85

Seq ID NO: 162 Protein sequence:
 Protein Accession #: AAA68877.1

1 11 21 31 41 51
 5 MSLEQRSPHC KPDEDLEAQQ EDLGLMGAQE PTGEEEEETS SSDSKEEEVS AAGSSSPFQS 60
 POGGASSSIS VYVTLWSQFD EGSSSQEIEEE PSSSVDPQAL EFMFQALKL KVAELVHFL 120
 HKYRVKEPVT KAEMLESVIK NYKRYFPVIF GKSEFMQVI FGTDVKEVDF AGHSYILVTA 180
 LGLSCDSMLG DGHSMKPAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKEHMPYGE 240
 PRKLLTQDWV QENYLEYRQV PGSDPAHYEF LWGSKAHAET SYEKVINYL 300
 PSLYEVLGE EQBGV

Seq ID NO: 163 DNA sequence
 Nucleic Acid Accession #: AF292100
 Coding sequence: 30-809

1 11 21 31 41 51
 15 GGGGGGGGAG AGGCCTGGAG GACACCAACA TGAACAAGTT GAAATCATCG CAGAAGGATA 60
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 CTCAAAAATGA CTGGAAGTTA GATGTTGCAA CAGATAATTT TTTCCAAAAAT CCTGAACTTT 180
 20 ATATACGAGA GAGTGTAATA GGATCATTGG ACAGGAAGAA GTTAGAACAG CTGTACATA 240
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 ATGACCTGGC ACTCGATCCA GCCAGCATTG GTGTGTTGAT TATTGCGTGG AAGTTCAGAG 360
 CAGCAACACA GTGCGAGTTC TCCAAACAGG AGTTTCATGGA TGGCATGACA GAATTAGGAT 420
 25 GTGACAGCAT AGAACCACTA AAGGCCAGTA TACCCAGAT GGAACAAGAA TTGAAAGAAC 480
 CAGGACGAT TAAGGATTTT TACCAGTTTA CTTTAAATTT TGCAAGAAT CCAGGACAAA 540
 AAGGATTAGA TCTAGAAATG GCCATTGCCT ACTGGAACCT AGTGCTTAAT GGAAGATTTA 600
 AATTCTTAGA CTTATGGAAT AAATTTTGTG TGGAAACATCA TAAACGATCA ATACCAAAAG 660
 ACATTGTGAA TCTTCTTTTA GACTTCAGTA CGATGATTGC AGATGACATG TCTAATTATG 720
 30 ATGAAGAAGG AGCATTCGCT GTTCTTATTG ATGACTTTGT GGAATTGCA CGCCCTCAA 780
 TTGCTGGGAC AAAAAGTACA ACAGTGTAGC ACTAAAGGAA CCTTTTAGAA TGTACATAGT 840
 CTGTACATAA AATACAAACG AAAATTGCAC AGTCAATTC TGCTGGCTGG ACTGAACTGA 900
 AGATCAATCC TCACAATTC GACTGAGGGT TGAGACAAAA CTTTAAAGAT ACATCTTGA 960
 CCATATCGTA TTTCTATCTT CTAATGGTGG TTTGGGCTTG TCTTCTAGTC TGGGCGGCTC 1020
 35 TAAACATTAA TATTTTCAAC ATTTGGAAT TCATCTTATA TCTGTGGACC ATCCTAGTTT 1080
 ATTCCTCCAT AAGTCTTAGA AGCTTTATGG TGATTTATTT GAGGTTTCA TTCTCGCATA 1140
 AAGCACAATG CTGTCTTCAT CAGAAAACAG TTGGCATAAG AATTAAACAT ATGAACATCA 1200
 CAAAACAATT TATAAAAACT TCTTAAATAT ACGCTTTGGG CTAGTTGCAA AGACTATGCT 1260
 AATAGCAGCT CCACTGAGAG TGATATATTT AAGTGTACTG GATCTGGAAT GGTGTTTGG 1320
 40 TTTGGGGGGA ATTTTTTTTT TTTCTGGCA AATCACATAT TCTGTGATG TGAGTATCTG 1380
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 CTGAAAAATG TATTTGTGTT TAGACTCTTG ATTTCAAAAG GTTCCACAGA ACTAGTCTCG 1500
 GCTTACCTTA CCCATGTTTA TATATAGCTG TCCTACAGGG AGCTTTTATT TAGAAAATGT 1560
 CTGCATAATG TTAGATCTTT CTCCTGTCTA CATTATGCAC TACATAATTG GACTTCATTA 1620
 45 TGCTTTTGA AATCTTATCT GCCTGTCA TAAGTTAAAC TATTTAATTT GTTTTGAATG 1680
 TTTTGGATTG CTACACAATA CAATATTCTA AATTTAGGCA TGAGGGTTT TTTGTTTAT 1740
 TTTTACTTTT TTTTGTTCAT TGCACTATGG AACACAATG AAATCTCTT AATTATAAG 1800
 AAGATAGTAG GAGTTAAATT TTGAAATGG TTGTGATGAG CCACGAAAT CAATCTTAT 1860
 AATATAGGTA CTGCTCTTTC AGACAAACAG TCCATTTTTA ATGACTTCTT ATTTTGTGTA 1920
 50 AATTACTTTA ACTGTGATTC ACTGTGGTTG CCAAAATATT ACTTCAGAA CAAAGATTTT 1980
 CAAACAAGCA TACACGATGC AAAATACCAAG TCTGGCTTCT AGTCTATTTA CTGTTTGTG 2040
 TCACCTAGAT TAGCTCAGTT TTCTCATCAA AGCAGAAATG TATCTTGCCT GTGTGTGTGT 2100
 GTGTGTGTGT GTGTGTGTGT GTATGTGTGT ATATATATAT ATATATATAT ATATATATTT 2160
 TTTTTTTTT TTTTTTTTAA ATTACAAAG CCATGAGCTG CTTTATGCT GAAATGGTC 2220
 55 ATTTCCCTGT TCACCTACTG ACATGTGAAG AAGGGTTTCT TGCTTCTTA AACATTTCCG 2280
 TAAGGCAGCG TAGAAATGTA ATACTTCAA TGTTTGATGA TTAGGTCTT TTGATAGGAA 2340
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 ATGACATATC AAAACTGCTT TTTACATGAT TTTGAAATAG ACTAGAAAGC TTTCCCTATA 2520
 60 GACATATTAA TATTCCAATC ATAACTTTAA TTCAAGAATG CAGTTTACC AAAAGAAAAA 2580
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 TGTCTTGAAG ATTTGAGTT ATGGTTATTG GTTTCAGATT GATTAATTCA CATATGCTGT 2820
 65 GTTTTCTTTA AAAGTCATAT GGGTTCGTGG CCTAATGCCT TGGATTTTAC ATATTTTCT 2880
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 TATAATTACT GTGTAATTAT AAACAAAAT ACATAAAGCT TTGAATATAA TTATGTAGCA 3000
 TAAAGTTTAA GGTGTTCAC TATGATGGCA TCTTAGAATT AAACAAAAT TTTACTAGGG 3060
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 70 AGGGAATATT TTGTACTAAA AAATGATTAC ACATATGGCT GTGTGTGTTT GAGTCTGTGT 3180
 CTGTGAGAGA GCCAGAGAGA GTGAGAGAGA TTGACAGAGA AAGGGAGAGA CACACACAG 3240
 CCCCTTGAAT TGCCTTAACT CCTAAGTGTG TCAGTCTCA TCCCGTAAA CTCCTCATGC 3300
 TGATTCTTGT TTTTAACTG AACCATAGGT ACAGTTTCTT TTTTGCCTAAA TGTCAAACA 3360
 75 GGTACAAAT TTAAATGTA ATGCTTTTAA AATAGAAAAA TGTATAAAAT TAGAAGTGCC 3420
 CACATATAAA AATACTTGA GATGAAGATT ATCTTTAGTG AATATCATCT GCATATCTCT 3480
 GTAAGTTCAA TTGTGTTTCT TACAGTCCCT GTCATATTAC CAACAGAGGC AATAAAAGCT 3540
 GCAGTGAAT TG

Seq ID NO: 164 Protein sequence:
 Protein Accession #: AAG00606

1 11 21 31 41 51
 80 MNKLKSSQKD KVRQFMIFTQ SSEKTAVSCL SQNDWKLDVA TDNFFQNPFL YIRESVKGSL 60
 DRKKLEQLYN RYKDPQDENK IGIDGIQFPC DDLALDPASI SVLIIAWKFR AATQCEFSKQ 120
 85 EFMDDGTELG CDSIEQLKQ IKPMEQELKE PGRFKDFYQF TFNFAKNPGQ KGLDLEMAIA 180
 YWNLVLNGRF KFLDLWNKFL LEHHRKSIPK DTWNLLDFFS TMIADDMSNY DEEGAWPVLI 240
 DDFVEFARPO IAGTKSTTV

Seq ID NO: 165 DNA sequence
Nucleic Acid Accession #: AF256215
Coding sequence: 220-2028

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	CTCCAGTCCG	CATGCTCAGT	AGTGTCTGCC	GGCCGGGCTG	CGGGGCGGCG	TCCGCTGCCG	60
10	GCCTACGGGC	TGCGGTGGCG	GCCTCCGCGG	CACCCGGCAG	GGCCCGCCAG	TCCCCGCTTC	120
	CCTGTCTCCG	AGCCCGCCGC	TGGCCCGGGG	CAGGGCGGGC	CCGGGGCTCC	TCCATGCTGC	180
	CAGCCCGCCG	GCTGCGGAGC	CGACCAAGTG	GCTCCTGCGA	TGGCGGCGGA	AGAGGAGGCT	240
	GCGGCGGGAG	GTAAGTGTTT	GAGAGAGGAG	AACCAGTGCA	TTGCTCCTGT	GGTTTCCAGC	300
	CGCGTGAGTC	CAGGGACAAG	ACCAACAGCT	ATGGGGTCTT	TCAGCTCACA	CATGACAGAG	360
15	TTTCCACGAA	AACGCAAAAG	AAGTGATTCA	GACCCATCCC	AAGTGGAAAG	TGGTGAACAC	420
	CAAGTTAAAA	TGAAGGCCTT	CAGAGAAGCT	CATAGCCAAA	CTGAAAACGG	GAGGAGAGAT	480
	AAATGAAATC	AACTGATTGA	AGAACTGTCT	GCAATGATCC	CTCAGTGCAA	CCCCATGGCG	540
	CGTAAACTGG	ACAACTTAC	AGTTTTAAGA	ATGGCTGTTC	AACACTTGAG	ATCTTTAAAA	600
	GGCTTGACAA	ATTCTTATGT	GGGAAGTAAT	TATAGACCAT	CATTCTTCA	GGATAATGAG	660
20	CTCAGACATT	TAATCCTTAA	GACTGCAGAA	GGCTTCTTAT	TTGTGGTGG	ATGTGAAAGA	720
	GGAAAAATTC	TCTTCGTTTC	TAAGTCAGTC	TCCAAAATAC	TTAATTATGA	TCAGGCTAGT	780
	TTGACTGGAC	AAAGTCTTAA	TGACTTCTTA	CATCCAAAAG	ATGTTGCCAA	AGTAAAGGAA	840
	CAACTTCTTT	CTTTTGATAT	TTACCAAGA	GAAAAGCTAA	TAGATGCCAA	AACCTGGTTG	900
	CAAGTTTACA	GTAATCTCCA	CGCTGGAAGG	ACACGTGTGT	ATTCTGGCTC	AAGACGATCT	960
25	TTTTTCTGTC	GGATAAAGAG	TTGTAAAATC	TCTGTCAAAG	AAGAGCATGG	ATGCTTACCC	1020
	AACCTCAAGA	AGAAAAGACA	CAGAAAATTC	TATACATATC	ATTGCATGG	TTACTTGAGA	1080
	AGCTGGCCTC	AAAGTATTGT	TGGAATGGAA	GAAGAAAGGA	ACAGTAAGAA	AGACAACAGT	1140
	AATTTTACCT	GCCTTGTGGC	CATTGGAAGA	TTACAGCCAT	ATATTGTTC	ACAGAACAGT	1200
	GGAGAGATTA	ATGTGAAACC	AACGCAATTT	ATAACCCGGT	TTGCAGTGAA	TGGAAAATTT	1260
30	GTCTATGTAG	ATCAAAGGGC	AACAGCGATT	TTAGGATATC	TGCCCTCAGG	ACTTTTGGGA	1320
	ACTTCTTGTT	ATGAATATTT	TCATCAAGAT	GACCCACAATA	ATTTGACTGA	CAAGCACAAA	1380
	GCAGTTCTAC	AGAGTAAAGG	GAATAACTCT	ACAGATTCCCT	ACAAATTTCAG	AGCAAAAGAT	1440
	GGCTCTTTTG	TAACTTTAAA	AAGCCAATGG	TTTAGTTTCA	CAAACTCCTG	GACAAAAGAA	1500
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35	TCATTTTTC	CTTGTAGCTC	TCAATCATCA	GAAGAATCCT	CTAGACAGTC	CTGTATGAGT	1620
	GTACCTGGAA	TGCTACTTGG	AACAGTACTT	GGTGCTGGTA	GTATTGGAAC	AGATATTGCA	1680
	AATGAAATTC	TGGATTTTCA	GAGGTTACAG	TCTTCTTCAT	ACCTTGATGA	TTGAGTCTCA	1740
	ACAGGTTTAA	TGAAAGATAT	TCATACTGTA	AACTGCAGGA	GTATGTCAA	TAAGGAGTTG	1800
	TTTCCACCAA	GTCCTTCTGA	AATGGGGGAG	CTAGAGGCTA	CCAGGCAAAA	CCAGAGTACT	1860
40	GTGTCTGTCC	ACAGCCATGA	GCCACTCCTC	AGTGATGGTG	CACAGTTGGA	TTTCGATGCC	1920
	CTATGTGACA	ATGATGACAC	AGCCATGGCT	GCAATTTATGA	ATTACTTAGA	AGCAGAGGGG	1980
	GGCCTGGGAG	ACCCTGGGGA	CTTCAGTGAC	ATCCAGTGG	CCCTCTAGCC	TTTGATTTTT	2040
	AACCTCAAAA	ATGAGAAACA	TTTTAAAGCA	TTATTTACGA	AAAAACTGTC	TCAACTATTTC	2100
	TTAAGTACTG	TATTGATATT	TTTGTATCT	TTTATTAATG	TTCTACCACT	TTTTATAGAT	2160
45	TTGCATCTTC	CTGTACAGG	GATGTGGGGA	AATACGTTTT	CCTCCCAAGA	GAACCAAGTT	2220
	TATTATAGAC	TCCTTTATTC	AGTGAATATG	CTTATAATCC	ACTAGTTGCC	ATATTTTTTG	2280
	TAAAAATATT	CTAAGCAAGA	ATACTACTTA	CATATTGTTT	TGGCTTTGTT	TTATTTTTGA	2340
	TGCAGTTTTT	TTAGTTGAG	GTAATGTAAT	ATATTGATGT	TTTCTTTGTT	GTCTAAGATT	2400
	GATTTATAAT	AGTAGTTTGG	TATAATTGG	AACATTTTCC	ATGCTTTGCG	AATTTCTCTA	2460
50	ATTGAGGATA	GGGCTTACAC	ACITTAAGAA	AACAGTGAGT	ACTTGAACAT	TTAAAGGGAC	2520
	AGTGCAATTT	ATAGTCATA	TCACATTGAA	TACTGTATTT	GATCTTTGGA	GACTTAGGCA	2580
	AGCACAGAGC	TGGGATATTT	ATGCTCAGTT	GAGCACTTTA	AGATGAATTT	TAAGTGAGAT	2640
	GATTTCTTGC	TAAAACCTCA	GAAAGTCAAA	AGAGTTTCAG	CTTTCCTTAC	AGAAAAGGAA	2700
	GGATCTTGGG	CCCTAGATCT	TGGGGATTAA	CCTCTGCATA	TAAGATTATC	TCTTAATAGG	2760
55	CCAGAGCTGG	TGCTCACGCC	TGTAATCCCA	GTACTTTGGG	AGGCTGAGAC	GGGCAGATCA	2820
	CTTGAGGTCA	GGAGTTCAAG	ACCAGCCTGG	CCAATATGGT	GAAACCCCGT	TTCTACTAAA	2880
	AATACAAAAA	AAATTACCCA	GGCACTCACT	CTTGAGGTAA	CTAACCAACT	CCCACGATAA	2940
	TGACAGTCCA	TTCTAGAGCG	CAAGGGCCTC	ATGACCTAAT	GGCACACACC	TGTAATCCCA	3000
	ACTGTCTGGG	AGGCTGAGGC	GAGAGGATTG	CTTGAACTTG	GGAGGCAGAG	GTGTCAGTGA	3060
60	CGCGAGATCG	CACCACTGCA	CTCCAGTCTG	GGCAACAGAG	TGAGACTTCA	TCTCAAAAAA	3120
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	TTTAAATGTT	TAATGTATAT	AAACCAAGTT	CTTTATACAC	ATTTGGGAAA	ACATTGGTCT	3360
65	CACAGATTAA	ATGATTAACT	AACTGACCCA	GGAACTAGTT	GTAGCTTTCT	AAGTAATTAG	3420
	GCAATTACAG	TTATTGCCGT	TAACCAAGAG	TAATAAAACA	AAATGACAAG	TACATGTTTA	3480
	AAATTATGAG	GCAATGAGAA	ATAATTTAAA	AACCAATTTT	CTAGTTATAA	TTTAAATTTT	3540
	GGAGAGCATT	TTTAACAGTA	ATTAATCCAG	AGGTGGCTCA	AATTGAGTAT	AAGAATTAA	3600
70	ATTATTAAAA	ATACTGCATG	TCTACCTTCT	CGGGGATCAT	ACTTTATAAC	ACTTTCTGCT	3660
	TCAGTAGCTC	TTCTAGCTTT	GCCAAAGTAT	CTCCCATATT	TTCTCTCTCG	TGCTTCGCAA	3720
	ATGAAAGTCA	GATAGGCTGG	GAACCTATGG	GGCAGCCCTC	AGACTTCAAT	GTGGGCTTCA	3780
	AATCCAGTTT	CCTGTTCTAT	ATGGTGCTAC	ATCTTTCCAG	AAATTTCCCC	TCAGAGCCCC	3840
	TCGCCAAAAA	AAAGCATTAT	TTTGACCTTG	CATGCTATTT	CTTTAGCTGT	AGGTGATAGA	3900
	TTAGAACTTC	TGTCAGACAT	GTTAATGACA	AACATACCAA	CAGACAATAA	CCAAAGCAAA	3960
75	TGTTTCTCTC	AAGTGTGAAA	TGTGCAGGGG	CTCGTGGGCA	AGGATGTATT	GGCAGACTGT	4020
	CCTCTTGAAC	TGATAGTGTC	CCAGCAATGT	TGGAGGTTGG	CACCAATCTC	GGTCCGACAC	4080
	TTGAGGACCT	GAGAGACATC	AGGTTTAGAA	TGAGCCAAAG	AAATCCTACA	AGATGGGGAG	4140
	AATTGGTGTG	CAGCAGCCTA	AGTGTATATG	TTAAGTCTAA	AGAAGTATGA	AAGATCCCCC	4200
	GTGTTCTCTA	AATTGAGCAG	AGGGGCTGCT	CTACCAATAT	CATTTTATGA	GGGACTGAAC	4260
80	CATTGCAGGT	TAGACTTGGC	TTCCAAAGAG	TCTGCCTAAG	CCAGGGGTGG	CAGGGTAGGC	4320
	CATCATAGCT	GGATGGCTCT	AAAGCAGAT	GGGGGCAGAC	TTGCCCTCGT	GATGCCAGGA	4380
	TTTGAGAGGC	AGAGTTTCTA	GAGGGAGACC	AGTGCTGCCT	CTCAGCTGG	CAGTTTCTTC	4440
	TCTTTGCAAG	AGGAGGGGCT	GTTCAATTCC	ATAGACCACT	GGGCAGATAG	CCAGTTGAAT	4500
	ACTCTGTGCA	TGGTTGATC	CTTTTATAGT	TGCTCTAAT	ATTTTCTGT	AGATCCTTTT	4560
85	GTCTGTGAGT	CAAAATCTAA	TCCATGCATT	GTATGATACC	GTAGCTCTCC	TAAGGTTTGT	4620
	GTTTCTCTCA	AAATGTTTTA	GTTTCTCTCA	ACTAAATTTG	ATTTTGTCTG	TTAGAAAGTG	4680
	CATATTTTAA	TGGTATACAC	TATGTTCTCT	TTTTCTACTG	CGAGTCAATT	TTTTGAATTT	4740
	TCGTGAGAAA	GAATATATCT	ACAAATGCA	CGAAAGTATC	ATAAAACAG	TACTCTAGAG	4800

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15
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CAGCGCTGTC CAATAGAAAT ATAATCTGAG CCACATGTAT AATTTTATTT TCTTCTAGCC 4860
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CAAAATATCA TTTGAACATG TAATTAATAT AAAATTATTA ATGTGATATT TTACATTCTT 4980
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GTACTAGCCA CATGTCAAGT GCTCAGTAGC CACATGTGGC TAGTGGCTAC TGCCTGGAC 5100
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CTGCTCTGGA GGCTGAGGCA GAATGGCGTG AACCACGGAG GCAGAGATGG CAGTGAGCCA 5580
AGATCGCGCC AGTGCACCCC AGCCTGGGCG ACAGAGCGAG ACTCCATCTC AAAAAAAAAA 5640
AAAAAAAAAA AAGAAAAGAA AAGAAAAGTC TAGAGAACAT TATATTAAAT GGTATTATT 5700
GAAGTAGACC AAAGTTTATA CCATAAGGAT ATTTTCTCTT AAATACCATG TTTGAAGAAC 5760
AATTATTATAT TGATCCTTGA ATCTGTAGA TCAAATAACA AGTCTCTATC CATGTTACCA 5820
AATTAAACCT TTTGAAATA ATAACTTTA AAATATCAGA TGTGTTATTA CAGGATGATA 5880
CTTGAATCA GTGGAATGA GTTATATGGT CATCACTAAA TTTAGAAATC TATTGTGAAA 5940
CAAGACGAAA CAGGAAGTCA CAGAATAGAG ACTTTTAGTA AATAAATGGA ATTTAAAGA 6000
AAGTGTATTAT TTACAGTGTG AGGATGTCTT TGTGTGCTA GTCTTTGAGG 6060
GATCTCCGTA AAATCTGGGG CACAGGTACA AGAAATAGCC AATATTAGT TCCAGACCA 6120
TGTTTAGTAG TGCTCAGTTT CAGATCATGC TGCCAGAGG TATCTCCCC TCAGGTGGT 6180
CATCACTGAG CCTTCCAGG GTGAGACTCAT ACTTGCCAG CACAATGTTA CGGGCAGACA 6240
GCCGACATC TATGATTAGC TAGAAGCCAT AAAGAAAAGC TGCTAAGTGG CCACTAGGTG 6300
CCACTTTTCT GTTTTGTGTA TGTCTTCTT AGCAGATCTT TTTTTCCTA GCTCCATGGG 6360
GCCTATGAGA GGCATTATG ATTTTGTGTC CTACAATAAG TCAGCCTGTC TGGTGTGAGT 6420
TGTTTATGTA GAAATGCTTT CCAAGGAGG TCTAGGAAGA TCCTGACACA TAAGAACTTT 6480
GGCTTAGAGA CCTTCCAGG GTGATGCCA ATAAAACTG ACCTGGAAAG AAAACCTGCC 6540
CAGCACGAAA CATGCTTTCT GAACTCACTT GAGAGTGTAT GGTGTATGTC ACTTCTCATA 6600
TATTCTTGAG TTTAGATTGT TCTTTTATC AATTTTATG TCTTTTCCAG TTCCTTGTG 6660
CTCGTCTGTA TATTGTGATT TTTAAATTTT TGTGGTAAAT AATGAAAAGA GTGAAATTAT 6720
ATTTTATAAT TACTCATTTG TAGTTTTTTT TTTTAAATTA ATAACTTCC TCCAAAAAGT 6780
GCTCCCTTAA AA

Seq ID NO: 166 Protein sequence:
Protein Accession #: AAG34652

40
45
50

1 11 21 31 41 51
MAAEERAAAG GKVLREENQC IAPVVSSRVS PGTRPTAMGS FSSHMTFFPR KRKGSDDSPS 60
QVEDGEHVQK MKAPREAHQ TEKRRDKMN NLIEELSAMI PQCNPMARKL DKLTVLRMAV 120
QHLRSLKGLT NSYVGSNYRP SFLQDNELRH LILKTAEGFL FVVGCGERGI LFVSKSVSKI 180
LNYDQASLFG QSLPDLFLPK DVAKVKEQLS SFDISPREKL IDAKTGLQVH SNLHAGTRTV 240
YSGRRSFFTC RIKSKCIKVK EEHGCLENSK KKEHRKFYTI HCTGYLRSWP PNIVGMSEER 300
NSKKDMSNPT CLVATIGRLQP YIVPQNSGEI NVKPTFEITR FAVNGKFFVY DQRATAILGY 360
LPQELGTSC YEYFQDDHN NLTDKHKAVL QSKKILTDS YKFRKDGSGF VTLKSQWFSF 420
TNFWTKLEY IVSNTLVLG HSEFGEASFL PCSSQSSEES SRQSCMSVPG MSTGTVLGAG 480
SIGTDIANEI LDQLRLQSS YLDDSSPTGL MKDTHTVNCR SMSNKELFPF SPSEMGELEA 540
TRQNQSTVAV HSHBELLSDG AQLDFDALCD NDDTAMAAFM NYLEAEGGLG DFGDFSDIQW 600
TL

55
Seq ID NO: 167 DNA sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86-1126

60
65
70
75
80
85

1 11 21 31 41 51
GGTTACTCAT CCTGGGCTCA GGTAAGAGGG CCCGAGCTCG GAGGCGGCAC ACCCAGGGGG 60
GACGCCAAGG GAGCAGGACG GAGCCATGGA CCCCGCCAGG AAAGCAGGTG CCCAGGCCAT 120
GATCTGGACT GCAGGCTGGC TGTGCTGCTG GCTGCTTCGC GGAGGAGCGC AGGCCCTGGA 180
GTGCTACAGC TGCGTGACAG AAGCAGATGA CGGATGCTCC CCGAACAAAG TGAAGACAGT 240
GAAAGTCGCG CCGGCGGTGG ACGTCTGCAC CGAGGCGGTG GGGGCGGTGG AGACCATCCA 300
CGGACAAATC TCGCTGGCAG TGCSSGGTGG CGGTTCGGGA CTCGCCGGA AGAATGACCG 360
CGGCTTGGAT CTTCACGGGC TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
CTGCAACGCC AAGCTCAACC TCACCTCGCG GCGCTCGAC CCGGCAGGTA ATGAGAGTGC 480
ATACCCGCCC AACGGCGTGG AGTGCTACAG CTGTGTGGGC CTGAGCCGGG AGGCGTGCCA 540
GGGTACATCG CCGCGGTGCG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600
CTTCGACGGC AACGTCACCT TGACGGCAGC TAAATGTGACT GTGTCTTTCG CTGTCCGGGG 660
CTGTGTCCAG GATGAATTCT GCACCTCGGA TGGAGTAACA GGCCAGGGT TCACGCTCAG 720
TGGCTCCTGT TGCCAGGGGT CCCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780
CCCTCGAATC CCACCCCTTG TCCGGCTGCC CCTCCAGAG CCCACGACTG TGGCCTCAAC 840
CACATCTGTC ACCACTTCTA CCTCGGCCCC AGTGAGACCC ACATCCACCA CCAAAACCCAT 900
GCCAGCGCCA ACCAGTCAGA CTCGAGACCA GGGAGTAGAA CACGAGGCTT CCGGGATGA 960
GGAGCCCAAG TTGACTGGAG GCGCCGCTGG CCACCAGGAC CGCAGCAATT CAGGGCAGTA 1020
TCTCGCAAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080
ATTGGCAGTG CTCTGTGGG CCGTGGCTGC TGGTGTCTTA CTGTGAGCTT CTCACCTTGG 1140
AAATTTCCCT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCTCTGT 1200
CCCACCACCT GACTGGGCTG GCCAGCCCC TGTTTTCCA ACATTCCCCA GTATCCCCAG 1260
CTTCTGCTGC GCTGGTTTGC GGCTTTGGGA AATAAAATAC CGTGTGTATAT ATTCTGGCAG 1320
GGGTGTCTGA GCTTTTGTAG GACAGCTCCT GTATCCTTCT CATCTTGTGC TCTCCGCTTG 1380
TCCTCTTGTG ATGTTAGAC AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG 1440
AGGATGCTAA GCTTCTACT CACTTCTCC TAGCCAGCCT GGACTTTGGA GCGTGGGGTG 1500
GGTGGGACAA TGGCTCCCCA CTTAAGCAC TGCTTCCCT ACTCCCGCA TCTTTGGGGA 1560
ATCGGTTCCC CATATGTCTT CCTTACTAGA CTGTGAGCTC CTCGAGGGCA GGGACCGTGC 1620
CTTATGTCTG TGTGTATCA GTTCTGGCA CATAAATGCC TCAATAAAGA TTTAATTACT 1680

TTGTATAGTG AAAAAAA

Seq ID NO: 168 Protein sequence:
Protein Accession #: NP_055215

1	11	21	31	41	51	
MDPARKAGAQ	AMIWTAGWLL	LLLLRGGAQA	LECYSCVQKA	DDGCSFNKMK	TVKCAPGV DV	60
CTEAVGAVET	IHGQFSLAVX	GCGSGLPGKN	DRGLDLHGLL	AFIQLQCCAQ	DRCNARLNLT	120
SRALDPAGNE	SAYPPNGVEC	YSCVGLSREA	CQGTSPFVVS	CYNASDHVYK	GCFDGNVTLT	180
AANVTVSLPV	RGCVDDEFCT	RDGVTGPGFT	LSGSCCQGSR	CNSDLRNKTY	FSPRIPLPLVR	240
LPPPEPTTVA	STTSVTTSTS	APVRPTSTTK	PMPAPTSTPT	RQGVHEEASR	DEEPRLTGGA	300
AGHQDRSNSG	QYPAKGFPQQ	PHNKGCVAPT	AGLAALLLAV	AAGVLL		

Seq ID NO: 169 DNA sequence
Nucleic Acid Accession #: NM_006875
Coding sequence: 186-1190

1	11	21	31	41	51	
GAATTCGGCA	CGAGCGCGCG	GCGAATCTCA	ACGCTGCGCC	GTCTCGGGC	GCTTCGGGC	60
CACCACTTTC	TCTGCTTTCC	ACCTTGGGCG	CCCCCAGCCC	TGGCTCCCCA	GCTGCGCTGC	120
CCCGGGCGTC	CACGCCCTGC	GGGCTTAGCG	GGTTCACTGG	GCTCAATCTG	CGCAGCGCCA	180
CCTCCATGTT	GACCAAGCCT	CTACAGGGGC	CTCCCGCGCC	CCCCGGGACC	CCCACGCCGC	240
CGCCAGGAGG	CAAGGATCGG	GAAGCGTTCG	AGGCCGAGTA	TGCACTCGCG	CCCCTCCTGG	300
GTAAGGGGGG	CTTTGGCAC	GTCTTCGCAG	GACACCGCCT	CACAGATCGA	CTCCAGGTGG	360
CCATCAAAAT	GATCCCCCGG	AATCGTGTGC	TGGGCTGGTC	CCCCCTGTCA	GACTCAGTCA	420
CATGCCCACT	CGAAGTCGCA	CTGCTATGGA	AAGTGGGTGC	AGGTGGTGGG	CACCTGGCG	480
TGATCGGCTT	GCTTGACTGG	TTTGAGACAC	AGSAAGGCTT	CATGCTGGTG	CTCGAGCGGC	540
CTTTGCCCGC	CCAGGATCTC	TTTGACTATA	TCACAGAGAA	GGGCCCACTG	GGTGAAGGCC	600
CAAGCCGCTG	CTTCTTTGGC	CAAGTAGTGG	CAGCCATCCA	GCACTGCCAT	TCCCGTGGAG	660
TTGTCCATCG	TGACATCAAG	GATGAGAACA	TCCTGATAGA	CCTACGCCGT	GGCTGTGCCA	720
AACTCATTTA	TTTTGGTTCT	GGTGCCCTGC	TTTATGATGA	ACCCTACACT	GACTTTGATG	780
GGACAAGGGT	GTACAGCCCC	CCAGAGTGGG	TCTCTCGACA	CCAGTACCAT	GCACTCCCGG	840
CCACTGTCTG	GTCACTGGGC	ATCCTCCTCT	ATGACATGGT	GTGTGGGGAC	ATTCCCTTTG	900
AGAGGGACCA	GTCAGTTCCT	GAAGCTGAGC	TCCTCTCCCG	AGCCCATGTC	TCCCCAGACT	960
GCTGTGCCCT	AATCCGCGCG	TGCCCTGGCC	CCAAACCTTC	TTCCCGACCC	TCACTGGAAG	1020
AGATCCTGCT	GGACCCCTGG	ATGCAAAAC	CAGCCGAGGA	TGTTACCCCT	CAACCCCTCC	1080
AAAGGAGGCC	CTGCCCTTTT	GGCCTGGTCC	TTGCTACCCT	AAGCCTGGCC	TGGCCTGGCC	1140
TGCCCCCAAA	TGGTCAGAA	AGCCATCCCA	TGGCCATGTC	ACAGGGATAG	ATGGACATTT	1200
GTTGACTTGG	TTTACAGGT	CATTACAGT	CATTAAAGTC	CAGTATTACT	AAGGTAAGGG	1260
ATTGAGGATC	AGGGGTTAGA	AGACATAAAC	CAAGTTTGCC	CAGTTCCTTT	CCCAATCCTA	1320
CAAGGAGGCC	TTCTCTCCAG	AACCTGTGGT	CCCTGATTTT	GGAGGGGGA	CTTCTTGCTT	1380
CTCATTTTGC	TAAGGAAGTT	TATTTTGGTG	AAGTGTGTC	CATTTTGAGC	CCCGGAGCTC	1440
TTATTTTGAT	GATGTGTGAC	CCCACATGG	CACCTCCTAC	TACCACCACA	CAAACTTAGT	1500
TCATATGCTT	TACTTTGGGC	AAGGGTGCTT	TCCTTCCAAT	ACCCAGTAG	CTTTTATTTT	1560
AGTAAAGGGA	CCCTTTCCCC	TAGCCTAGGG	TCCTATATTG	GGTCAAGCTG	CTTACCTGCC	1620
TCAGCCCAAG	ATTTTATTAT	TTGGGGGAGG	TAATGCCCTG	TGTTTACCCC	AAGGCTTCTT	1680
TTTTTTTTTT	TTTTTTTTTG	GGTGAGGGGA	CCCTACTTTG	TTATCCCAAG	TGCTCTTATT	1740
CTGGTGAGAA	GAACCTTAAT	TCCATAATTT	GGGAAGGAAT	GGAGATGGA	CACCACCGGA	1800
CACCCACAGA	CAATAGATGG	GGATGGATGG	TTTTTTGGGG	GATGGGCTAG	GGGAAATAAG	1860
GCTTGCTGTT	TGTTTCTCTG	GGGCGCTCCC	TCCAATTTTG	CAGATTTTGG	CAACCTCCTC	1920
CTGAGCCGGG	AATGTCCAAT	TACTAAATG	TAAATAATCA	CGTATTGTGG	GGAGGGGAGT	1980
TCCAAGTGTG	CCCTCCTTTT	TTTTCTTGCC	TGGATTATTT	AAAAAGCCAT	GTGTGGAAC	2040
CCACTATTTA	ATAAAGTAA	TAGAATCAGA	AAAAAAAAAA	AAAAAAAA		

Seq ID NO: 170 Protein sequence:
Protein Accession #: NP_006866

1	11	21	31	41	51	
MLTKPLQGGP	APPGTPTPPP	GGKDREAFEA	EYRLGPLLKG	GGFGTVFAGH	RLTDRLOQVAI	60
KVIPRNRVLG	WSPLSDSVTC	PLEVALLWKV	GAGGGHPGVI	RLLDWFETQE	GFMLVLERPL	120
PAQDLFDYIT	EKGPLGEGPS	RCFFGQVVAA	IQHCHSRGVV	HRDIKDNIL	IDLRRGCAKL	180
IDFGSGALLH	DEPYTDFDGT	RVYSPPPEWIS	RHQYHALPAT	VWSLGILLYD	MVCGDIPFER	240
DQEILEAEHL	FPAHVSPDCC	ALIRRCCLAPK	PSSRPSLEEI	LIDPWWQTPA	EDVTPQLQQR	300
RPCPFGLVLA	TLSLAWPLGA	PNGQKSHFMA	MSQG			

Seq ID NO: 171 DNA sequence
Nucleic Acid Accession #: NM_003646
Coding sequence: 89..2875

1	11	21	31	41	51	
GCGGCGCGGA	GCGGCGGTGC	TGAGCCCCCG	CCGCGGCGCC	GGCATGGGCG	TCTCCGCGCG	60
GCCTCCGCC	GGCCGGGGCT	AGGGCCCGAT	GGAGCCGCGG	GACGGTAGCC	CCGAGGCGCG	120
GAGCAGCGAC	TCCAGTCTGG	CTTCGCTCTC	GTCCAGCGCG	TCCGAGCGCG	ACGCGGCTCC	180
CGAGCCGGAC	AAGGCGCGCG	GGCGACTCAA	CAAGCGGCGC	TTCCCGGGCG	TGCGGCTCTT	240
CGGCGACAGG	CAAGCCATCA	CCAAGTCGGG	CCTCCAGCAC	CTGGCCCCCG	CTCCGCCAC	300
CCCTGGGGCC	CGGTGACAGC	AGTCAGAGCG	GCAGATCCGG	AGTACAGTGG	ACTGGAGCGA	360
CTCAGCGACA	TATGGGGAGC	ACATCTGGTT	CGAGACCAAC	GTGTCCGGGG	ACTTCTGCTA	420
CGTTGGGGAG	CAGTACTGTG	TAGCCAGGAT	GCTGAAGTCA	GTGTCTCGAA	GAAAGTCGCG	480
AGCCTGCAAG	ATTGTGTGTC	ACAGCCCTCG	CATCGAGCAG	CTGGAGAAGA	TAAATTTCCG	540
CTGTAAAGCG	TCCCTTCCGTG	AATCAGGCTC	CAGGAATGTC	CGCGAGCCAA	CCTTTGTACG	600
GCACCACTGG	GTACACAGAC	GACGCCAGGA	CGCAAGTGT	CGGCACTGTG	GGAGGGGATT	660
CCAGCAGAAG	TTCACCTTCC	ACAGCAAGGA	GATTGTGGCC	ATCAGCTGCT	CGTGGTGCAA	720

	GCAGGCATAC	CACAGCAAGG	TGTCCTGCTT	CATGCTGACG	CAGATCGAGG	AGCCGTGCTC	780
	GCTGGGGGTC	CACGACGCG	TGTCATATCCC	GCCACCTGG	ATCCTCCGCG	CCCGGAGGCC	840
	CCAGAAATCT	CTGAAGACAA	GCAAGAAGAA	GAAGAGGGCA	TCCTTCAAGA	GGAAGTCCAG	900
5	CAAGAAAGGG	CCTGAGGAGG	GCGGCTGGAG	ACCCCTTCATC	ATCAGGCCCA	CCCCCTCCCC	960
	GCTCATGAAG	CCCTGTCTGG	TGTTTGTGAA	CCCCAAGAGT	GGGGGCAACC	AGGGTGCAAA	1020
	GATCATCCAG	TCTTTCCTCT	GGTATCTCAA	TCCCCGACAA	GTCTTCGACC	TGAGCCAGGG	1080
	AGGGCCCAAG	GAGGCGCTGG	AGATGTACCG	CAAAGTGAC	AACCTGCGGA	TCCTGGCGTG	1140
	CGGGGGGAC	GGCAGCGTGG	GCTGGATCCT	CTCCACCCTG	GACCAGCTAC	GCCTGAAGCC	1200
10	GCCACCCCT	GTTGCCATCC	TGCCCCGCG	TACTGGCAAC	GACTTGGCCC	GAACCTCAA	1260
	CTGGGGTGGG	GGCTACACAG	ATGAGCCTGT	GTCCAAGATC	CTCTCCACG	TGGAGGAGGG	1320
	GAAOCTGGTA	CAGCTGGACC	GCTGGGACCT	CCACGCTGAG	CCCAAGCCCG	AGGCAGGGCC	1380
	TGAGGACCGA	GATGAAGGCG	CCACCGACCG	GTTGCCCTTG	GATGTCTTCA	ACAACACTT	1440
	CAGCCTGGGC	TTTGACGCCC	ACGTCACCTT	GGAGTTCAC	GAGTCTCGAG	AGGCCAACCC	1500
	AGAGAAATTC	AACAGCGGCT	TTCCGAATAA	GATGTTCTAC	GCCGGGACAG	CTTTCTCTGA	1560
15	CTTCTGATG	GGCAGCTCCA	AGGACCTGGC	CAAGCACATC	CGAGTGGTGT	GTGATGGAAT	1620
	GGACTTGACT	CCCAAGATCT	AGGACCTGAA	ACCCAGTGT	GTTGTTTTCC	TGAACATCCC	1680
	CAGGTACTGT	GCGGGCACCA	TGCCCTGGGG	CCACCTGGG	GAGCACCAAG	ACTTTGAGCC	1740
	CCAGCGGCAT	GACGACGGCT	ACCTCGAGGT	CATTGGCTTC	ACCATGACGT	CGTTGGCCGC	1800
20	GCTGCAAGTG	GGCGACGAGG	GCGAGCGGCT	GACGCAAGTG	GCGAGGTGG	TGCTCAACCA	1860
	ATCCAAGGCC	ATCCCGGTGC	AGGTGGATGG	CGAGCCCTGC	AAGCTTGACG	CCTCACGCAT	1920
	CCGCATCGCC	TGTCGCAATC	AGGCCACCAT	GGTGCAAGAG	GCCAAGCGGC	GGAGCGCGGC	1980
	CCCCCTGCAC	AGCAGACGAG	AGCCGCTGCC	AGAGCAGTTG	CGCATCCAGG	TGAGTCGGCT	2040
	CAGCATGCAC	GACTATGAGG	CCCTGCACTA	CGACAAGGAG	CAGCTCAAGG	AGGCCCTCTGT	2100
25	GCOGCTGGGC	ACTGTGGTGG	TCCAGGAGA	CAGTGACCTA	GAGCTCTGCC	GTGCCACAT	2160
	TGAGAGACTC	CAGCAGGAGG	CCGATGGTGC	TGGAGCCAA	TCCCGACAT	GCCAGAACT	2220
	GTCCCCCAAG	TGGTCTTCC	TGACGCGCAC	CACTGCCAGC	CGCTTCTACA	GGATCGACCG	2280
	AGCCCCAGAG	CACCTCAACT	ATGTGACTGA	GATCGCACAG	GATGAGATT	ATATCTCTGA	2340
	CCCTGAGCTG	TGAGGGGACT	CGGCCCGGCC	TGACCTCCCA	ACCCCACTT	CCCCCTCTCC	2400
30	CACCTCACCC	TGCTCACCCA	CGCCCCGGTC	ACTGCAAGGG	GATGCTGAC	CCCCCAAGG	2460
	TGAAGAGCTG	ATTGAGGCTG	CCAAGAGGAA	CGACTTCTGT	AAGCTCCAGG	AGCTGCACCG	2520
	AGCTGGGGGC	GACCTCATGC	ACGAGACGAA	GCAGAGTCGC	ACGCTCTG	ACCACGAGT	2580
	CAGCACTGGC	AGCAAGGATG	TGGTCCGCTA	CCTGCTGGAC	CACGCCCTCC	CAGAGATCTC	2640
	TGATGCGGTG	GAGGAAAAAG	GGGAGACCTG	TTTGACCAAA	GCAGCGGGCC	TGGGCCAGCG	2700
35	CACCATCTGC	CACATACATG	TGGAGGCGCG	GGCCTCGCTC	ATGAAGACAG	ACCAGCAGGG	2760
	CGACACTCCC	CGGCAGCGGG	CTGAGAAGGC	TCAGGACACC	GAGCTGGCGG	CCTACTCTGA	2820
	GAACCGGCAG	CATTACAGAA	TGATCCAGCG	GGAGGACCAG	GAGACGGCTG	TGTAGCGGGC	2880

Seq ID NO: 172 Protein sequence:
Protein Accession #: NP_003637

40	1	11	21	31	41	51	
	MEPRDGSPEA	RSSDSSESASA	SSSGSERDAG	PEPDKAPRRL	NKRRFPGLRL	FGHRKAITKS	60
45	GLQHLAPPPP	TPGAPCSESE	RQIRSTVDWS	ESATYGEHIW	FETNVSGDFC	YVGEQYCVAR	120
	MLKSVSRKRC	AACKIVVHTP	CIEQLEKINF	RCKPSFRESG	SRNVREPTFV	RHHVHRRRQ	180
	DGKCRHCKGK	FQKFTPHSK	EIVAISSWC	KQAYHSKVC	FMLQQIEBPC	SLGVHAAVVI	240
	PPTWILRARR	PONTLKASKK	KKRASFKRKS	SKKGPBEGRW	RPFIIRPTPS	PLMKPLLVFV	300
	NPKSGGNQGA	KIIQSFLWYL	NPRQVFDLSQ	GGPKALEMY	RKVHNLILA	CGGDGTGVGI	360
50	LSTLDQLRLK	PPFPVAILPL	GTGNDLARTL	NWGGGYTDEP	VSKILSHVEE	GNVVQLDRWD	420
	LHAEPNPEAG	PEDRDEGATD	RLPLDVFNNY	FSLGFDAAHT	LEFHESREAN	PEKFNRSFRN	480
	KMFYAGTAFS	DFLMGSSKDL	AKHIRVVCVG	MDLTPKIQDL	KPQCVVFLNI	PRYCAGTMFW	540
	GHPGHEHDFE	PQRHDDGYLE	VIGFTMTSLA	ALQVGGHGER	LTQCREVVL	TSKAIPVQVD	600
	GEPCKLAAAR	RIALRNQAT	MVQKAKRRA	APLHSDQPFV	PEQLRIQVSR	VSMHDEYALH	660
55	YDKEQLKEAS	VPLGTVVVPG	DSLELCRAH	IERLQEPDQ	AGAKSPTCQK	LSPKWCFLEA	720
	TTASRFYPIQ	RAQSHLNYVT	ETIAQDEIYIL	DEPLLGAASR	PDLPPTPSPL	PTSPCSPPTFR	780
	SLQGDAAFPD	QEGELIEAQR	NDPCKLQELH	RAGGDLMHDR	EQSRITLHHA	VSTGSKDVVR	840
	YLLDHAPPEI	LDAVEENGET	CLHQAAALGQ	RTICHYIVEA	GASLMKTDQ	GDTPRQRAEK	900
	AQDTLAAAYL	ENRQHYQMIQ	REDQETAV				

Seq ID NO: 173 DNA sequence
Nucleic Acid Accession #: AF232772
Coding sequence: 1-1662

65	1	11	21	31	41	51	
	ATGCCCGTGC	AGCTGACGAC	AGCCCTGCGT	GTGGTGGGCA	CCAGCCTGTT	TGCCCTGGCA	60
	GTGCTGGGTG	GCATCCTGGC	AGCCTATGTG	ACGGGCTACC	AGTTCATCCA	CACGGAAAG	120
	CACATCTGTT	CCTTCGGCCT	GTACGGCGCC	ATCCTGGGCC	TGCACCTGCT	CATTGAGAGC	180
70	CTTTTTCGCT	TCCTGGAGCA	CCGGCGCATG	CGACGTGCGG	GCCAGGCCCT	GAAGCTGCC	240
	TCCCCGCGGC	GGGGCTCGGT	GGCACTGTGC	ATTGCGGCAT	ACCAGGAGGA	CCCTGACTAC	300
	TTGCGCAAGT	GCCTGCGCTC	GGCCAGGCGC	ATCTCCTTCC	CTGACCTCAA	GGTGGTCATG	360
	GTGGTGGATG	GCAACCGCCA	GGAGGACGCC	TACATGTCTG	ACATCTTCCA	CGAGGTGCTG	420
	GGCGGCACCG	AGCAGGCGCG	CTTCTTTGTG	TGGCGCAGCA	ACTTCCATGA	GGCAGGCGAG	480
75	GGTGAGACGG	AGGCCAGCCT	GCAGGAGGGC	ATGGACCGTG	TGCGGGATGT	GGTGCGGGCC	540
	AGCACCTTCT	CGTGATCAT	GCAGAAGTGG	GGAGGCAAGC	GCGAGGTCT	GTACACGGCC	600
	TTCAAGGCC	TGCGGATTC	GGTGGACTAC	ATCCAGGTGT	GCGACTCTGA	CACTGTGCTG	660
	GATCCAGCCT	GCACCATCGA	GATGCTTCGA	GTCTGGAGG	AGGATCCCCA	AGTAGGGGGA	720
	GTCCGGGAGG	ATGTCTAAGT	CTCAACAAG	TACGACTCAT	GGATTTCTCT	CCTGAGCAGC	780
80	GTGCGGTACT	GGATGGCCTT	CAACGTGGAG	CGGGCCTGCC	AGTCCTACTT	TGGCTGTGTG	840
	CAGTGTATTA	GTGGGCGCTT	GGGCATGTAC	CGCAACAGCC	TCCTCCAGCA	GTTCTTGAG	900
	GACTGGTACC	ATCAGAAGTT	CCTAGGCAGC	AAGTGCAGCT	TCGGGGATGA	CCGGCACCTC	960
	ACCAACCGAG	TCCTGAGCCT	TGGCTACCGA	ACTAAGTATA	CCGCGCGCTC	CAAGTGCTCT	1020
	ACAGAGACCC	CCACTGAGG	CTCCCGGTGG	CTCAACCGAG	AAACCCGCTG	GAGCAAGTCT	1080
85	TACTTCCGGG	AGTGGCTCTA	CAACTCTCTG	TGGTTCCTCA	AGCACCACT	CTGGATGACC	1140
	TACGAGTCAG	TGGTCAAGGG	TTTCTTCCCC	TTCTTCTCTA	TTGCCACGGT	TATACAGCTT	1200
	TTCTACCGGG	CCCGCATCTG	GAACATTCTC	CTCTTCTCTG	TGACGGTGCA	GCTGGTGGGC	1260
	ATTATCAAGG	CCACCTACGC	CTGCTTCTCT	CGGGGCAATG	CAGAGATGAT	CTTCTATGTC	1320

5	CTCTACTCCC	TCCTCTATAT	GTCCAGCCTT	CTGCCGGCCA	AGATCTTTGC	CATTGCTACC	1380
	ATCAACAAT	CTGGCTGGGG	CACCTCTGGC	CGAAAAACCA	TTGTGGTGAA	CTTCATTGGC	1440
	CTCATTCCTG	TGTCCATCTG	GGTGGCAGTT	CTCCTGGAGG	GGCTGGCCTA	CACAGCTTAT	1500
	TGCCAGGACC	TGTTCACTGA	GACAGAGCTA	GCCTTCCTTG	TCTCTGGGGC	TATACTGTAT	1560
	GGCTGCTACT	GGGTGGCCCT	CCTCATGCTA	TATCTGGCCA	TCATCGCCCG	GCGATGTGGG	1620
	AAGAAGCCGG	AGCAGTACAG	CTTGGCTTTT	GCTGAGGTGT	GACATGGCCC	CCAAGCAGAG	1680
	CGGGTAAAGT	GCAATGGGTA	AGGGAGGGAA	GGGGAATGGA	AGAGAAAAGA	CAGGGTGGGA	1740
	GGGAGGAGGG	AGTGCTGTGT	TTTAGTCTCT	TAATGGTCCA	AAGSACAAT	CTAAATGCA	1800
10	AAGAACGGTG	ATGTAGTATG	GCCTGCACAG	TCTGTTTGA	GGAGGCAACA	CTGATCCCCC	1860
	AGATGCAGGG	CTGCAGGGGA	TTCTGTGTTT	TCAGACTGCC	TGTCGTCTTG	CATCTGCACA	1920
	TAGGCAGTAG	CCTCCTCCTG	GGCTCCAGAG	GGCACTCAGA	AGTTGTGCTA	AACCAAGTTA	1980
	AGTCCCATTC	AGTGGCAACT	TGTGATAGGT	ACCTGAGTGA	CGGCAACCTG	CGGAAGGAGG	2040
	TTCTCCACAG	CCATCTGAAC	ACAACCAGAG	GTGGCAGGAG	AATTTCTACT	GAGCGAGGTG	2100
	GGCGGGTTAG	TGTATGTAC	CCCCACCCCA	CCCATAAGTA	GTCAATCAATG	CAATAAGATT	2160
15	GGCGGTGAGA	TACAAAGCCC	AGAAGCCCTGA	TCTTTGGGCA	TCAGAAAACA	GGGTCCAGGA	2220
	ATGGTGCTTT	ATGTGAGATA	CCCACTCCA	CATCAACATT	CCAGGGATGA	GCCAAACCAG	2280
	CAGGGAGTTA	GCACTGAAC	GCTTTTAAAA	GTGCACATTA	AAAAGGAAAG	TTTGCCAGGA	2340
	GGAAACAAAG	GATTGTGGTG	GTGCTAAAGG	AGGCCATAAG	CTACACAGAG	GCCTTGGGTG	2400
20	TTCCACCTGG	AAACTGCTGA	GACGTCTAGA	TGGGTTCTTA	GCTTGTCTGT	GATCTCTGCT	2460
	GGGGAGATAA	AAAGATTAA	CCCCAACATG	TTCAAGAAAG	AAGTGAAGTC	TTGGGTATT	2520
	TAACCTGTAT	ACTCTTGAAT	TCTCTCAAA	TTCAAGCTCTG	ATCTGAGGCT	AAGACACACT	2580
	CCCCACTTCA	CTTTCTTCAA	AGCCACATTT	TTTGAGGTAT	CACTGCAGTC	ACCTCTTCTA	2640
	CCCTCATCAT	CATAGGTAA	GTTTTCAGAG	TGGCAATTGG	GGCGGAGCCC	CGGCTTCTTA	2700
25	TAGAAGCTTC	AGCAGGAGGC	AAGCGTGTTC	TCAGCACATA	TGGGAACTAT	GAGGAGCCTC	2760
	TGATCAAAAT	GGCTCAACAT	TTGGAGCTGC	TTGGACGGAT	TCCTTGGCAG	CCGGGTAGC	2820
	ATGTGTGACT	TTGAGGCTAC	TGTTCTTGAC	AATCATCTCC	AATGGAAGC	TTTTCAGTGT	2880
	TCCCAAAGTG	AACTCTCAAA	TCCAAATGG	TTATCTTTGA	GACCATCCAT	TCTCCTCAGT	2940
	GGCTTCTCCA	GGGAATTCCT	ACAGCCAAAGT	TGTGACAGTC	ACTGCATTGG	CCTGCTTCTT	3000
30	TCAGAAACCG	AGACTAGGAG	ATGAAACTGG	TTCTTACATC	CTAAGGTTC	TGCTTTCTCT	3060
	CTCATGCCCT	CTGAGGCTGT	TTTTGGCTGT	TTTCCCTCTG	CTGCTTTTGG	GGAAATGAGG	3120
	GAAGCCATT	TCCAAGTGAC	TGCAATCCA	GGCTGTTCTC	AGCGTTTGA	GTTTAAACCC	3180
	TGGGATCCTG	ACTAAGCCTT	TGACTTAAGG	GTGCTTGCT	TGCCCTCCAA	ATGCTCTTTC	3240
	TCAAAGGGGC	CAACTAAACC	GTGCAGAAC	AGCACTAAGG	TGGACAGCAG	ACAAGAGGGC	3300
35	AAGCCTCTAA	TGTACCAAGT	GCTTCCTACA	AAGACGCAAG	GTGTGCTCCG	AACACAGAT	3360
	GGGCAAAACC	TGGTGCTTTC	CTTCATCTCC	CACGAACTCA	AGGGTTTTC	AAGTGTAGCT	3420
	AACAGTTGCC	ACATCACACA	GACCTCCAGT	TTCTGGTAAG	ACTGCTGGTT	GACATCAGAG	3480
	CCAACCCATT	GAAGGCTGGA	AGGCAGCAGG	CATTGCTAA	GGCAGCTGAT	CCAGGCAATC	3540
	GTTCGTCTGG	CCAAGAAATT	AACTATTTT	GAGCATTAGA	ATGAGAGAAA	TCCGCTCAGC	3600
40	CAAGTGCAGA	GTTTCAGACT	CGCTAAGGGC	TTGTTTTTCT	TCAGCATTTA	CTTGAAGATT	3660
	AATGTAGGAT	GACAGGCTCT	CCTGGCTGTC	CTACCATCAG	CTCTGCCTTG	CAGTGTGGTC	3720
	CTCAACTTTC	CTCAAACTCA	AAACAGGCAG	GTACAGGTAG	TGGGCTCACA	ACGTTTGACC	3780
	TCGACTGGTT	TTTCTAAGTT	ATTTTGTACA	TTTTTCAGCA	GCAAAACCAA	ACTGGGTCTT	3840
	CAGCTTTATC	CCCGTTTCTT	GCAAGGGAAG	AGCCTTTATA	CAATTGGACG	CATTTTGGTT	3900
45	TTTCCTCAT	GAGAATTCAA	ATCCTCTTTT	GTATTGTTTC	TACAATAATT	TGTAACATA	3960
	TTTATTTTAA	CCTGCTTTT	TTTTTTTTTT	TAATTTTCAG	GTCAGATTTT	TTTACTGCA	4020
	CTTATTGTGC	AAAAATAAGA	TTCTCACAT				

Seq ID NO: 174 Protein sequence:
Protein Accession #: AAF36984

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	MPVQLTTLAL	VVGTSFLPALA	VLGGILAAV	TGYQFIHTEK	HYLSFGLYGA	ILGLHLIIQS	60
	LFAPLEHRRM	RRAGQALKLP	SPRRGSVALC	IAAYQEDPDY	LRKCLRSQR	ISFPDLKVV	120
55	VDVGNQEDA	YMLDIFHEVL	GGTEQAGFFV	WRSNFHEAGE	GETEASLQEG	MDRVDRVVRA	180
	STFSCIMQKW	GCKREVMYTA	FKALGDSVDY	IQCDSDDTLV	DPACTIEMLR	VLEEDPQVGG	240
	VGGDVQILNK	KCSFSDSFLSS	VRYWMAFNVE	RACQSYFGCV	QCISGPLMGY	RNSLLQQFLE	300
	DNVHKFPLGS	YCSFQDDRLH	TNRVLSLGYR	TKYTARSKCL	TETPTKYLRLW	LNQOTRWSKS	360
60	YFREWLNSL	WEFKHHLWMT	YESVVTGFFP	FPLIATVIQL	FYRGRIWNIL	LFLTLVLQLVG	420
	IIRATYACPL	RGNAMIFMS	LYSLLYMSSL	LPKIFAIAT	INKSGWGTSG	RKTIVVNFIG	480
	LIPVSIWVAV	LLEGLAYTAY	QDLFSETEL	APLVSGAILY	GCYVVALML	YLAIARRCG	540
	KKPEQYSLAF	AEV					

Seq ID NO: 175 DNA sequence
Nucleic Acid Accession #: NM_000691
Coding sequence: 43..1404

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	GCCGTGAAGC	GGCCCGCGC	CGCCTTCAGC	TCGGGCAGGA	CCCGTCCGCT	GCACTTCCGA	120
70	TTCCAGCAGC	TGGAGGCGCT	GCAGCGCCTG	ATCCAGGAGC	AGGAGCAGGA	GCTGGTGGGC	180
	GCCTGGCCG	CAGACTCGCA	CAAGAATGAA	TGGAACGCCT	ACTATGAGGA	GGTGGGTGAC	240
75	GTCTAGAGG	AGATCGAGTA	CATGATCCAG	AAGCTCCCTG	AGTGGGCCGC	GGATGAGCCC	300
	GTGGAGAAGA	CGCCCCAGAC	TCAGCAGGAC	GAGCTCTACA	TCCACTCGGA	GCCACTGGGC	360
	GTGGTCTCTG	TCATTGGCAC	CTGGAACATC	CCCTTCAACC	TCACCATCCA	GCCCATGGTG	420
	GGCGCCATCG	CTGACGGGAA	CGCAGTGGTC	CTCAAGCCCT	CGGAGCTGAG	TGAGAACATG	480
	GCAGCCCTGC	TGGCTACCAT	CATCCCCCAG	TACCTGGACA	AGGATCTGTA	CCCAAGTAATC	540
80	AATGGGGGTG	TCCCTGAGAC	CACGGAGCTG	CTCAAGGAGA	GGTTCGACCA	TATCCTGTAC	600
	ACGGGCAGCA	CGGGGGTGGG	GAAGATCATC	ATGACGGCTG	CTGCCAAGCA	CCTGACCCCT	660
	GTCAACGCTG	AGCTGGGAGG	GAAGAGTCCC	TGCTACGTGG	ACAAGAACTG	TGACCTGGAC	720
	GTGGCCTGCC	GACGCATCGC	CTGGGGGAAA	TTCATGAACA	GTGGCCAGAC	CTGCTGGGCC	780
	CCAGACTACA	TCTCTGTGTA	CCCCTCGATC	CAGAACCAAA	TTGTGGAGAA	GCTCAAGAA	840
85	TCACTGAAAG	AGTTCTACCG	GGAAGATGAT	AAGAAATCCC	GGGACTATGG	AAGAATCATT	900
	AGTGCCCGGC	ACTTCCAGAG	GGTGATGGGC	CTGATTGAGG	GCCAGAGGTG	GGCTTATGGG	960
	GGCACCGGGG	ATGCCCGCAC	TCGCTACATA	GCCCCACCA	TCTTCACGGA	CGTGAGCCCC	1020

CAGTCCCCGG TGATGCAAGA GGAGATCTTC GGGCCTGTGC TGCCCATCGT GTGCGTGGCG 1080
 AGCCTGGAGG AGGCCATCCA GTTCATCAAC CAGCGTGAGA AGCCCTGGCG CCTCTACATG 1140
 TTCTCCAGCA ACGACAAGGT GATTAAGAAG ATGATTGCAG AGACATCCAG TGGTGGGGTG 1200
 GCGGCCAAGC ATGTATCGT CCACATCACC TTGCACCTC TGCCCTTCGG GGGCGTGGGG 1260
 AACAGCGGCA TGGGATCCCTA CCATGGCAAG AAGAGCTTGG AGACTTTCTC TCACCGCGCG 1320
 TCTTGCTCTG TGAGGCTCTCT GATGAATGAT GAAGGCCTGA AGGTGAGATA CCCCCGAGC 1380
 CCGGCCAAGA TGACCCAGCA CTGAGGAGGG GTTGCTCCGC CTGGCTGGCG CATACTGTGT 1440
 CCCATCGGAG TCGGGACAC CCTCACTGGC TCTCTGGCC CTGGAGAATC GCTCTGCGAG 1500
 CCCCAGCCCA GCCCCACTCC TCTGCTGACC TGCTGACCTG TGCACACCCC ACTCCACAT 1560
 GGGCCAGGCG CTCACCATTC CAAGTCTCCA CCCCTTTCTA GACCAATAAA GAGACAAATA 1620
 CAATTTTCTA ACTCGG

Seq ID NO: 176 Protein sequence:
 Protein Accession #: NP_00682

1 11 21 31 41 51
 MSKISEAVKR ARAAFSSGRT RPLQFRFQQL EALQRLIQEQ EQELVGALAA DLHKNEWNAY 60
 YEEVVVLEE IEYMIQKLPE WAADEPVEKT PQTQDELYI HSEPLGVVLV IGTWNYFFNL 120
 TIQPMVGAIA AGNAVVLKPS ELSENMAELL ATIIQPYLDK DLYPVGINGV PETTELLKER 180
 FDHILYTGST GVGKIIMTAA AKHLTPVTL E LGGKSPCYVD KNCOLDVACR RIAWGFPMNS 240
 GQTCVAPDYI LCDPSIQNQI VEKLKSLKE FYGEDAKSR DYGRISARH FORVMGLIEG 300
 QKVAYGGTD AATRYIAPTI LTDVDPQSPV MQEEIFGPVL PIVCVRSLEE AIQFINQREK 360
 PLALYMFSSN DKVIKMLAE TSSGGVAAND VIVHITLHSL PFGGVGNSGM GSYHGKKSFE 420
 TFSHRRSCLV RPLMDEGLK VRYPPSPAKM TQH

Seq ID NO: 177 DNA sequence
 Nucleic Acid Accession #: NM_001067.1
 Coding sequence: 108-4703

1 11 21 31 41 51
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 CATTGCGACC TGTAATGAA AATATGCAAG TCAACAAAAT AAAGAAAAAT GAAGATGCTA 180
 AGAAAAGACT GTCTGTGAA AGAATCTATC AAAAGAAAAC ACAATTGGAA CATATTTTGC 240
 TCCGCCCAGA CACCTACATT GGTCTGTGG AATTAGTGAC CCAGCAAAATG TGGGTTTACG 300
 ATGAAGATGT TGGCATTAACT TATAGGGAAG TCACITTTGT TCCTGGTTTG TACAAAAATCT 360
 TTGATGAGAT TCTAGTTAAT GCTGCGGACA ACAAAACAAAG GGACCCAAAA ATGTCTTGTA 420
 TTAGATGCAC AATTGATCCG GAAAAACAAT TAATTAGTAT ATGGAATAAT GAAAAAGGTA 480
 TTCCTGTTGT TGAACACAAA GTTGAAAAGA TGTATGTCCC AGCTCTCATA TTTGGACAGC 540
 TCCTAACTTC TAGTAATAT GATGATGATG AAAAGAAAAGT GACAGGTGGT CGAAATGGCT 600
 ATGGAGCCAA ATTGTGTAACT ATATTGAGTA CCAAAATTTAC TGTGGAAGCA GCCAGTAGAG 660
 AATACAAGAA AATGTTCAAA CAGACATGGA TGGATAATAT GGAAGAGAGT GGTGAGATGG 720
 AACTCAAGCC CTTCAATGGA GAAGATTATA CATGTATCAC CTTTCAGCCT GATTGTCTTA 780
 AGTTTAAAT GCAGAGCCTG GACAAAGATA TGTGTGCACT AATGGTCAGA AGAGCATATG 840
 ATATTGCTGG ATCCACCAAA GATGTCAAAG TCTTCTTAA TGGAAATAAA CTGCCAGTAA 900
 AAGGATTTGG TAGTTATGTG GACATGTATT TGAAGGACAA GTTGGATGAA ACTGGTAAT 960
 CCTGAAAGT AATGATGAA CAAGTAAACC ACAGGTGGGA AGTGTGTTTA ACTATGAGTG 1020
 AAAAAAGGCT TCAGCAAAAT AGCTTTGTCA ACAGCATTGC TACATCCAAG GGTGGCAGAC 1080
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 ACAAGGGTGG TGTGCACTA AAAGCACATC AGGTGAAAAA TCACATGTGG ATTTTGTAA 1200
 ATGCCTTAAT TGAAAACCCA ACCTTTGACT CTCAGACAAA AGAAACATG ACTTTACAAC 1260
 CCAAGAGCTT TGGATCAACA TGCCAATTGA GTGAAAAAAT TATCAAGACT GCTTATGGCT 1320
 GTGGTATTGT AGAAGAGATA CTAACTGGG TGAAGTTTAA GGCCCAAGTC CAGTTAAACA 1380
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 AAGATTCAAT GAAGACGCTT CGTTATGGGA AGATAATGAT TATGACAGAT CAGGACCAAG 1740
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 TGGGACATCG TTTTCTGGAG GAATTTATCA CTCCATTGT AAAGGTATCT AAAAAACAAGC 1860
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 TGTCTCAAA TTCTGATAAC GAGAGATCTA TCCCTTCTAT GGTGGATGGT TTGAAACCAG 2280
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 CCCAATTAGC TGGATCAGTG GCTGAAATGT CTTCTTATCA TCATGGTGAG ATGTCACTAA 2400
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 AGCCCATTTG TCAGTTTGGT ACCAGGCTAC ATGGTGGCAA GGAATCTGCT AGTCCAGGAT 2520
 ACATCTTTAC AATGCTCAGC TCTTTGGCTC GATTGTTATT TCCACCAAAA GATGATCACA 2580
 CGTTGAAGTT TTTATATGAT GACAACCAGC GTGTGAGGCC TGAATGGTAC ATTCCTATTA 2640
 TTCCATGGT GCTGATAAAT GGTGCTGAAG GAATCGGTAC TGGGTGGTCC TGCAAAATCC 2700
 CCAACTTTGA TGTGCGTGAA ATTTGAAATA ACATCAGGCG TTTGATGGAT GGAGAAGAAC 2760
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 ACGTAGGCTG TTTAAAGAAA TATGACACGG TGTGGATAT TCTAAGAGAC TTTTTTGAAC 3180
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 CTGCTAAACT GAATAATCAG GCTCGCTTTA TCTTAGAGAA AATAGATGGC AAAATAATCA 3300

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	TTGAAAATAA	GCCTAAGAAA	GAATTAATTA	AAGTTCGTAT	TCAGAGGGGA	TATGATTCGG	3360
	ATCCTGTGAA	GGCCTGGAAA	GAAGCCCAGC	AAAAGGTTCC	AGATGAAGAA	GAAAATGAAG	3420
	AGAGTGACAA	CGAAAAGGAA	ACTGAAAAGA	GTGACTCCGT	AACAGATTCT	GGACCAACCT	3480
5	TCAACTATCT	TCTTGATATG	CCCTTTGGT	ATTTAACCAA	GGAAAAGAAA	GATGAACCTCT	3540
	GCAGGCTAAG	AAATGAAAAA	GAACAAGAGC	TGGACACATT	AAAAAGAAAG	AGTCCATCAG	3600
	ATTTGTGGAA	AGAAGACTTG	GCTACATTTA	TTGAAGAATT	GGAGGCTGTT	GAAGCCAAGG	3660
	AAAAACAAGA	TGAACAAGTC	GGACTTCCTG	GGAAAGGGGG	GAAGGCCAAG	GGGAAAAAAA	3720
	CACAAATGGC	TGAAGTTTIG	CCTTCTCCGC	GTGGTCAAGG	AGTCATTCCA	CGAATAACCA	3780
10	TAGAAATGAA	AGCAGAGGCA	GAAAAGAAAA	ATAAAAAGAA	AATTAAAGAA	GAAAAACTGT	3840
	AAGGAAGCCC	TCAAGAAGAT	GGTGTGGAAC	TAGAAGGCCT	AAAAACAAGA	TTAGAAAAGA	3900
	AACAGAAAAG	AGAACCAGGT	ACAAAGACAA	AGAAACAAAC	TACATTGGCA	TTTAAGCCAA	3960
	TCAAAAAAGG	AAAGAAGAGA	AATCCCTGGC	CTGATTGAGA	ATCAGATAGG	AGCAGTGACG	4020
	AAAGTAATTT	TGATGTCCCT	CCAGAGAGAA	CAGAGCCACG	GAGAGCAGCA	ACAAAAACAA	4080
	AATTCACAAT	GGATTCTGGAT	TCAGATGAAG	ATTTCTCAGA	TTTTGATGAA	AAAACTGATG	4140
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	GTAACAAAGA	ACTGAAACCA	CAGAAAAGTG	TCGTGTCAGA	CCTTGAAGCT	GATGATGTTA	4260
	AGGGCAGTGT	ACCACTGTCT	TCAAGCCCTC	CTGCTACACA	TTTCCCAGAT	GAAACTGAAA	4320
	TTACAAAACC	AGTTCCTAAA	AAGAATGTGA	CAGTGAAGAA	GACAGCAGCA	AAAAGTCAGT	4380
20	CTTCCACCTC	CACCTACGGT	GCCAAAAAAA	GGGCTGCCCC	AAAAGGAAAG	AAAAGGGGAT	4440
	CAGCTTTGAA	TTCTGGGTCT	TCTCAAAAGC	CTGATCCTGC	CAAAACCAAG	AATCGCCGCA	4500
	AAAGGAAGCT	ATCCACTTCT	GATGATTCTG	ACTCTAATTT	TGAGAAAATT	GTTTCGAAAG	4560
	CAGTCACAAG	CAAGAAATCC	AAGGGGGAGA	GTGATGACTT	CCATATGGAC	TTTGACTCAG	4620
	CTGTGGCTCC	TGGGGCAAAA	TCTGTACGGG	CAAGAAACCC	TATAAAGTAC	CTGGAAGAGT	4680
25	CAGATGAAGA	GGATTCTGTT	TAAAATGTGA	GGCGATTATT	TAAAGTAATT	ATCTTACCAA	4740
	GGCCAGAGCT	GGTTTAAAG	TTACCTGAAG	CTCTTAACTT	CCTCCCCCTC	GAATTTAGTT	4800
	TGGGGAAGGT	TTTTTATAGT	CAAGACATCA	AAGTGAAGTA	AAGCCCAAGT	GTTCTTTAGT	4860
	TTTTTATAAT	ACTGTCTAAA	TAGTGACCAT	CTCATGGGCA	TTGTTTTCTT	CTCTGCTTTG	4920
	TCTGTGTTTT	GAGTCTGCTT	TCTTTTGTCT	TTAAAACCTG	ATTTTAAAGT	TCTTCTGAAC	4980
30	TGTAGAAATA	CACTTCTGAT	CACCTCAGCG	TAAAGCAGTG	TGTTTATTAA	CCATCCCACT	5040
	AGCTAAAACT	AGAGCAGTTT	GATTAAAAAG	TGTCACTCTT	CCTCCTTTTC	TACTTTCACT	5100
	AGATATGAGA	TAGAGCATTA	TATCTGTTT	TATCTTAGTT	TTATACATAA	TTTACATCA	5160
	GATAGAACTT	TATGGTTCTA	GTACAGATAC	TCTACTACAC	TCAGCCTCTT	ATGTGCCAAG	5220
	TTTTTCTTTA	AGCAATGAGA	AATTGCTCAT	GTCTTCTCAT	TTCTCAAATC	ATCAGAGGCC	5280
35	AAAGAAAAAC	ACTTTGGCTG	TGTCTATAAC	TTGACACAGT	CAATGAAGAT	AAGAAAAATTA	5340
	GAGTAGTTAT	GTGATTATTT	CAGCTCTTGA	CCTGTCCCCT	CTGGCTGCCT	CTGAGTCTGA	5400
	ATCTCCCAAA	GAGAGAAACC	AATTCTAAG	AGGACTGGAT	TGCAGAAAGC	TGCGGGACAA	5460
	CATTGTATCC	AAGATCTTAA	ATGTTATATT	GATAACCATG	CTCAGCAATG	AGCTATTAGA	5520
	TTCAATTTGG	GAAATCTCCA	TAATTTCAAT	TTGTAACCTT	TGTTAAGAGC	TGCTACATT	5580
40	GTTATATGTG	TGTGACTTGA	GTAATGTTAT	CAACGTTTTT	GTAATATATT	ACTATGTTTT	5640
	TCTATTAGCT	AAATTCACAC	AATTTGTATC	TTAATAAAAA	TGTTCTAAAC	ATTGC	

Seq ID NO: 178 Protein sequence:
Protein Accession #: NP_001058.1

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	MWVYDEDVGI	NYREVTFPVG	LYKIFDEILV	NAADNKQRDP	KMSCIRVTID	PENNLISIWN	120
50	NGKGIPVVEH	KVEKMYVPAL	IFGQLLTSSN	YDDDEKKVTG	GRNGYGAKLC	NIPSTKFTVE	180
	TASREYKKNF	KQTWMDNMGR	AGEMELKPFN	GEDYTCITFQ	PDLSKPKMQS	LDKDIVALMV	240
	RRAYDLAGST	KDVVVFLLGN	KLPVKGFRSY	VDMLKDKLKD	ETGNSLVKVIH	EQVNRHWEVC	300
	LTMSEKGFQO	ISFVNSIATS	KGGRHVDYVA	DQIVTKLVDV	VKKKNKGGVA	VKAHVKNHNM	360
	WTFVNALIEN	PTFDSQTKEN	MTLQPKSFGS	TCQLSEKPIK	AAIGCGIVES	ILNWVKFKAQ	420
55	VQLNKKCSAV	KHNRIKGIPI	LDDANDAGGR	NSTECTLILT	EGDSAKTLAV	SLGLVGVGRDK	480
	YGVVFLRGLI	LNVREASHKQ	IMENAEINNI	IKIVGLQYKK	NYEEDSLKT	LRGKIMIMT	540
	DQDDQDGHK	GLLNFIIHNN	WPSLLRHRFL	EEPTIPIVKV	SKNKQEMAFY	SLPEPEEWKS	600
	STPNHKKWV	KYYKGLGTST	SKEAKEVFAD	MKRHRIQFKY	SGPEDDAAIS	LAPSKKQIDD	660
	RKEWLTNFM	DRRQRKLGL	PEDYLYGQTT	TYLTYNDFIN	KELILFSNSD	NERSIPSMVD	720
60	GLKPGQRKVL	PTCFKRNDRK	EVKVAQLAGS	VAEMSSYHHG	EMSLMNTIIN	LAQNFVGSNN	780
	LNLLQPIGQF	GTRLHGGKDS	ASPRYIPTML	SSLARLLFPP	KDDHTLKFLLY	DDNQREPEW	840
	YPIIIPMVL	NAGBIGITGW	SKIPNFDVR	EIVNNIRRLM	DGEEFLPMLP	SYKNFKGTIE	900
	ELAPNQYVVS	GEVAILNSTT	IEISELPVRT	WTQTYKEQVL	EPMLNGTEKT	PPLITDYREY	960
	HTDITVKFV	KMTEEKLAEA	ERVGLHKVFK	LQTSLTCSNM	VLFHDVGCCLK	KYDITVLDILR	1020
65	DPFELRLKYV	GLRKEWLLGM	LGAESAKLNN	QARFILEKID	GKII IENKPK	KELIKVLIQR	1080
	GVDSDPVKAW	KEAQKQVPDE	EENEESDNEK	ETEKSDSVTD	SGPTFNVLID	MPLWYLTKEK	1140
	KDELCLRLNE	KEQELDTLKR	KSPSLWKED	LATFIEELEA	VEAKEKQDEQ	VGLPGRGKKA	1200
	KGKKTQMAEV	LPSPRGQRTI	PRITIEMKAE	AEKKNKKIK	NENTEGSPQE	DGVELEGLKQ	1260
	RLEKKQKREP	GTKTKKQTTL	AFKPIKKGKK	RNFWDSESD	RSSDESNEFDV	PPRETEPRRA	1320
70	ATKTKFTMDL	DSDEDFSDFD	EKTDDDFVFP	SDASPPKTKT	SPKLSNKKELK	PQKSVVSDLE	1380
	ADDVKGVSPL	SSSPFATHFP	DETEITNFVP	KKNVTVKKTA	AKSQSSTSTT	GAKKRAAPKG	1440
	TKRDPALNSG	VSQKPDPAKT	KNRRKRKPST	SDDSDSNFEK	IVSKAVTSKK	SKGESDDPHM	1500
	DFDSAVAPRA	KSVRAKFKIK	YLESEDDDL	P			

Seq ID NO: 179 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-7095

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	CGCGAGGGGG	CCGCAGACCG	TCTGGAAATG	CGAATCTTAA	AGCGTTTCTC	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGGCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
85	CTGTGTGAAG	AGATTGGGCTG	GCTCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420

	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTCAGCGGAG	GAGTTTCAGA	AATGGTGTIT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATT	TGTCACTCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
5	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGBAGG	AGCAGTCRAA	660
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Nucleic Acid Accession #: Eos sequence

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	AACTTTCTGG	TCACCTCAGAA	GAGTGTGCAA	GTGCTTGCTT	ATTATACTGT	GAGGAATTTT	3180
	ACTCTAAGAA	ACACAAAGAA	AAAAAAGGGC	TCCCAAGAAAG	GAAGACCCAG	TGGACGTGTG	3240
60	GTGACACAGT	ATCACTACAC	GCACTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
	GTGCTGACCT	TTGTGAGAAA	GCGACGCTAT	GCCCAAGCGCC	ATGCAGTGGG	GCCTGTTGTG	3360
	GTCCACTGCA	GTGCTGGAGT	TGGAAGAACA	GGCACATATA	TTGTGCTAGA	CAGTATGTTG	3420
	CAGCAGATTG	AACACGAAAG	AACTGTCAAC	ATATTGGGCT	TCTTAAACAA	CATCCGTTCA	3480
	CAAAAGAAAT	ATTTGGTACA	AACTGAGGAG	CAATATGTCT	TCATTCTATG	TACACTGGTT	3540
65	GAGGCCATAC	TTAGTAAGAA	AACTGAGGAG	CTGGACAGTC	ATATTCTATG	CTATGTTAAT	3600
	GCATCTCTCA	TTCTGTGACC	AGCAGGCCAA	ACAAAGCTAG	AGAAACCAAT	CCAGCTCCTG	3660
	AGCCAGTCAA	ATATACAGCA	GAGTGAATAT	TCTGCAGCCC	TAAAGCAATG	CAACAGGGAA	3720
	AAGAATCGAA	CTTCTCTAT	CATCCCTGTG	GAAAGATCAA	GGGTTGGCAT	TTTATCCCTG	3780
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70	GAATTCTATC	TTACCCAGCA	CCCTCTCCTT	CATACCATCA	AGGATTTCTG	GAGGATGATA	3900
	TGGGACCATG	ATGCCCAACT	GGTGGTTATG	ATTCTGTATG	GCCAAAACAT	GGCAGAAAGT	3960
	GAATTTGTTT	ACTGCCCAAA	TAAAGATGAG	CCTATAAATT	GTGAGAGCTT	TAAGGTCACT	4020
	CTTATGGCTG	AAGAACACAA	ATGCTATATC	AATGAGGAAA	AACTTATAAT	TCAGGACTTT	4080
	ATCTTAGAAG	CTACACAGGA	TGATTATGTA	CTTGAAGTGA	GGCACTTTCA	GTGCTCTAAA	4140
75	TGGCCAAATC	CAGATAGCCC	CATTAGTAAA	ACTTTTGAAC	TTATAAGTGT	TATAAAGAAA	4200
	GAAGCTGCCA	ATAGGGATGG	GCCTATGATT	GTTTATGATG	AGCATGGAGG	AGTGACGGCA	4260
	GGAACTTTCT	GTGCTCTGAC	AACCTTATG	CACCAACTAG	AAAAAGAAAA	TTCCGTGGAT	4320
	GTTTACCAGG	TAGCCAAGAT	GATCAATCTG	ATGAGGCCAG	GAGTCTTTGC	TGACATTGAG	4380
	CAGTATCAGT	TTCTCTACAA	AGTGATCCCT	AGCCTTGTGA	GCACAAGGCA	GGAGAGAAAT	4440
80	CCATCCACCT	CTCTGGACAG	TAATGGTGCA	GCATTGCGCT	ATGGAAATAT	AGCTGAGAGC	4500
	TTAGAGTCTT	TAGTTTAAAC	CAGAAAGGGG	TGGGGGGGAC	CACATCTGAG	CATTGTTTTC	4560
	CTCTTCTTAA	AATTAGGCAG	GAAATTCAGT	CTAGTTCTGT	TATCTGTTGA	TTTCCCATCA	4620
	CCTGACAGTA	ACTTTCTATG	CATAGGATTC	TGCCGCCAAA	TTTATATCAT	TAACATGTG	4680
	TGCCTTTTTG	CAAGACTTGT	AAITTTACTTA	TTATGTTTGA	ACTAAAATGA	TTGAATTTTA	4740
85	CAGTATTTCT	AAGAAATGAA	TTGTGGTATT	TTTTTCTGTA	TTGATTTTAA	CAGAAAAATT	4800
	CAATTTATAG	AGGTAATGAA	TTCCAAACTA	CAGAAAAATG	TTGTTTTTAG	TGTCAAATTT	4860
	TTAGCTGTAT	TTGTAGCAAT	TATCAGGTTT	GCTAGAAATA	TAACCTTTAA	TACAGTAGCC	4920
	TGTAAATAAA	ACACTCTTCC	ATATGATATT	CAACATTTTA	CAACTGCAGT	ATTACCTTAA	4980

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Seq ID NO: 182 Protein sequence:
 Protein Accession #: Bos sequence

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FKASKITFWH	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSPEEAV	KGKGLRALS	180
ILFEVGTENG	LDPKAIIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPFC	240
TDTVDWIVFK	DTVHSISBSQL	AVPCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
TGKEBIHEAV	CSSEFENVQA	DPENYTSLLV	TWERPRVVDY	TMIEKFAVLV	QQLDGEDQTK	360
HEFLTDGYQD	LGAILNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLPFE	420
LIGTEEIIKE	EEBEGDIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
RSPTRGSEFS	GKGVDPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPFHT	VEGTSASLND	540
GSKTVLRSPH	MNLGGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
TAQPDVGSGR	ESPLQTNYTE	IRVDESEKTT	KSFSAQPVMS	QGPSVTDLEM	PHYSTFAYFP	720
TEVTPHAFPT	SSRQDLVST	VNVVYSQTTO	PVYNAEASNS	SHESTRIGLAE	GLESEKKAVI	780
PLVIVSALTF	ICLVVLVGIL	IYWRKCFQTA	HFYLEDSTSP	RVISTPPTPI	FPISDDVGAI	840
PKHFPKHVA	DLHASSGTE	EPETLKEFYQ	EVQSCITVDLG	ITADSSNHDP	NKHKNRYINI	900
VAYDHSRVKL	AQLAEKDGKL	TDVINANYVD	GYNRPKAYIA	AQGPLKSTAE	DFWRMIWEHN	960
VEVIVMITNL	WEGRRKCDQ	WPDAGSEEEY	GNPLVTQKSV	QVLAYYTVRN	FTLRNTKIKK	1020
GSQKGRPSGR	VVTQYHYTQW	PDMGVPEYSL	PULTFVRKAA	YAKRHAQGVF	VVHCSAGVGR	1080
TGTIVLDSM	QLQIQHEGTV	NIFGFLKHIR	SQRNYLVQTE	EQYVFIHDTL	VEAILSKETE	1140
VLDSHIHAYV	NALLIPGPAG	KTKLEKQFQL	LSQSNIQQSD	YSAALKQCNR	EKNRTSIIIP	1200
VERSRVGISS	LSGGGTVDYIN	ASYIMGYYS	NEFIITQHPL	LHTIKDPWRM	IWDHNAQLVV	1260
MIPDQNMMAE	DEFYVWPNKD	EPINCESFKV	TLMAEHEKCL	SNEEKLIQD	FILEATQDDY	1320
VLEVRHFQCP	KWPNPDSFIS	KTFELISVIK	EEAANRDGFM	IVHDEHGGVT	AGTFCALITL	1380
MHQLKENSIV	DVYQVAKMIN	LMRPGVFADI	EQYQFLYKVI	LSLVSTRQEE	NPSTSLDSNG	1440
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Seq ID NO: 183 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 148-4494

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CAGCTCCTCT	TGTGTTCCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
CTTGTGAAAG	AGATTGGCTG	GTCTATACAC	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAG	300
AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
CAAGTAATGT	TGAATCTTAA	GAACCTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
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GTCAGCGGAG	GAGTTTCAGA	AATGGTGTIT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
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ACAGTTAGCA	TCTCTGAAGG	CCAGTTGGCT	GTTTCTTGTG	AAGTCTTCTT	AATGCAACAA	960
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	TACTTAGAGG ACAGTACATC CCCTAGAGTT ATATCCACAC CTCCCAACACC TATCTTTCCA 2640
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Seq ID NO: 184 Protein sequence:
Protein Accession #: EOS sequence

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60		ILFEVGTEN LDFKAIIDGV ESVSFRGKQA ALDPPILLNL LPNSTDKYYI YNGSLTSPPC 240
		TDVTDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVLMMDY LQNNFREQQY KFSRQVSSY 300
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Seq ID NO: 185 DNA sequence
Nucleic Acid Accession #: EOS sequence
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35	CAACTTCTGC	TATCCCATTC	ATCTCTGAGA	ACATATCCCA	AGGGTATATA	TTTTCTCCG	1980
	AAAACCCAGA	GACATAACCA	TATGATGTCC	TATACACAGA	ATCTGTCTAGA	AATGCTTCCG	2040
	AAGATTCAAC	TTCACTAGGT	TCAGAAGAAT	CACTAAGGAA	TCCTTCTATG	GAGGGAAATG	2100
	TGTGGTTTCC	TAGCTCTACA	GACATAACAG	CACAGCCCGA	TGTTGGATCA	GGCAGAGAGA	2160
40	GCCTTTCTCCA	GACTAATTAC	ACTGAGATAC	GTGTTGATGA	ATCTGAGAAG	ACAACCAAGT	2220
	CCTTTTCTGC	AGGCCCAAGT	ATGTCCACAG	GTCCCTCAGT	TACAGATCTG	GAAATGCCAC	2280
	ATTATTCTAC	CTTTGGCTAC	TTCCCAACTG	AGGTAACACC	TCATGCTTTT	ACCCCATCCT	2340
	CCAGACAACA	GGATTGTGTC	TCCACGGTCA	ACGTGGTATA	CTCGCAGACA	ACCCAACCGG	2400
	TATACAATGA	GAAGGCAAGT	ATACCCCTTG	TGATCGTGTC	AGCCCTGATC	TTTATCTGTC	2460
45	AATCCGAGAA	GAAGGCAAGT	ATACCCCTTG	TGATCGTGTC	AGCCCTGATC	TTTATCTGTC	2520
	TAGTGGTTCT	TGTGGGTATT	CTCATCTACT	GGAGGAAATG	CTTCCAGACT	GCACACTTTT	2580
	ACTTAGAGGA	CAGTACATCC	CCTAGAGTTA	TATCCACACC	TCCAACACCT	ATCTTTCCAA	2640
	TTTCAGATGA	TGTCCGAGCA	ATCCCAATAA	AGCACTTTCC	AAAGCATGTT	GCAGATTTAC	2700
	ATGCAAGTAG	TGGGTTTACT	GAAGAATTTG	AGCACTGAA	AGAGTTTAC	CAGGAAGTGC	2760
	AGAGCTGTAG	TGTTGACTTA	GGTATTACAG	CAGACAGCTC	CAACCAACCA	GACACCAAGC	2820
50	ACAAGAATCG	ATACATAAAT	ATCGTTGCCT	ATGATCATAG	CAGGGTTAAG	CTAGCACAGC	2880
	TTGCTGAAAA	GGATGGCAAA	CTGACTGATT	ATATCAATGC	CAATTATGTT	GATGGCTACA	2940
	ACAGACAAAA	AGCTTATATT	GCTGCCCAAG	GCCCCACTGA	ATCCACAGCT	GAAGATTTCT	3000
	GGAGAATGAT	ATGGGAACAT	AATGTGGAAG	TTATTGTAT	GATAACAAAC	CTCGTGGAGA	3060
	AAGGAAGGAG	AAAATGTGAT	CAGTACTGGC	CTGCCGATGG	GAGTGAGGAG	TACGGGAAGT	3120
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	TAAGAAACAC	AAAAATAAAA	AAGGGCTCCC	AGAAAGGAAG	ACCCAGTGA	CGTGTGGTCA	3240
	CACAGTATCA	CTACAGGACG	TGGCCTGACA	TGGGAGTACC	AGAGTACTCC	CTGCCAGTGC	3300
	TGACCTTTGT	GAGAAAGGCA	GCCTATGCCA	AGCGCCATGC	AGTGGGGCCT	GTGTGCTGCC	3360
	ACTGCAGTGC	TGGAGTTGGA	AGAACAGGCA	CATATATTGT	GCTAGACAGT	ATGTTGCAGC	3420
60	AGATTCAACA	CGAAGGAATC	GTCAACATAT	TTGGCTTCTT	AAAACACATC	CGTTTCAAAA	3480
	GAAATATTAT	GGTACAAACT	GAGGAGCAAT	ATGCTTTCAT	TCATGATACA	CTGGTTGAGG	3540
	CCATACTTAG	TAAAGAAACT	GAGGTGCTGG	ACAGTCATAT	TCATGCCCTT	GTTAATGCAC	3600
	TCCTCATTC	TGGACCAGCA	GGCAAAACAA	AGCTAGAGAA	ACAATTCAG	CTCCTGAGCC	3660
	AGTCAAAATAT	ACAGCAGAGT	GACTATTCTG	CAGCCCTAAA	GCAATGCAAC	AGGGAAAAAG	3720
65	ATCGAACTTC	TTCTATCATC	CCTGTGGAAA	GATCAAGGGT	TGGCATTTC	TCCTGAGTG	3780
	GAGAAGGCAC	AGACTACATC	AATGCCTCCT	ATATCATGGG	CTATTACCAG	AGCAATGAAT	3840
	TCATCATTAC	CCAGCACCCCT	CTCCTTCATA	CCATCAAGGA	TTTCTGGAGG	ATGATATGGG	3900
	ACCATAATGC	CCAATCTGGT	GTTATGATTC	CTGATGGCCA	AAACATGGCA	GAAGATGAAT	3960
	TTGTTTACTG	GCCAAATAAA	GATGAGCCCTA	TAAATTGTGA	GAGCTTTAAG	GTCACTCTTA	4020
70	TGGCTGAAGA	ACACAAATGT	CTATCTAATG	AGGAAAACCT	TATAATTGAG	GACTTTTATCT	4080
	TAGAAGCTAC	ACAGGATGAT	TATGTACTTG	AAGTGAGGCA	CTTTCAGTGT	CCTAAATGGC	4140
	CAAAATCCAGA	TAGCCCCATT	AGTAAAACTT	TTGAACTTAT	AAGTGTATATA	AAAGAAGAAG	4200
	CTGCCAATAG	GGATGGGCCCT	ATGATTGTTC	ATGATGAGCA	TGGAGGAGTG	ACGCCAGGAA	4260
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75	ACCAGGTAGC	CAAGATGATC	AATCTGATGA	GGCCAGGAGT	CTTGTCTGAC	ATTGAGCAGT	4380
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	CCACCTCTCT	GGACAGTAAT	GGTGACGAT	TGCTGATGG	AAATATAGCT	GAGAGCTTAG	4500
	AGTCTTTAGT	TTAAACAGAA	AAGGGGTGGG	GGGACTCACA	TCTGAGCATT	GTTTTCTCTT	4560
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	AATAAAACAC	TCTTCCATAT	GATATTCAAC	ATTTTACAAC	TGCAGTATTC	ACCTAAAGTA	4980
85	GAAATAATCT	GTACTTATT	GTAAATACCT	CCCTAGTGTG	TCCATGGACC	AAATTTATAT	5040
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	TTTAGTTTAA	TGACGTAGTT	CATTAGCTGG	TCTTACTCTA	CCAGTTTCTT	GACATTGTAT	5160

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5

Seq ID NO: 186 Protein sequence:
 Protein Accession #: EOS sequence

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15	SYTGKEEIEH	AVCSSEPENV	QADPENYTSI	LVTWERPRVV	YDTMIEKFAV	LYQQLDGEDQ	240
	TKHEFLTGGY	QDEGAILNNL	LPNMSYVLQI	VAICTNGLYG	KYSDQLIVDM	PTDNPELDF	300
	PELIGTEBII	KEBEEGKDIE	EGAIYNPGRD	SATNQIRKKE	PQISTTTHYN	RIGTKYNEAK	360
	TNRSPTRGSE	FSGKGDPVNT	SLNSTSQPV	KLATEKDIDL	TSQTVTELP	HTVEGTSASL	420
	NDGSKTVLRS	PHMNLSTGAE	SLNTVSITEY	EEESLLTSFK	LDTGAEDSSG	SSPATSAIPF	480
20	ISENISQGYI	FSSSENPETIT	YDVLIPESAR	NASEDSTSSG	SEESLKDPSM	EGNVNFPSSST	540
	DITAGPQVGS	GRESFLQNTY	TEIRVDESEK	TTKSFSAGPV	MSQGPSVTDL	EMPHYSTFAY	600
	PFTVTPHAF	TPSSRQQLDV	STVNVVYSQT	TQPVYNEASN	SSHESRIGLA	EGLESEKKAV	660
	IFLVIVSALT	FICLVVLVGI	LIYWRKCFQT	ARFYLEDSTS	PRVISTPPTP	IFPISDDVGA	720
	IPKHFPPKHV	ADLHASSGTA	EEFETLKEFY	QEVQSCVLDL	GITADSSNHP	DNKHKNRYIN	780
25	IVAYDHSRVK	LAQLAEKDGK	LTDYINANYV	DGYNRPKAYI	AAQGPLKSTA	EDFWRMIWEH	840
	NVEVIVMITN	LVEKGRKRC	QYWPADGSEB	YGNFLVTQKS	VQVLAAYTVR	NFTLRNTKIK	900
	KGSQKGRPSG	LRVTQYHYTQ	WPDMDGVPEYS	LPVLTFFVRKA	AYAKRHAVGP	VVVHCSAGVG	960
	RTGTYIVLDS	MLQIQHEGT	VNIFGFLKHI	RSQRNYLVQT	EEQYVFIHDT	LVEAILSKET	1020
	EVLDSHIAHY	VNALLIPGA	GKTKLEKQFO	LLSQSNIQSS	DYSAALKQCN	REKNRTSSII	1080
30	PVERSRVIGS	SLSGEGTDYI	NASYIMGYQ	SNEFIITQHP	LLHTIKDFWR	MIWDHNAQLV	1140
	VMIIDGQNMA	EDFVYWPNK	DEPINCESFK	VTLMAEHKK	LSNEEKLIQ	DFILEATQDD	1200
	YVLEVRHFQC	PKWPNPDSPI	SKTFELISVI	KEEAANRDGP	MIVDEHGGV	TAGTFCALTT	1260
	LMHQLKEKNS	VDVYQVAKMI	NLMRPGVFAD	IEQYQFLYKV	ILSLVSTRQE	ENPSTSLDSN	1320
	GAALPDGNIA	ESLESILV					

35

Seq ID NO: 187 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 148-4632

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	CGGCGAGGGG	CCGCAGACCG	CTGGGAAATG	CGAATCCTAA	AACGTTTCCT	CGCTTGCAAT	180
45	CAGCTCCTCT	GTGTTTCCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTGAAG	AGATTGGCTG	GTCCCTATCA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCAAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTTGGA	420
	AACACATTCA	TTGCATAACAC	GTGGAAAAACA	ATCTCACTAA	TGACTACCGT		480
	GTACAGCGAG	GAGTTTCAGA	AATGGTGTIT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
50	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTCCTA	GTCTTGAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTGT	720
	GATTTCAAG	CGATTATTTGA	TGGAGTCGAA	AGTGTTAGTC	GTCTTGAGGA	CGAGGCTTGT	780
	TTAGATCCAT	TCATACTGTT	GAACTTCTG	CCAAACTCAA	CTGACAGATA	TTACATTTC	840
55	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTCTTTTGTG	AAGTCTTCTAC	AATGCAACAA	960
	TCTGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGACA	ACAGTACAG	1020
	TCTCTAGAC	AGGTGTTTTC	CTCATACACT	GGAAAAGGAA	AGATTCTATG	AGCAGTTTGT	1080
	AGTTCAAGAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAAAT	ATACCAAGCT	TCTTGTATCA	1140
60	TGGGAAAGAC	CTCAGTCTGT	TTATGATACC	ATGATTGAGA	AGTTTGCACT	TTGTATCCAG	1200
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	GGTGCTATTC	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCATAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCCAGAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACTG	AAGAAATAAT	CAAGGAGGAG	1440
65	GAAGAGGGAA	AGACATTGGA	AGAAAGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
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	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACAAA	GAGGAAGTGA	ATTCTCTGGA	1620
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	ACAGAAAAAG	ATATTTCTTT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
70	GAAGGTACTT	CAGCTTCTTT	AAATGATGGC	TCTAAAACTG	TTCTTAGATC	TCCCATATG	1800
	AACCTGTGCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
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75	GAAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACAGG	AATCTGCTAG	AAATGCTTCC	2040
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	AGCTTCTCTC	AGACTAATTA	CATCTGAGTA	CGTGTGATG	AATCTGAGAA	GACAACCAAG	2220
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80	TCCAGACAAC	AGGATTGTGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAG	AACCCCAACC	2400
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	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTATCTGT	2520
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	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTC	3000
5	TGGAGAAATGA	TATGGGAACA	TAATGTGGAA	GTTATTGTCA	TGATAACAAA	CCTCGTGGAG	3060
	AAAGGAAGGA	AAAAATGTGA	TCAGTACTGG	CCTGCCGATG	GGAGTGAGGA	GTACGGGAAC	3120
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20	GAAGGCACAG	ACTACATCAA	TGCTCTCTAT	ATCATGGGCT	ATTACCAGAG	CAATGAATTC	3960
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25	GAAGCTACAC	AGGATGATTA	TGTACTTGAA	GTGAGGCAC	TTCAGTGTCC	TAAATGGCCA	4260
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Seq ID NO: 188 Protein sequence:
Protein Accession #: EOS sequence

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	FKASKITFFHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSFEEAV	KGKGLRLALS	180
55	ILFVEVGTEN	LDPKATIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVNDVIFK	DTVSISESQL	AVFCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIEHAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVDY	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLLN	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLPPE	420
60	LIGTEBIIKE	EEEGKDIEEG	AIVNPGRDSA	TNQRKKEPK	ISTTTHYNR	GTKYNEAKTN	480
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65	TEVTPHAFPT	SSRQQLVST	VNVVYSQTTQ	PVYNEAGNS	HESRIGLAEG	LESEKKAVIP	780
	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	FYLEDDSTSP	VISTPPTPIF	PISDDVGAIP	840
	IKHFFKHVAD	LHASSGFTTE	FETLKEFYQE	VQSCVTDLGI	TADSSNHPDN	RHKRYINIV	900
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	EVIVIMTNLV	EKGRRKCDQY	WPADGSEYEG	NFLVTQKSVQ	VLAYYTVRNF	TLRNTKIKKG	1020
70	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFRKAAY	AKRHAUGPVV	VHCAGVGR	1080
	GTIYIVLDSML	QQIQHEGTVN	IFGFLKHIRS	QRNYLVQTEE	QYVFIHDTLV	EAILSKBTEV	1140
	LDSDIHAYVN	ALLIPGPAGK	TKLEKQFQGL	TLSPRLRCRG	TISAHCNLPL	PGLTDPPTSA	1200
	SRVAGTILLS	QSNIIQSDYS	AALKQCNREK	NRTSSIIPE	RSRVGISSLS	GEGTDYINAS	1260
	YIMGYYSQNE	FIITQHPLH	TIKDFWRMIW	DHNAQLVVM	PDGQNMAGE	FVYWFNKDEP	1320
75	INCESPKVTL	MAEHEKCLSN	EELIIQDFI	LEATODDYVL	EVRRHFQCPKW	PNPDSPIST	1380
	FELISVIKEE	AANRDGPMIV	HDEHGGVTAG	TFCALTTLMH	QLEKENSVDV	YQVAKMINLM	1440
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Seq ID NO: 189 DNA sequence
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	CGTGTAACAC	CACACTATTAT	CATTGATGCA	TATATAAACC	CATTTTATTT	TGCTATTAT	180

5 TTCAGAGGAA GCGCCTCTGA TTTGTTTCTT TTTTCCCTTT TTGCTCTTTC TGGCTGTGTG 240
 GTTTGGAGAA AGCAGAGTTG GAGTAGCCGG TTGCTAAATA AGTCCCAGAG GCGAGCGGAG 300
 ACAGATCAGC GGAGACTGGT TCAGCAGTGG AGCGTCGCGG TGTTCCCTGCT GAGCTACGGG 360
 GTGCCCTCCT GCGGCGGCTC GGTGGAGGGT CTCAGCGCGC GCCTCAAAAG AGCTGTGTCT 420
 GAACATCAGC TCCTCCATGA CAAGGGGAAG TCCATCCAG ATTTACGGCG ACGATTCTTC 480
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 10 AAGACACCTG GGAAGAAAAA GAAAGGCAAG CCCGGGAAAC GCAAGGAGCA GGAAAAGAAA 720
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 25 GGTTCCTCTC ATGTATCTTT TTGTTCAATG GCAAGATGAA ATAATTTTTC TAGGGTAATG 1560
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Seq ID NO: 190 Protein sequence:
Protein Accession #: NP_002811

30 1 11 21 31 41 51
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 HHLLIAEIHIA EIRATSEVSP NSKPSPTNKN HPVRFGSDDE GRYLTQETNK VETYKEQPLK 120
 35 TPGKKKKKGP GKRKEQEKKK RRTSAWLDS GVTGSGLEGD HLSDTSTTSL ELDSR

Seq ID NO: 191 DNA sequence
Nucleic Acid Accession #: XM_059328
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 60 CCCCAGCTTG CCCAGGATGG CGTGACGCTT TGCCTCCCTG ACACCTTGA CTCCAAGAGG 960
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Seq ID NO: 192 Protein sequence:
Protein Accession #: XP_059328

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 75 GLHANLSEGR PVGPARRGAS SLLGPEGFFL GKMGPREAVA AGVDLPQVR EELEAQLSCF 120
 RELLGRAPTH ADGHQHVHVL PGVCQVFAEA LQAYGVRPFR LFLERGVGCG TWLEAPARAF 180
 ACAVERDARA AVGPFSRHGL RWTDAFVGLS TCGRHMSAHR VSGALARVLE GTLAGHTLTA 240
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Seq ID NO: 193 DNA sequence
Nucleic Acid Accession #: NM_005688.1
Coding sequence: 126..4439

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	GGAGAACTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
5	TCTCTCTTGA	TGCCTTCCATG	CATTCTCAGC	TCAGAAATCCT	GGATGAGGAG	CATCCCAAGG	360
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	ACCCAGTGGA	CAATGCTGGG	CTTTTTTCCT	GTATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
	CCCGTGTGGC	CCACAAGAAG	GGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
10	AAGTTGGGCC	AGACGCTGCT	TCCCTGCGAA	GGTTGTGTG	GATCTTCTGC	CGCACCAGGC	660
	TCATCCTGTC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAGCCT	720
	TCATGGTGAA	ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CAGTACAGCT	780
	TGTTGTAGT	GCTGGGCTTC	CTCCTGACCG	AAATCGTGG	GTCTTGGTGG	CTTGCACTGA	840
	CTTGGGCATT	GAAATTACGA	ACCGGTGTCC	GCTTGGCGGG	GGCCATCCTA	ACCATGGCAT	900
15	TTAAGAAGAT	GCCTTAAGTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
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	GCTTCTCTGG	ATCAGCTGTT	TTTATCTCT	TTTACCCAGC	AATGATGTTT	GCATCACGGC	1140
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30	COGAAGAGGA	GAAAGAGGAG	CACATCCACC	TGGGCCACCT	CGCCTTACAG	AGGACACTGC	1860
	ACAGCATCGA	TCTGAGATTC	CAAGAGGGTA	AACTGGTTGG	AATCTGCGGC	AGTGTGGGAA	1920
	GTGGAAAAAC	CTCTCTCAT	TAGGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGGAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCCTC	AATGCTACTC	2040
	TGAGAGACAA	CATCTGTTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAAC	TCTGTGCTGA	2100
35	ACAGCTGCTG	CCTGAGGCTC	GACCTGGCCA	TTCTTCCCAG	CAGCGACCTG	ACGGATGTTG	2160
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	TGTATAGTGA	CAGGAGCATC	TACATCCTGG	ACGACCCCTC	CAGTGCCTTA	GATGCCCATG	2280
	TGGGCAACCA	CATCTTCAAT	AGTGCTATCC	GGAAACATCT	CAAGTCCAAG	ACAGTTCTGT	2340
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40	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AACTGATGAA	TTTAAATGGT	GACTATGCTA	2460
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45	TCTGTGTTAT	TATGGCCCTT	TTCATGCTGA	ATGTAGGCAG	CACCGCCTTC	AGCACCTGGT	2760
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	CCCTCTCCAT	GGCAGTCAAG	CTGATCTCTG	AAGCCATTCC	AGGAGTTGTC	TTTGTCAAGG	2940
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50	CTATGAAGTT	TTTTGACACG	ACCCCCACAG	GGAGGATTCT	CAACAGGTTT	TCCAAAGACA	3060
	TGGATGAAGT	TGACGTGGCG	CTGCCGTTC	AGGCCGAGAT	GTTTCATCCAG	AACGTTATCC	3120
	TGGTGTCTCT	CTGTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCTCT	GTGGCAGTGG	3180
	GGCCCCCTGT	CATCTCTTTT	TCAGTCTGTC	ACATTGTCTC	CAGGGTCTCT	ATTGGGGAGC	3240
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55	AGGGCCCTTG	CACCATCCAC	GCCTACAATA	AAGGGCAGGA	GTTTCTGTC	AGATACCAGG	3360
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	CTGTGCGGCT	GGACCTCATC	AGCATCGCCC	TCATCACACC	CACGGGGCTG	ATGATCGTTC	3480
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	TAACGGGGCT	GTTCCAGTTT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTCACTC	3600
60	CGGTGGAGAG	GATCAATCAC	TACATTAAGA	CTCTGTCTCT	GGAAAGCACT	GCCAGAATTA	3660
	AGAACAAGGC	TCCCTCCCCC	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	GAGAAGCAG	3720
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65	GTGATATTGG	CCTTGGCGAC	CTCCGAAGCA	AACTCTCTAT	CATTCTCTCA	GAGCCGGTGC	3960
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70	CCATGGACAC	AGAGACAGAC	TTATTGATTC	AAGAGACCAT	CCGAGAAGCA	TTTGACAGCT	4260
	TGACCATGCT	GACCATTGCC	CATCGCCTGC	ACACGGTCTC	AGGCTCCGAT	AGGATTATGG	4320
	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GGTCTTCTGT	TCCAACGACA	4380
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75	CCCTCATCG	CGTCTCTCTA	CCGAAACCTT	GCCTTTCTCG	ATTTTATCTT	TGCGACAGCA	4560
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	ATTCCATATT	CATGTAAACA	AAATTTAGTT	TTTGTCTCTA	ATTGCACCTC	AAAAGGTTCA	4680
	GGGAACCGTT	ATTATAAATTG	TATCAGAGGC	CTATAATGAA	GCTTTATACG	TGTAGCTATA	4740
	TCTATATATA	ATTCTGTACA	TAGCCTATAT	TTACAGTGAA	AATGTAAGCT	GTTTATTTTA	4800
80	TATTAAAAA	AGCACTGTGC	TAATAACAGT	GCATATTCTC	TTCTATCATT	TTGTACAGT	4860
	TTGCTGTACT	AGAGATCTGG	TTTGCTTATT	AGACTGTAGG	AAGAGTAGCA	TTTCACTTCT	4920
	CTCTAGCTGG	TGGTTTCAGG	GTGCCAGGTT	TTCTGGGTGT	CCAAAGGAAG	ACGTGTGGCA	4980
	ATAGTGGGCC	CTCCGACAGC	CCCCCTGTCC	GCCTCCCCAC	AGCCGCTCCA	GGGGTGGCTG	5040
	GAGACGGGTG	GGCCCTGGGA	GACCATGCAG	AGCGCCGTGA	GTTCTCAGGG	CTCCTGCCTT	5100
	CTGTCTCTGT	GTCACTTACT	GTTTCTGTCA	GGAGAGCAGC	GGGGCGAAGC	CCAGGCCCTC	5160
85	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
	TTTCTGCTCT	CTCTCTTTTT	GCTGTTGTTT	CTAAACAAGA	ATCAGTCTAT	CCACAGAGAG	5280
	TCCACTGCTC	TCAGGTTCTT	ATGGCTGGCC	ACTGCACAGA	GCTCTCCAGC	TCCAAGACCT	5340

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Seq ID NO: 194 Protein sequence:
 Protein Accession #: NP_005679.1

1 11 21 31 41 51
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 VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEEELNEV GPDAASLRV VWIFCRTRLI 180
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 ALNYRTGVRL RGAILTMAPK KILKLNKE KSLGELINIC SNGQRMFEA AAVGSLLAGG 300
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Seq ID NO: 195 DNA sequence
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 TTTGTATTT TAGTAGAGAT GGGGTTTCAC CATGTTGGCC AGGCAGATCT CAAACTCCTG 2340

ACCTCGTGAT GCACCCACCT CGGCCTCCCA AAGTGCTGGG ATTACATGCG TGAGCCACTG 2400
 CGCCCTGCCT GTTTGTAGTA ATTTTATAGC ACCAAATCTC CCTCATCTTC TAGTGCCATT 2460
 CTCCTCTCTG TTCAGGTAAA TGTCACACTG TGCCCGAAT GGATGACCAG GAACCTTAAA 2520
 GAGTGGCTGA AAAGATTGCA GAGTTATCAT AATAAATTGC TAACCTGCGT

5

Seq ID NO: 196 Protein sequence:
 Protein Accession #: NP_006461

10 1 11 21 31 41 51
 MAELDLMAPG PLPRATAQPP APLSPDSGSP SPDSGSSAPV EEDVGSSEK LGRETEEQDS 60
 DSAEQDQDPAG EGKEVLCDFC LDDTRRVKAV KSCCLTCMVNY CEEHLQPHQV NIKLQSHLLT 120
 EPVKDHNWRY CPAHHSPLSA FCCPDQQCIC QDCQEHSGH TIVSLDAARR DKEALQCTQ 180
 15 LDLEKRLKLN ENAISRLQAN QKSVLVSVE VKAVAEMQFG ELLAAVRKAQ ANVMLFLEEK 240
 EQAALSQANG IKAHLEYRSA EMKSKQELE RMAAISNTVQ FLEEYCKFKN TEDITFPSVY 300
 VGLKDKLSGI RKVITESTVH LIQLLENYKK KLQEPSKEEE YDIRTQVS AV VQRKYWTSKP 360
 EPSTREQFLQ YAYDITDPD TAHKYLRLOE ENRKVTINTP WEHPYPDLPS RFLHWRQVLS 420
 20 QQSLYLHRY YVEIIFGAGT YVGLTCKGID RKGEERNSCI SGNNFWSLQ WNGKEFTAWY 480
 SDMETPLKAG PFRLGLVYID FPGGILSFYG VEYDTMTLVH KFAKCFSEPV YAAFWSLKE 540
 NAIRIVDLGE BPEKPAPSLG VTAP

Seq ID NO: 197 DNA sequence
 Nucleic Acid Accession #: NM_004316
 Coding sequence: 433-1149

25 1 11 21 31 41 51
 CCGGAGACCC GGCAGAGAG AGCGCAGCCT TAGTAGAGA GGAACGCGAG ACGCGGCAGA 60
 GCGCGTTCCG CACTGACTTT TGCTGCTGCT TCTGCTTTT TTTTCTTAG AAACAAGAAG 120
 GCGCCAGCGG CAGCTCACA CGCGAGCGCC ACGCGAGGCT CCCGAAGCCA ACCCGCAAG 180
 GGAGGAGGGG AGGGAGGAGG AGCGCGCGTG CAGGGAGGAG AAAAAGCATT TTCACCTTTT 240
 TTGCTCCAC TCTAAGAAGT CTCCCGGGGA TTTGTATAT ATTTTAAAC TTCCGTCAGG 300
 GCTCCCGCTT CATATTTCTT TTTCTTTCCC TCTCTGTTCC TGCACCCAAG TTCTCTCTGT 360
 35 GTCCCCCTCG CGGGCCCGCG ACCTCGCGTC CCGGATCGCT CTGATTCGCG GACTCCTTGG 420
 CGCGCGCTGC GCATGGAAG CTCTGCCAAG ATGGAGAGCG GCGGCGCGG CCAGCAGCCC 480
 CAGCCGCGAG CCCAGCAGCC CTTCCTGCGG CCCGCGCCT GTTCTTTGC CACGCGCGCA 540
 GCGCGCGCGG CCGCAGCGCG CGCAGCGGCA GCGCAGAGCG CGCAGCAGCA GCAGCAGCAG 600
 CAGCAGCAGC AGCAGCAGCA GCAGCGCGCG CAGCTGAGAC CGCGCGCCGA CGGCCAGCCC 660
 40 TCAGGGGCGG GTCAACAAGT AGCGCCCAAG CAAGTCAAGC GACAGCGCTC GTCTTCGCCC 720
 GAACGTGATC GCTGCAACG CCGGCTCAAC TTCAGCGGCT TTGGCTACAG CCGTGGCAG 780
 CAGCAGCGCG CCGCGTGGC GCGCGCAAC GAGCGCGAGC GCAACCGCT CAAGTTGGTC 840
 AACCTGGGCT TTGCGACCTT TCGGGAGCAC GTCCCCAAG CCGCGGCCAA CAAGAAGATG 900
 AGTAAGGTGG AGACACTGCG CTCGGCGGTC GAGTACATCC GCGCGCTGCA GCAGCTGCTG 960
 45 GACGAGCATG ACGCGGTGAG CGCGCGCTTC CAGGCAGCGC TCCTGTGCGC CACCATCTCC 1020
 CCAACTACT CCAACGACTT GAACTCCATG GCGGCTGCG CGGTCTCATC CTAAGTCTCG 1080
 GACGAGGCT CTTACGACCC GCTCAGCCCC GAGGAGCAGG AGCTTCTCGA CTTACCAAC 1140
 TGGTCTGAG GGGCTCGGCC TGGTCAGGCC CTGGTGCAG TGGACTTGG AAGCAGGGTG 1200
 50 ATCGCACAA CTGCATCTT AGTGCTTTCT TGTCAGTGGC GTTGGGAGGG GGAGAAAAGG 1260
 AAAAGAAAA AAAAGAGAA GAAGAAGAA AGAGAAGAG AAAAAACGA AAACAGTCAA 1320
 GCAACCCCT CCGCAACTA CGAGGAGCAT CTGAGAGAC ATGGCTTCA GAAACCGGGA 1380
 AGCGCTCAGA ACAGTATCTT TGCACTCAA TCAATCACGG AGATATGAG AGCAACTGGG 1440
 ACCTGAGTCA ATGCGCAAAA TGCACTTGT GTGCAAAAG AGTGGGCTCC TGGCAGAAAG 1500
 55 GAGCAGCACA CGCGTTATAG TAACCTCCAT CACCTCTAAC ACGCACAGCT GAAAGTCTT 1560
 GCTCGGCTCC CTTACCTCC CCGCCCTTC TTAGAGTGCA GTTCTTAGCC CTGTAGAAAC 1620
 GAGTTGGTGT CTTTC

Seq ID NO: 198 Protein sequence:
 Protein Accession #: NP_004307

60 1 11 21 31 41 51
 MESSAKMESG GAGQQPQPP QPPFLPPAAC FPATAAAAA AAAAAAQSA QQQQQQQQQ 60
 QQQQAPQLRP AADQPPSGGG HKSAPKQVKR QRSSPELMR CKRRLNFSGF GYSLPQQQPA 120
 AVARRNERER NRVLVNLGF ATLREHVPNG AANKKMSKVE TLRSAVEYIR ALQQLLDEHD 180
 AVSAAFQAGV LSPTISPNYS NDLNSMAGSP VSSYSSDEGS YDPLSPEEQE LLDFTNWF

Seq ID NO: 199 DNA sequence
 Nucleic Acid Accession #: NM_007015
 Coding sequence: 1-1005

70 1 11 21 31 41 51
 75 ATGACAGAGA ACTCCGACAA AGTTCCTCATT GCCCTGGTGG GACCTGATGA CGTGGGAATTC 60
 TGCAGCCCCC CGCGTACGCG TACGCTGACG GTGAAGCCCT CCAGCCCCCG CGGGCTGCTC 120
 AAGGTGGGAG CCGTGGTCTT CATTTGCGGA GCTGTGCTGC TGCTCTTTGG GGCCATCGGG 180
 GCGTCTTACT TCTGGAGAGG GAGCGACAGT CACATTACA ATGTCCATTA CACCATGAGT 240
 ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTGGAGAGCC 300
 80 TTTAAATGGA GAGTGAGAG TGAAGAAGCA ATTGCAGTTA ATGATTCCCA GAATGGCATC 360
 ACAGGAATTC GTTTTGTGG AGGAGAGAAG TGCTACATTA AAGCGCAAGT GAAGGCTCGT 420
 ATTCTGAGG TGGCGCGCGT GACCAACAG AGCATCTCCT CCAACTGGA AGGCAAGATC 480
 ATGCCAGTCA AATATGAGA AAATCTCTT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540
 85 GACCAAGCT TCTTGAAGTC TAAGGTGTTA GAACTCTCG GTGACCTTCC TATTTTCTGG 600
 CTTAAACCAA CCTATCCAAA AGAAATCCAG AGGGAAGAA GAGAAGTGGT AAGAAAAATT 660
 GTTCAACTA CCACAAAAG ACCACACAGT GGACCAAGG GCAACCCAGG CGCTGGAAGA 720
 CTGAATAATG AAACCAGACC CAGTGTCAA GAGGACTCAC AAGCCTTCAA TCCTGATAAT 780

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CCTTATCATC AGCAGGAAGG GGAAGCATG ACATTGACC CTAGACTGGA TCACGAAGGA 840
ATCTGTTGTA TAGAATGTAG GCGGAGCTAC ACCCACTGCC AGAAGATCTG TGAACCCCTG 900
GGGGGCTATT ACCCATGGCC TTATAATTAT CAAGGCTGCC GTTCGGCTCG CAGAGTCATC 960
ATGCCATGTA GCTGGTGGGT GGCCCGTATC TTGGGCATGG TGTGAATCA CTTCATATAT 1020
CACGTGCTGT AAAATAAGAA CTAGCTGAAG AGACAACCAA AGAAGCATT AAGCAGGTTG 1080
ATGCTGATGG GACCATAAAA TATTTTACA CGCAGCCTGA GCGGTTATTC TTGACACTCT 1140
TAACAGAAAT TTTTAAATCG TTTTCCAGAA CTTTAGTATA TGCAAATGCA CTGAAAGGGT 1200
AGTTCAAGTC TAAATGCCA TAACCCCGTT ATTTGTTATT TTTTATTGCG ATTGATTGCG 1260
CATAAGTCTT CCCTTGCTTG CATCTTCCAA AGCTATTTCG AAATAAACAC GAAATTTTAC 1320
AGTTTGCC
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Seq ID NO: 200 Protein sequence:
Protein Accession #: NP_008946

1 11 21 31 41 51
MTENS DKVPI ALVGPDDVEF CSPPAYATLT VKPSSPARLL KVGAVVLISG AVLLLFGAIG 60
AFYFWKSGDS HIYNVHYTMS INGKLQDGS EIDAGNNLET PKMGSGAEEA IAVNDFQNGI 120
TGIRFAGGEK CYIKAQVKAR IPEVGAVTQK SISKLESGKI MPVKYEENSL IWVAVDQPVK 180
DNSPLSSKVL ELCGDLPIFW LKPTYPKEIQ RERREVVRI VPTTTKRPHS GFRSNFGAGR 240
LNNETRPVQ EDSQAFNPDN PYHQEGESM TFDPRLDHEG ICCIECRSSY THCQKICEPL 300
GGYYFWPYN YQGCRSACRVI MPCSMWVARI LGMV

Seq ID NO: 201 DNA sequence
Nucleic Acid Accession #: NM_000728.2
Coding sequence: 112..495

1 11 21 31 41 51
GTAATAAGAG CGGGGTCTCC GCGGGGAAGG CGCCCAAGC AGGTGTGGTG TTCATCCCGG 60
GTCGACCGGC CGCTCGCGCT GCCCTGAAAC TCTAGTCGCC AGAGAGGCGG CATGGGTTTC 120
CGGAAGTTCT CCCCTTCTCT GGCTCTCAGT ATCTTGGTCC TGTACCAGGC GGGCAGCCTC 180
CAGGGCGGCG CATTGAGTTC TGCCCTGGAG AGCAGCCAGC ACCCGGCCAC ACTCAGTAAA 240
GAGGACGCGC GCCCTCTGCT GGCTGCACTG GTGCAGGACT ATGTGCAGAT GAAGGCCAGT 300
GAGCTGAAGC AGGAGCAGGA GACACAGGGC TCCAGCTCCG CTGCCAGAA GAGAGCCTGC 360
AACACTGCCA CCTGTGTGAC TCATCGGCTG GCAGGCTTGC TGAGCAGATC AGGGGGCATG 420
GTGAAGAGCA ACTTCGTGCC CACCAATGTG GGTTCCAAAG CCTTTGGCAG GCGCCGAGG 480
GACCTTCAAG CCTGAGCAGA TGAATGACTC CAGGAAGAAG GTGTGTCTTA AATCCAATGA 540
CATATCTTAA TAAGAGATTC ACTCAGAAGA CACATGTGGA GAAGGTGACA TGACAGAGGC 600
AAGGAGGCAC AAGCCAAGGA AGTCTGTGTC TACCAGAAGC CAGAATCACA GAACAGTCTC 660
TGGAAGAAGA GCAGCCCTGC TGACACCTAG AGTTTGACTC TCCAGCTTCC AGAAGTGTGA 720
GAGAATAATT TCTGTGTGTT TAAGCCACAA AGTTTGTGGT AATTGTGTTAT GACAGCCCTA 780
GGAAACTAAT ACAATACATT TTCAATTTATT TTGGGTAATG GCCTTGGAGT GGGATTGCTG 840
GGTTATTTGG AAAGTGTGTA TTTAACTCTG TAAGAAACTG CCAAACTATT TTCTGAAAGT 900
ACTGTACCACT TCGCCTTCT TGCCAGCCAC ATATGAGAGC TCTAGTATT CCACAAATAG 960
GTATGTAGCA GTATCTCATT GCTGTTTAA TTTGTATTTC CCAATGACT AATGACGTTG 1020
AGCATCTATT TTACCATATG TTTATCACCT TTATTGAAGG GTCGTGTTAA ATCTTCTGCT 1080
AAATTTTGTG TGGCTTGCTT GCCTTATTAG TGTGAGTTT TTAGAGCTCT TTATATGTTG 1140
TGATGTCAAG ATTGTCTTCA GATATATAGT TTGGAACCTT CCTTCCCTCG AATCTGCGGA 1200
TTGCTTTTTC ATTTTCTTAG CAGTGTCTCT CACAGAGAAA AAGTTGTAAT TTGAATAAGA 1260
TCCAATTCAT CTTTTTTTTT CTTTTATGTA TTGTGCTTTT AGTTCATGTC TAAGAACTCT 1320
TTGCCTAATC AAGGTCCCAA GGTCAACAATA ACCTTATTCT ATACTTTCTT GTAAAAGTTT 1380
TATAGTTTAA TATTTTATAT GTAGATTAGT GATCTATTTT GAGTTAATTT TTGTATAAGG 1440
TGAGAGGTGT AGGTGAAAT TCATACCTGT GAATATAGAT ACCCAATGT TTCAAGTCCA 1500
TTTGTAAATA AGACTGTAT TTCAACATTT AATTGCCCCC GCACCTTTGT CAAAAGCAA 1560
CTGATCATAT TTGTGTGGGT ATATTTCTGG GTTCTCAATT CTGTCTCATT GATTGATTTG 1620
ACCATTTCTT TGCCAATGTC ATACTGCCTT GATTAGTGA GTGTAAAGT GAATCTCAAA 1680
ACCAGATAAT GTGGGTCTAC CAACATTTGT CATTCTTGT CAAAAGATT TTAGCTACAT 1740
CTAAATATTT TTCTACATCT TTTATACATT TTAGAATCAG TGTGTTACTA TCTACAAAAT 1800
TTCTGATGAG ATTTTAAATG GGATGTGTTT AAATCAGTGG GTTAATTTTG GGAGAATTAG 1860
CATATTAATA ATATTAAGTC GTTCAATTC TGAACACAAT ACATGTTTTT ACTTATTTAG 1920
GTTTTCTCTG TTTTTTTTTT TTTAACAGTG TTCTCAGTTT TCAACAGAAA TATTCTACAC 1980
ATATCTTGTT AGATTTTAA CTATTTTATT TTTTGGTGCT AATGTAAATG GTACTTAAAC 2040
ATTTTGTGTT TTAATGTTC ATTGCTAGTA GATAGAAATA CAATATTTAA AATATTAGGA 2100
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 202 Protein sequence:
Protein Accession #: NP_000719.1

1 11 21 31 41 51
MGPRKFPFPL ALSILVLVQA GSLQAAPFRS ALESSPDPAT LSKEDARLLL AALVQDYVQM 60
KASELKQEQE TQSSSSAAQK RACNTATCVT HRLAGLLSRG GGMVKSNEVP TNVGSKAFGR 120
RRRDLQA

Seq ID NO: 203 DNA sequence
Nucleic Acid Accession #: NM_001741
Coding sequence: 71..496

1 11 21 31 41 51
CTCTGGCTGG ACGCCGCGCC CGCCGCTGCC ACCGCTCTG ATCCAAGCCA CCTCCCGCCA 60
GAGAGGTGTC ATGGGCTTCC AAAAGTTCTC CCCCTTCTG GCTCTCAGCA TCTTGGTCTC 120
GTTGCAGGCA GGCAGCCTCC ATGCAGCACC ATTCAGGTCT GCCCTGGAGA GCAGCCAGC 180
AGACCCGGCC ACCTCAGTG AGGACGAAGC GCGCTCTCTG CTGGCTGCAC TGGTGCAGGA 240
CTATGTGCAG ATGAAGGCCA GTGAGCTGGA GCAGGAGCAA GAGAGAGAGG GCTCCAGCCT 300

5 GGACAGCCCC AGATCTAAGC GGTGCGGTAA TCTGAGTACT TGCAATGCTGG GCACATACAC 360
 GCAGGACTTC AACAGTTTC ACACGTTCCC CCAAAGTCA ATTGGGTTG GAGCAGCTGG 420
 AAAGAAAAGC GATATGTCCA GCGACTTGGG GAGAGACCAT CGCCCTCATG TTAGCATGTC 480
 CCAGAAATGCC AACTAACTC CTCCCTTCC TTCTTAATTT CCCTTCTTGC ATCCTTCCTA 540
 TAACCTTGATG CATGTGGTTT GGTTCCTCTC TGGTGGCTCT TTGGGGTGGT ATTGGTGGCT 600
 TTCCTTGTGG CAGAGGATGT CTCAAACTTC AGATGGGAGG AAAGAGAGCA GGAATCACAG 660
 GTTGAAGAG AATCACCTGG GAAAATACCA GAAAATGAGG GCCGCTTTGA GTCCCCCAGA 720
 GATGTCATCA GAGCTCCTCT GTCTGCTTC TGAATGTGCT GATCATTGA GGAATAAAAT 780
 TATTTTCCC C

Seq ID NO: 204 Protein sequence:
Protein Accession #: NP_001732

15 1 11 21 31 41 51
 MGFKQFSPFL ALSILVLLQA GSLHAAPFRS ALESSPADFA TLSEDEARLL LAALVQDYVO 60
 MKASELEQEQ EREGSSLDSP RSKRCGNLST CMLGTYTQDF NKFHTFPQTA IGVGAPGKKR 120
 DMSSDLERDH RPHVSMQNA N

Seq ID NO: 205 DNA sequence
Nucleic Acid Accession #: NM_005361
Coding sequence: 1-945

25 1 11 21 31 41 51
 ATGCCTCTTG AGCAGAGGAG TCAGCACTGC AAGCCTGAAG AAGGCCTGA GGCCCGAGGA 60
 GAGGCCCTGG GCCTGGTGGG TGCGCAGGCT CCTGCTACTG AGGAGCAGCA GACCGCTTCT 120
 TCCTCTTCTA CTCTAGTGGG AGTTACCTTG GGGGAGGTGC CTGCTGCCGA CTCACCGAGT 180
 30 CCTCCGCCCA GTCTCTCAGG AGCTCCAGC TTCTCGACTA CCATCAACTA CACTCTTTGG 240
 AGACAATCCG ATGAGGGCTC CAGCAACCAA GAAGAGGAGG GGCCAAGAA GTTTCCCGAC 300
 CTGGAGTCCG AGTTCCAAGC AGCAATCAGT AGGAAGATGG TTGAGTTGGT TCATTTTCTG 360
 CTCTCTCAAG ATCAGGCCAG GGAGCCGCTC ACAAAGGCAG AAATGTCTGA GAGTGTCTCT 420
 AGAAATTGCC AGGACTTCTT TCCTCGTATC TTCAGCAAG CCTCCGAGTA CTTCAGCTGT 480
 35 GTCTTTGGCA TCGAGGTGGT GGAAGTGGTC CCCATCAGCC ACTTGATACAT CCTTGTCAAC 540
 TGCTTGGGCC TCTCTACGA TGGCTGCTG GCGACAATC AGGTCAATGCC CAGACAGGCG 600
 CTCTGATAAA TCGTCTGGC CATAATCGCA ATAGAGGGCG ACTGTGCCCC TGAGGAGAAA 660
 ATCTGGGAGG AGCTGAGTAT GTTGGAGGTG TTTGAGGGGA GGGAGGACAG TGTCTTCGCA 720
 CATCCAGGA AGCTGCTCAT GCAAGATCTG GTGCAGGAAA ACTACCTGGA GTACCGGCAG 780
 40 GTGCCCGGCA GTGATCTCTG ATGCTACGAG TTCTGTGGG GTCCAAGGGC CCTCATTTGA 840
 ACCAGCTATG TGAAGTCCCT GCACCATACA CTAAAGATCG GTGGAGAACC TCACATTTC 900
 TACCCACCCC TGCATGAACG GGCTTTGAGA GAGGGAGAAG AGTGA

Seq ID NO: 206 Protein sequence:
Protein Accession #: NP_005352

45 1 11 21 31 41 51
 MPLEQRSQHC KPBEGLLEARG EALGLVGAQA PATEEQQTAS SSSTLVEVTL GEVPAADSPS 60
 50 PPHSPQGASS PSTTINTYTLW RQSDGESSNQ EEEGPRMPFD LESEFQAAIS RKMVELVHFL 120
 LKRYRAREPV TRAMLESVL RNQDFFPVI FSKASEYLQL VFGIEVVEVV PISHLYILVT 180
 CLGLSYDGLL GDNQVMPKTG LLIIVLAIIA IEGDCAPEEK IWELSLMLEV FEGRSDSVFA 240
 HPRKLLMQDL VQENYLEYRQ VPGSDPACYE FLWGPRALIE TSYVKVLHHT LKIGGEPHIS 300
 YPFLHERALR EGEE

Seq ID NO: 207 DNA sequence
Nucleic Acid Accession #: NM_021115
Coding sequence: 743-2893

60 1 11 21 31 41 51
 AAAGGAAGGG AGGGAGGGAG AAAGGAGAAG TTGGTTTAGA GGCCAGCCGG ACGAGCTTTG 60
 GGCACCGCCC TTAGGAGGGC CACCTCAGA GTCTGACAGC AGGTGAAGGT CCTAAATCTC 120
 65 CCCAACTAA CTGGTGTCTT TTCTCTCTTT CCAAGATGCT CTTCOCGAGG GAGATGCTAG 180
 CCCTTTGGGT CCTTACCTTC TGCCCTCAGG AGCCCCGGAG AGAGGCAGTC CTGGCAAAGA 240
 GCACCTGAA GAGAGAGTGG TAACAGCGCC CCCAGTTCC TCACAGTCGG CGGAAGTGCT 300
 GGGCAGCTG GTGCTGGATG GGACCGCACC CTCTGCACAT CACGACATCC CAGCCCTGTC 360
 ACCGCTGCTT CCAGAGGAGG CCGGCCCAA GCACGCCTTG CCCCCAAGA AGAAACTGCC 420
 70 TTCGCTCAAG CAGGTGAAC CTGCCAGGAA GCAGCTGAGG CCCAAGGCCA CTTCGCGAGC 480
 CACTGTCCAA AGGGCAGGGT CCCAGCCAGC GTCCAGGGC CTAGATCTCC TCTCTCTCTC 540
 CACGAGAAAG CTTGGCCAC CGGGGACCC GGACCCCATC GTGGCTCCG AGGAGGCATC 600
 AGAAGTGCCC CTTTGGCTGG ACCGAAAGGA GAGTGCGGTC CCTACACAC CCGCACCCCT 660
 GCAATCTCC CCCTTCACTT CGCAGCCCTA TGTGGCCAC ACACTCCCC AGAGGCCAGA 720
 75 ACCCGGGAG CCTGGGCTG ACATGGCCCA GGAGGCCCCC CAGGAGGACA CCAGCCCAT 780
 GGCCCTGATG GACAAAGGTG AGAATGAGCT GACTGGGTCA GCCTCAGAG AGAGCCAGGA 840
 GACCACTACC TCCACATTA TCACCAACC GGTCTACACC ACCGAGCAGG CACCACTCT 900
 CTGCACTGTG AGCTTCTCCA ATCTGAGGG GTACATTGAC TCCAGCGACT ACCCACTGCT 960
 GCGCTCAAC AACTTTCTGG AGTGACATA CAACGTGACA GTCTACACT GCTATGGGGT 1020
 80 GGAGCTCCAG GTGAAGAGTG TGAACCTGTC CGATGGGAA CTGCTCTCCA TCCGCGGGGT 1080
 GGAAGGCCCT ACCCTGACCG TCTTGGCCAA CAGACACTC CTGGTGGAGG GGCAGTAAT 1140
 CCGAAGCCCC ACCAACACCA TCTCCGTCTA CTTCCGACC TTCCAGGAG ACGGCCCTTG 1200
 GACCTTCCAG CTTCACTACC AGGCCTTCAT GCTGAGCTGC AACTTTCCCC GCGGCGCTGA 1260
 CTCTGGGGAT GTCACGTGTA TGGACCTGCA CTCAGTGGG GTGGCCCACT TTCAGTGCCA 1320
 85 CTGTGGCTAT GAGCTCAGG GCGCTAAGAT GCTGACATG ATCAATGCCT CCAAGCCGCA 1380
 CTGGAGCAGC GACGAGCCCA TCTGCTCAGC TCTTGTGGA GGGGCACTGC ACAATGCCAC 1440
 CATCGGCCGC GTCTCTCCC CAAGTTACCC TGAACAACA AATGGGAGCC AATTCTGCAT 1500
 CTGGACGATT GAAGCTCCAG AGGGCCAGAA GCTGCACCTG CACTTTGAGA GGCTGTGTCT 1560

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GCATGACAAG GACAGGATGA CGGTTACAG CGGGCAGACC AACAAAGTCAG CTCTTCTCTA 1620
CGACTCCCTT CAAACCGAGA GTGTCCCTTT TGAGGGCCCTG CTGAGCGAAG GCAACACCAT 1680
CCGCATCGAG TTCAGTCCG ACCAGGCCCG GGCGGCCCTCC ACCTTCAACA TCCGATTGGA 1740
AGCGTTTGAG AAAGGCCACT GCTATGAGCC CTACATCCAG AATGGGAAGT TCACTACATC 1800
CGACCCGACC TATAACATTG GGACTATAGT GGAGTTCACC TCGACCCCGC GCCACTCCCT 1860
GGAGCAGGGC CCGGCCATCA TCGAATGCAT CAATGTGGCG GACCCATACT GGAATGACAC 1920
AGAGCCCTTG TGCAGAGCCA TGTGTGGTGG GGAGCTCTCT GCTGTGGCTG GGGTGGTATT 1980
GTCCCAAAAC TGGCCCGAGC CCTACGTGGA AGGTGAAGAT TGTATCTGGA AGATCCACGT 2040
GGGAGAAGAG AAACGGATCT TCCTAGATAT CCAGTTCCTG AATCTGAGCA ACAGTGACAT 2100
CTTGACCATC TACGATGGCG ACAGGTCAT GCCCACATC TTGGGGCAGT ACCTTGGGAA 2160
CAGTGGCCCG CCGGCACTGT ACTCCTCCAC GCCAGACTTA ACCATCCAGT TCCATTCCGA 2220
CCCTGCTGGC CTCATCTTTG GAAAGGCCCA GGGATTATC ATGAACTACA TAGAGGTATC 2280
AAGGAATGAC TCCTGCTCGG ATTTACCCGA GATCCAGAAT GGCTGGAAAA CCACTTCTCA 2340
CACGGAGTTG GTGCGGGGAG CCAGAATCAC CTACAGTGT GACCCCGGCT ATGACATCGT 2400
GGGGAGTGAC ACCCTACCT GCCAGTGGGA CCTCAGCTGG AGCAGCGACC CCCCATTTTG 2460
TGAGAAAAAT TGTACTCTG ACAGCCCGG AGAGGTGGAT CACTCGACCC GCTTAATTTT 2520
GGATCTCTGT CTGCTGGTGG GGAACCCAT CCAATACACC TGCAACCCCG GTTTTGTGCT 2580
TGAAGGAGT TCTCTTCTGA CTTGCTACAG CCGTGAAACA GGAAGTCCCA TCTGGACGTC 2640
TCGCTGCCCC CACTGCGTTT CAGAAGCGGC AGCAGAGAGC TCGCTGGAAG GGGGGAACAT 2700
GGCCCTGGCT ATCTTCATCC CGTCTCTCAT CATCTCCTTA CTGCTGGGAG GAGCCTACAT 2760
TTACATCACA AGATGCTCGT ACTATTCCAA CCTCGCCTG CCTCTGATGT ACTCCACCC 2820
CTACAGCCAG ATCACCCTGG AAACCGAGTT TGACAACCCC ATTTACGAGA CAGGGGGAAC 2880
CCAAAAAGTT TAGGTTTCA TTTAAAAAGA GGTACCCCTT AAAAAGGGGC TTGTGAACTC 2940
AACCCCAATT TCCCCGAGAC ATTTATCCAA AGGCCCTGGG GGCCTTGATT TAAACCCCA 3000
AAAGGCGGCT GTTTTGTGGT TAAACTTTTT AACAAAGGAT TACGGGTTTT TTCCCGGAT 3060
TTTATAAAT TTTAAAGTG

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Seq ID NO: 208 Protein sequence:
Protein Accession #: NP_066938

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1 11 21 31 41 51
MAQEAPOEDT SPMALMDKGE NELTGSASEE SQETTTSTII TTTVITTEQA PALCSVSFSN 60
PEGYIDSSDY PLLPLNNFLE CTYNVTVTYTG YGVELQVKS V NLSDGELLSI RGV DGP LTLV 120
LANQTLLVEG QVIRSEPTNTI SVYFRTFQDD GLGTFQLHYQ AFMLSCNPPR RPD SG DVTVM 180
DLHSGGVAIF HCHLGYELQG AKMLTCINAS KPHWSSQEP I CSA PCG GAVH NAT IGRV LSP 240
SYPTNTGSG FCIWTFEARE GQKLHLHFER LLLHDKDRMT VHSQGTNKA LLYDSLQTES 300
VPFEGLLSEG NTIRIEFTSD QARAASTFNI RFEAFKGH C YEPY IONGNF TSDPTYNIG 360
TIVEFTCDPF HSLEQGPAII ECINVRDPY W NDTEPLCRAM CGGELSAVAG VVLSPNWPEP 420
YVEGEDCIWK IHVGEKRIF LDIQFLNLSN SDILTIYDGD EVMPHILQY LGNSGPQKLY 480
SSTFDLTIQF HSDPAFLIFG KGQGFIMNYI EVSRNDS CSD LPEIQNGWKT TSHTELVRGA 540
RTTYQCDPY DIVGSDTLTC QWDLSSWSDP PFCEKIMYCT DPEVDHSTR LISDPVLLVG 600
TTIQTCTNPG FVLEGGSSLLT CYSRETGTPI WTSRLPHCVS EAAAE TSLEG GNMALAI FIP 660
VLIISLLLG AYIYITRCRY YSNLRLPLMY SHPYSQITVE TEFDNPIYET GGTQKV

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Seq ID NO: 209 DNA sequence
Nucleic Acid Accession #: NM_001327.1
Coding sequence: 89-631

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1 11 21 31 41 51
AGCAGGGGGC GCTGTGTGTA CCGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT 60
CTGAGAGCCG GGCAGAGGCT CCGGAGCCAT GCAGGCCGAA GGCCGGGGCA CAGGGGGTTC 120
ACGCGGCGAT GCTGATGGCC CAGGAGGCC C TGCCATTCT GATGGCCAG GGGGCAATGC 180
TGGCGGCCCA GGAGAGGCGG GTGCCACGGG CGGCAGAGGT CCCC GGGGCG CAGGGGCAGC 240
AAGGGGCTCG GGGCGGGGAG GAGGCGCCCC GCGGGGTCCG CATGGCGGCG CGGCTTCAGG 300
GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCCGGAG AGCCGCTGCT TTAGGTCTTA 360
CCTCGCCATG CCTTTCGGCA CACCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA 420
GGATGCCCA CGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCAGT TGTCCGGCAA 480
CATACTGACT ATCCGACTGA CTGCTGCAGA CCACCGCCAA CTGCAGCTCT CCATCAGCTC 540
CTGTCTCCAG CAGCTTTCCT TGTGATGTG GATCAGCAG TGCTTCTGTC CCGTGTTTTT 600
GGCTCAGCCT CCTCAGGGC AGAGGCGCTA AGCCAGCCT GGCGCCCTCT CCTAGGTCAT 660
GCCTCCTCCC CTAGGGAATG GTCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT 720
GTTTGTGCGT GGAGGAGGAC GGCTTACATG TTTGTTCTCG TAGAAAAATAA AACTGAGCTA

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Seq ID NO: 210 Protein sequence:
Protein Accession #: NP_001318.1

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75

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1 11 21 31 41 51
MQAEGRGTTG STGDADGPGG POIPDGPQGN AGGPGEAGAT GGRGFRGAGA ARASGPGGGA 60
PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EAELARRSLA QDAPPLVPVG 120
VLLKEFTVSG NILTIRLTAA DHRQLQLSIS SCLQLSLLM WITQCPLFVF LAQPPSGQRR

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Seq ID NO: 211 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 52-459

80
85

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1 11 21 31 41 51
CCTCGTGGGC CCTGACCTTC TCTCTGAGAG CCGGGCAGAG GCTCCGGAGC CATGCAGGCC 60
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CCTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CGGGTGCCAC GGGCGGCAGA 180
GGTCCCCGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCGCGGGGT 240
CCGATGGCG GTGCCGCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGC CAGGAGGCCG 300

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PCT/US02/12476

GACAGCGGCC TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC 360
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GTGTTTTTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCTTGG CGCCCTTTC 480
TAGGTATGTC TCCTCCCTCT AGGGAATGGT CCCAGCACGA GTGGCCAGTT CATTGTGGGG 540
GCCTGATTGT TTGTGCTGG AGGAGGACGG CTTACATGTT TGTTCCTGTA GAAAAATAAG 600
CTGAGCTA

Seq ID NO: 212 Protein sequence:
Protein Accession #: E08 sequence

1 11 21 31 41 51
MQAEGGQGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA 60
PRGPHGGAAS AQDGRCPGCA RRPDSRLQLF RLTAADHRQL QLSISSCLQQ LSLLMWITQC 120
FLPVFLAQAQ SQQRR

Seq ID NO: 213 DNA sequence
Nucleic Acid Accession #: NM_000555
Coding sequence: 416..1498

1 11 21 31 41 51
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TCTGGGGGGA GGGGATGCAC ACATTAGAGT AGGAAAGAGG GCTTGGAATA AAATGAAAC 180
ACTCCCCCTT CATAGTCATT GTACTGAAAT GCAAAGACTG CTTCTTAAGC TGGAGATGCT 240
AACCTTGGGT AGCTCCTTCT GTTCTCTTCA AGGGGAATTT TGTCAAGGTA TGGATTCATT 300
TACAACGTGT AGTCATGTGG GCATGTGTGA GGAACAGAT GCCAGTTTTA ATGTATTTAG 360
CCGAAAGTTT CAATTGTGTA GGAGCCACTG TCAGTCTCTG AGGTTCCACC AAAATATGGA 420
ACTTGATTTT GGACACTTTG ACGAAAGAGA TAAGACATCC AGGAACATGC GAGGCTCCCC 480
GATGAATGGG GTGCTGAGCC CCCTCACAG CGCCCACTGT AGCTTCTACC GAACCCAGAA 540
CTTGCAAGCA CTGAGTAATG AGAAGAAAGC CAAGAAGGTA CGTTTCTACC GCAATGGGGA 600
CCGCTACTTC AAGGGGATGG TGTACGCTGT GTCTCTGAC CGTTTTCGCA GCTTTGACGC 660
CTTGCTGGCT GACCTGACGC GATCTCTGTC TGACACATC AACCTGCCTC AGGGAGTGGC 720
TTACATTTAC ACCATTGATG GATCCAGGAA GATCGGAAGC ATGGATGAAC TGGAGGAAGG 780
GGAAAGCTAT GTCTGTCTCT CAGACAACTT CTTTAAAAAG GTGGAGTACA CCAAGAAATG 840
CAATCCCAAC TGGTCTGTCA ACCTAAAAAC ATCTGCCAAT ATGAAAGCCC CCCAGTCCCT 900
GGCTAGCAGC AACAGTGCAC AGGCCAGGGA GAACAAGGAC TTTGTGCGCC CCAAGCTGGT 960
TACCATCATC CGCAGTGGGG TGAAGCCTCG GAAGGCTGTG CGTGTGCTTC TGAACAGAA 1020
GACAGCCCACT CTTTGTGAGC AAGTCTCTAC TGATATCACA GAAGCCATCA AACTGGAGAC 1080
CGGGGTGTCT AAAAATCTCT ACCTCTGGA TGGAAACAGG GTAACCTGTC TCCATGATTT 1140
CTTTGGTGAT GATGATGTGT TTATTGCTG TGGTCTGAA AAATTTGCTG ATGCTCAGGA 1200
TGATTTTTCT TGGATGAAA ATGAATGCCG AGTCATGAAG GGAACCCAT CAGCCACAGC 1260
TGGCCCAAGG GCATCCCAAA CACCTCAGAA GACTTCAGCC AAGAGCCCTG GTCTATGCG 1320
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CAAGTCTAAG CAGTCTCCCA TCTCTACGCC CACCACTCCT GGCAGCCCTC GGAAGCACAA 1440
GGACCTGTAC CTGCTCTGTG CCTTGGATGA CTGCGACTCG CTTGGTGATT CCAATGTAAG 1500
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TCTGCTCAAG TGTCCAACAG GGCTATTGGT GCTTTCAGT TTTTATTTTG TTTTGTGTGT 1620
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CACTGATCCA CAGTCTAACAT TTATGAGAGA TAGATTGATA ACCATCTCTT GGGGCAGCAT 1740
TCCAGGGATG CAAAATGTGC TAGTCCATGA CCTTCAATG GAAAGCTTAG GGGCCTGGGG 1800
TAAATTTGCC CCGTTTAAAT TTGCCCAAAC AGTTTTCTCT TGTAGAGGG GTGTTTAAAT 1860
ATACAGCAAT TAAAAAGTTT GTGTGGGAAA AAAAAAAACT CATTTGCCAG TCCAAGAATG 1920
ACAAACACAA GTGCCCTTT TCTCTGGATC TCAAGAATGG TGGAGGACCC TGAAGGACA 1980
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TGCTTAGGAT CCGTGTGCTG GGTAGCTAA GAGAATAGAC AGAATTGGAA AATACTCAG 2160
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TCTAGAAGGC TGTCTAACAT ACCACATGAT TACATGAAC GTATGGTATC CATCTATCTC 2340
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GGTCTGACAG CTTTCACTCT CTTTTATAG CAAGAAATCA ATATCCTTTT TATAAAAAAT 2460
CATGTCTGTA TTTCAGGAGC AAACCTCTCA GGCTCCTTTT TTATAAACTG GTGATTTTTC 2520
TTTTGTCTAA AAAACACATG AAGAAAATTT ACCAGAAAAA AAAAAAAAG CCGAAGAATA 2580
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CATTAAATAT TTCAATGTGG ACCAGACATT CTAATTATAT TTTAAATGAA ATGTTACAGC 2760
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CTTTCCTTG TCTTTAACAT TAGAAAGGAT TTCTCTTAC TAAGGACTGA TCATTTGAAA 2880
TAGTTTTTCA TCTTTTGAGA TACAGGTTTA TAACACTGCT TTTTTTTCC TGTAAACATA 2940
GCCCATAAAT GCAAAAAACAA CTAATTTTAA TTGAAGGTCT TGCTTGCCAN TCCTGTGTG 3000
GCTTTNACCA AATATAAAAA TTCCCTTATT CCTTGTAAT GGTGCAATN TTTGGAAGG 3060
CACAGCATCC AAACCAAGCT GCTGTTTGGC TACTGAATGG CTTGCAGTTG TTCCTCCACT 3120
CTAAATGGAA TGAGCTTGCT GTGTGTGTGT GTGGTGGTGG TGGGAGGGGG TGGTGCAATG 3180
GTGTGTGTGT GTGTGCATCT GCAGCTGCTT CAAAATTAAG AAATACTACA AGACACCCCT 3240
GTAATGGATT GGTGGCACT GGGTGGCACT GCTGATGTGC ACTGTGTAGG GGGGAACCCA 3300
GTGGTGGTGG GGTATCTCAA ATGCCCTTAG ACAAGCTTCA GATGTCTGTA GCTACCAAAA 3360
ACATTTTCCG TTCAAGAAAA GTGAGATGAT GGTAGTACTG GTTCTGCTG AAATGAAAA 3420
ACCCCAATG ATGAGGAGCT CTTTGTGCC CCTCTCTTT TTTTGTAAAC CCATTCAAAA 3480
CCATTAAATA GCCCATTTTA CTAANCCCTT ATTTCTTTCT AGAAGCTCAG GGTTTNCTTA 3540
GTGCTCCCA NAACATTTTG TAGTTAATTG GGAAGAAAGT ATACTTGGAT TAGGGGGTGT 3600
GGGCATAAAG AATGTGTGGA GGCTGATTTT TAAATTCAG GCCAGAACCC CCAATGACTC 3660
CACCCATAGT NTCATTTAG GTCTCATTTA GTCCATCACC TTTATTTTAA GTTGAGGAAG 3720
TGGAGGCTGG TGAAGAGCAG GACCAGAGGA AGAATCCAGA TTTCTTATG CTTGGGCTC 3780
ACACTAGCTC TMTAGATATT TCCTTGATTG CGGTATATGT ACTACTAGAA AATACCAAT 3840
GGATATATT TCTTTAGGAT AACCTTTGAA CCAACAATNT TCAATAACAA TAGTACATCT 3900

	TCCATCTTAC	TTTTAATCGA	GTATAAGGAA	ATGTTTCTTT	ATGGCCATT	TGGAGGGAGC	3960
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5	TTGTTTTTAA	TTGGCCCACT	TTCAAGGCAA	TTTTTTTTGT	GTGCTGTGTA	CTGAGCTCCT	4080
	CCACCCCTGT	CATTCACTTC	CAATTTTACC	CAATCCAAAT	TTAGCACTCA	AGTTCCATTG	4140
	TGTTAATTTT	TGCACGGTCT	ACACACATCA	AGTCAGCAAG	CATTTGCCAC	CACCTCCCTAT	4200
	ACTTCTCCCT	CTTTTTTACA	CACACACACA	CACACACACA	CACATCCAT	CTCTTGCTTG	4260
	TTCTACCTC	CCTGATTTT	CTTCCCTACA	GAAATAGAAA	TAGGGACAAA	GAAGGGGAAA	4320
	ATGTATATAT	TGGGGCTGGG	CTGAACAACT	AACCTTCATA	GTAGTATTAA	CTAGGGGTAA	4380
10	ATTGAGAGAA	AAGCTCCTTT	TCTCTTCACT	GTTTTGGAAA	GGATAGCCAT	TAGCATGACT	4440
	GCTTTGTGTC	CTTATGGACT	TTAGTATTAG	CCTAGATTGA	ATTATAGCGT	TTTTCTAGCT	4500
	GAAGGAACCT	TAAGATCACA	TCATCTACTC	CTCTACTCCA	AATTTCTCAT	TCTTCAGGCC	4560
	AGGAAACCGA	GACACAGAGG	TAAAGTAATT	TCCCCAAGGT	CACACAGCTG	GCTGGGGCAG	4620
	GATTGGGTTT	ACAACCCACA	TCTCCTGGCT	CTTATTCAG	GGCCTTTTCC	CACTAAGTAG	4680
	TATTGCCTTC	CATTGCTGTC	CTGAGAGTTA	TTTCTCAGGG	TCATGTTGCA	TCTTGGAGCC	4740
15	ACATGTCTGT	GGCCTGATCT	CAGTGGGAAA	TNACCACCAGC	AACCTTAATAC	AGCCCCTTTT	4800
	CCCTGCATT	CTCTGGTTCC	CATCCACATG	GGTTGCAGAT	GTCCCTGAAG	AGAGTGAGGC	4860
	ATTGAGGGCC	AATAGGAGCA	ATGGGGTCCC	TGGCCTTGTC	CATCTGATT	AGGAGATCAC	4920
	TGCTCCATCG	TGAGGAGCCC	TCTGAATAGC	CCCCCACTGA	ATGCTTGCCCT	TGCCCAATG	4980
20	GAATGGAGGA	AGATTGATTT	TCTCCATCAG	TTCACTTGT	GTCTCTCAT	AATGGTTGGT	5040
	CTTTCCAGGC	TGAGGGAAAT	GTCTCTGTT	TCCANAGTAN	AAAAAAGAAA	GAGTGGAACA	5100
	ATANCTTTGT	TCTACTGAGT	GGCTTTTCAA	CATTTAAAAA	AAACTAGTGT	5160	
	GGTACCATT	CTGCGCANGA	TTTNTTTTAG	AATATGGGAG	TAAAGTAGAG	TAGAGAAAAT	5220
	AACTGGTCT	CAGTGTGGTT	GGCCTCATCC	ACAATGTCCC	CAAAGCCATC	CTGCTNTGAT	5280
25	GAGGACAATT	TCCAGGTATA	AGCAAGGGGC	TTTGTGACAA	AAATGTACCC	TGGCTGATGT	5340
	TAAACATTGG	CTCCTGTGTT	TGCACCAAAA	TAGCAAGCTG	TGTGCTCTAT	ACACTCTTCC	5400
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	CAACACATG	GTTCCTCTTG	CTGCAAGGCT	NTTCTGGGA	ACTAAGGGGG	TATTTATTAG	5520
	TTCACTNTA	AGAGACCTCC	TTCTGGGCTT	ACCCCACTCC	TCAGTACTT	CTCTCTCCTT	5580
30	CTCCTTCTC	CTCCACAGTC	ACAAGTAACC	AAGGAACCTG	AAAGTGGATG	TGTAGCTATT	5640
	TGAAGAAGGC	AAGGAACCTT	GAGATCTTTC	TTTGAATCCT	TTAGTCCAAG	TCTTAGACCA	5700
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	GGTACAATGC	TCCCAATCAC	CCTGCACATT	TGATTCTAAA	TGGCTTTTAT	TTTTTAAAAA	5820
	TCCATATCCC	TAGGACAAGA	NAACAGGATG	CCTATATCCC	CAAAATGAGC	TCCAGGACAC	5880
35	TGATGGGAAT	GATTCGCAAG	ATCACCACAC	CTCAGAAAAC	GTCTGTGCCA	ANAGACTTCC	5940
	CCAGATAGAA	NCAGTGGGAC	AGTGGTTTGA	ACGACTTCTT	TTATGGTTGT	CCAGTTTGCT	6000
	ATGGAATAAA	AAGGCAATGA	TTTTTAAAAA	AAGATGATTG	GAACCTGTCT	TTGGCCACAT	6060
	AGGGCCACTT	GGATCCATTT	CCAGGCCCTTA	CTCATATATT	GCCTTCAGTG	AAGGGCTTTG	6120
	GCTTTAAGTC	CCAGACTGGT	CTCCCAAGTG	AACCATAAGT	GTTCCTGGAG	TCATCTGGGG	6180
40	TGAGGCATGA	GAATGTTGCC	CCATCTATCC	CTTCAGGAAA	AGGTGCCTTC	CCTCCCTTTC	6240
	TCCTAAAGCC	TGGTCCCCAA	AAATGTTTGT	TGTCTCCAAA	AGTCTAGTAT	GGTCTTTATA	6300
	CACCCANACT	CTTAGTGTGG	CGTCTGCTTC	TGTTTCTTGG	TAAAGGATCT	ATGCANACCT	6360
	CCCGCTTTGG	CTTAGCTAGC	GTGACATTGG	CTATCATTGG	ACAAGACTAA	CTTTTTTTTT	6420
	TTTTTTTTTG	ACTGAGTCTC	CCTCTGTAC	CTAGGCTGGA	GTGCACTGGC	ACAATCTTGG	6480
45	CTGCTGCAAA	CTTCAACCTT	TCACCTCCCA	GGTCGAAGCG	ATTCTCTGCG	CTCAGCTCC	6540
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	ATTATCTGCC	CACCTCGGCC	TCCCAAAGTG	CTGGGATTAC	AGGCATGAGC	ACCATGCCCA	6720
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50	GGTGATTTTT	TCTTACCTTG	GATGCCTGAG	ACTAGGGGAG	TATAGAATTC	CAATTGGTAA	6840
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55	AGTCTCTCTT	TCCACAGTAC	AAACATCCAT	CCTTCTCTCT	GTGCAATCTC	GTCTCTCCCT	7140
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	GTGGTCTTAC	CCCACTCCAA	TCAGAAATAT	GTGGTGGGGG	AATCAACCTG	ATCCTGGCCC	7320
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60	TATAGCTCAT	GTATCTTTAG	GTCTTTGCTC	TCCAAGCACT	GTACAGAATA	CTTTGTGGTT	7440
	CCTTTTATAG	CTGACATTTT	GTGGAGCAGT	GAAGCGTGCT	CAGAGACATA	ATCAGCTGAA	7500
	GAGAAAAAAT	CAACCAATGG	ATTTATATCA	GCTAAATACT	AATAATTGAT	TTTGTGTTAT	7560
	GTGCCCATAA	TTTTTAAAGC	TGCAATATAA	TATAATGAGG	GACCACAGGT	AATTTCTCCT	7620
	GTCAATTGTT	TGGCTGGGAT	GGGGGTGGGG	GAGTAATTGC	TAAAGTTT	ACCATTACAC	7680
65	ATTAAACTCT	CTATAATAAT	CTTGTGTTGG	GCTTGCTAAC	TGTTGAGCTG	TTTAACTAA	7740
	ACTGGTAGGC	AATCGGAGTT	GATTTAAATG	AAAAGATAAT	TTAACAAATC	TATACTATAA	7800
	AAAGAGACAT	TGCTTAAATT	GACATGTATT	TTTCTCTTCT	GAGTCACCTA	AACATTACTT	7860
	CTTGACACCA	ACTGTTCAAT	ATACTGAATA	GACAGTCCAT	ATAAGAGAAA	TTAGTGGACC	7920
	TAAAGAAGCC	AGATTGTAGG	TGTTAAATTA	TTAAACAGAA	TTGCAAGGCC	CTTGGAAATG	7980
70	TCACTGCTTG	GCAATACCAT	ATGGCATGCC	AAAATTTACA	ATGACTTTTC	TTTATAAGTT	8040
	ATCCAAAAGG	GATTTGAACA	AGTAAGAGGT	TATGCCAAAA	TGTCCTCAAT	GTATGGTCTT	8100
	GTAATATATT	GCAGCTTGAA	GCCAATGATC	CCTTATGACT	TGTATACAAC	TAATGCATGT	8160
	TTTATTGAAT	TTTGCAATTC	CCACGTGTGG	TAACTCTTTA	AAATGTTTTT	GATCACCTTT	8220
	NTGTGCCATT	AACTTGTATC	AGAAAATGTT	TTTATGGCCA	TTTTCAAAGG	GAGAAAAGTT	8280
75	AAAATGGAAA	CAGCCCAACC	TTTCTGCCCT	ATAGCTGTAG	TAGAATTTGA	GTACCTGTAG	8340
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80	AGTTATTGAT	CATTTCTTAA	GGAACAGCAT	TGTGATCAAA	GACTCAACTT	TACGTAAAAA	8700
	TCAGTGTGAA	ATTGGGGTTG	TATTGGCCAT	TGATTACATT	CAGGATTGAA	TAGTTTTTCAG	8760
	AATCAGATGT	AATCCAAAGA	CAGTAGGTAG	TGATGTCCCT	TATCCCTGCA	GCTGTTTTAA	8820
	GATAGAGACC	TCAGAAGACT	CTGCTTGACC	GATGACCAAT	AATATTGTA	AAAAAAGAGA	8880
	AAAAATGAGA	GAATTAACAA	AGATATTATA	GAACCTTAGC	CACCTATTTA	GAATAGTTAT	8940
85	AGCCAGAAAA	AAAAACAAGG	GCATGAGTTC	AAATGCATTA	CTATCAGTGT	CCTAGGCAAT	9000
	ACCTAACCTA	CTCTGAAATT	GTGATTCAAA	AGCAGTATTT	CAAGAGGCAT	TCTCCTTTTT	9060
	TGGTTTGCTG	ACCCCACTTG	GACTGGTAGG	TTTGGTGAGG	CCCCCATAAA	CCAGCTGGAG	9120

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CAGACCCCTT TCATCTCTG TGCTGTAAC ACCCCTCTTC CCCCACCCCC TCCGCAATTC 9180
AATGAGGGCT TTCTTGGGTC AGAGGACTTC AAGGTTGTCT AGAGAAGTTT GCCATGTGTG 9240
TAAGGTGCTG TGAAGCTGTGA GTGCTGAAGA TTCGCAGCAT TCAATACCAG GCAGCCAAAG 9300
AGCTGCTCTT GCAATTATTT TGGCTCTCAA GCTCTGTCTT TCATCGCATT CTCATTCTCTG 9360
TGTACATTG CAAGATGTGT GTAATGTCAT TTTCACAAA TAAATTTGA TTTCAAT

Seq ID NO: 214 Protein sequence:
Protein Accession #: NP_000546

1 11 21 31 41 51
MELDFGHFDE RDKTSRNRMG SRMNGLPSP T HSAHCSFYRT RTLQALSNEK KAKKVRFYRN 60
GDRYFKGIVY AVSSDRFRSF DALLADLTRS LSDNINLPQG VRYIYTDGS RKIGSMDELE 120
EGESYVCCSD NFFPKVEYTK NVNPNWSVNV KTSANMKAPQ SLASSNSAQ A RENKDFVRPK 180
LVTIIRSGVK PRKAVRVLN KKAHSFEQV LTDITEAIKL ETGVVKKLYT LDGKQVTC LH 240
DFPGDDVFI ACGPEKFRYA QDDPSLDENE CRVMKGNPSA TAGPKASPTP QKTSKSPGP 300
MRRSKSPADS ANGTSSSQLS TPKSKQSPIS TPTSPGSLRK HKDLYLPLSL DSDSLGDSM

Seq ID NO: 215 DNA sequence
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Coding sequence: 312..644

1 11 21 31 41 51
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CTTTCCAACA TCTTCGTCTT TTCTCACTGA CCGAGACTCA GCCGGTAGGT CTGCAGAGTG 120
GTCTTCTGGG TAATTTAGTT GTGAGTGAAT GTGTGGAGGA GCCAGCGGGC TTAGGACAGG 180
TCTCTGGGCA CAGTCCGTTG CTTTGAAGGA AAAGGCCCTC GCGGTGGTCC TCGGCTTCC 240
CCAGGTCCTT GATGCAGCGC CCATGGGCGG GTAATCGTGG CTGGGCTGGA ACGAGGGAGG 300
AAGTGAGAGA TATGAGTGAG CATGTAACAA GATCCCAATC CTCAGAAAGA GGAAATGACC 360
AAGAGTCTTC CCAGCCAGTT GGACCTGTGA TTGTCCAGCA GCCCACTGAG GAAAAACGTC 420
AAGAAGAGGA ACCACCAACT GATAATCAGG GTATTGCACC TAGTGGGGAG ATCAAAAATG 480
AAGGAGCACC TGCTGTTCAA GGGACTGATG TGGAAAGCTT TCAACAGGAA CTGGCTCTGC 540
TTAAGATAGA GGATGCACCT GGAGATGGTC CTGATGTGAG GGAGGGGACT CTGCCCACTT 600
TTGATCCCA TAAAGTGCTG GAAGCAGGTG AAGGGCAACT ATAGGTTTAA ACCAAGACAA 660
ATGAAGACTG AAACCAAGAA TATTGTTCTT ATGCTGGAAG TTTGACTGCT AACATTCTCT 720
TAATAAAGTT TTACAGTTTT CTGCAAAAAA AAAAAAAAAA AAA

Seq ID NO: 216 Protein sequence:
Protein Accession #: NP_569734

1 11 21 31 41 51
MSEHVTRSQS SERGNDQESS QPVGPFVIVQ PTEBKREQEE PPTDNQGIAP SGEIKNEGAP 60
AVQGTDEAP QQELALLKIE DAPGDGPDVR EGTLPFTDPT KVL EAGEGQL

Seq ID NO: 217 DNA sequence
Nucleic Acid Accession #: NM_001476.1
Coding sequence: 82..435

1 11 21 31 41 51
GCCAGGGAGC TGTGAGGCAG TGCTGTGTGG TTCTGCGCGT CCGGACTCTT TTTCCTCTAC 60
TGAGATTTCAT CTGTGTGAAA TATGAGTTGG CGAGGAAGAT CGACCTATTA TTGGCCTAGA 120
CCAAGGCGCT ATGTACAGCC TCCTGAAGTG ATTGGGCCTA TGCGGCCCGA CGAGTTTCACT 180
GATGAAGTGG AACCAAGCAAC ACCTGAAGAA GGGGAACCAAG CAACTCAACG TCAGGATCCT 240
GCAGCTGCTC AGGAGGGAGA GGATGAGGGA GCATCTGCAG GTCAAGGGCC GAAGCCTGAA 300
GCTGATAGCC AGGAACAGGG TCACCCACAG ACTGGGTGTG AGTGTGAAGA TGGTCTGAT 360
GGCAGGAGG TGGACCCGCC AATCCAGAG GAGGTGAAAA CGCCTGAAGA AGGTGAAAAG 420
CAATACAGT GTTAAAGAA GACACGTTGA AATGATGCAG GCTGCTCTTA TGTGGAAAT 480
TTGTTTACAT AAATCTCTCC AATAAAGCTT TACAGCCTTC TGCAAAA

Seq ID NO: 218 Protein sequence:
Protein Accession #: NP_001467.1

1 11 21 31 41 51
MSWRGRSTYY WPRPRRYVQF PEVIGPMRPE QFSDEVEPAT FEEGEPATQR QDPAAAQEGE 60
DEGASAGQGP KPEADSQEQG HPQTGCCECD GPDGGQEVDPF NPEVKTPEE GEKQSQC

Seq ID NO: 219 DNA sequence
Nucleic Acid Accession #: NM_001476
Coding sequence: 90-3671

1 11 21 31 41 51
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AGACAGAGAC TGAGCGGCGCC GGCACCGCCA TGCCCTGCGCT CTGGCTGGGC TGCTGCCTCT 120
GCTTCTCGCT CCTCCTGCCG GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
ATGGGAAGTC CAGGCAAGTG ATCTTTGATC GGGAACTTCA CAGACAAATC GGTAATGGAT 240
TCCGCTGCGT CAACTGCAAT GACAACACTG ATGGCATTCA CTGCGAGAAG TGCAAGAAATG 300
GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTTGCCCTG CAATTGTAAC TCCAAAGGTT 360

	CTCTTAGTGC	TCGATGTGAC	AACCTCTGGAC	GGTGCGAGCTG	TAAACCAAGGT	GTGACAGGAG	420
	CCAGATGCGA	CCGATGTCTG	CCAGGCTTCC	ACATGCTCAC	GGATGCGGGG	TGCACCCAAG	480
	ACCAGAGACT	GCTAGACTCC	AAGTGTGACT	GTGACCCAGC	TGGCATCGCA	GGGCCCTGTG	540
5	ACGCGGGCCG	CTGTGTCTGC	AAGCCAGCTG	TTACTGGAGA	ACGCTGTGAT	AGGTGTGAT	600
	CAGGTTACTA	TAACTCTGGAT	GGGGGGAACC	CTGAGGGCTG	TACCCAGTGT	TTCTGCTATG	660
	GGCATTACAG	CAGCTGCCGC	AGCTCTGCAG	AATACAGTGT	CCATAAGATC	ACCTCTACCT	720
	TTATCAAGA	TGTTGATGGC	TGGAAGGCTG	TCCAAACGAA	TGGGTCTCCT	GCAAAGCTCC	780
	AATGGTCACA	GCGCCATCAA	GATGTGTTTA	GCTCAGCCCA	ACGACTAGAC	CCTGTCTATT	840
10	TTGTGGCTCC	TGCCAAATTT	CTTGGGAATC	AACAGGTGAG	CTATGGGCAA	AGCCTGTCTT	900
	TTGACTACCG	TGTGGACAGA	GGAGGCAGAC	ACCCATCTGC	CCATGATGTG	ATTCTGGAAG	960
	GTGCTGGTCT	ACGGATCACA	GCTCCCTTGA	TGCCACTTGG	CAAGACACTG	CCTGTGGGC	1020
	TCACCAAGAC	TTACACATTC	AGGTTAAATG	AGCATCCAAG	CAATAATTGG	AGCCCCCAGC	1080
	TGAGTTACTT	TGAGTATCGA	AGGTTACTGC	GGAACTCTAC	AGCCCTCCGC	ATCCGAGCTA	1140
	CATATGGAGA	ATACAGTACT	GGGTACATTG	ACAATGTGAC	CCTGATTTC	GCCCCCCTG	1200
15	TCTCTGGAGC	CCCAGCACCC	TGGGTTGAAC	AGTGTATATG	TCCTGTGTGG	TACAAGGGGC	1260
	AATTCTGCCA	GGATTGTGCT	TCTGGCTACA	AGAGAGATTC	AGCGAGACTG	GGGCTTTTGG	1320
	GCACCTGTAT	TCCTTGTAAAC	TGTCAAGGGG	GAGGGGCTGT	TGATCCAGAC	ACAGGAGATT	1380
	GTTATTACAG	GGATGAGAAAT	CCTGACATTG	AGTGTGCTGA	CTGCCCAATT	GGTTTCTACA	1440
	ACGATCCGCA	AGCAGCTGAC	AGCTGCAAGC	CATGTCCCTG	TCATAACGGG	TTGAGCTGCT	1500
20	CAGTGATGCC	GGAGACCGAG	GAGGTGGTGT	GCAATAACTG	CCCTCCCGGG	GTCAACGGTG	1560
	CCCGCTGTGA	GCTCTGTGCT	GATGGCTACT	TTGGGGACCC	CTTTGGTGAA	CATGGCCAG	1620
	TGAGGCTTGT	TCAGCCCTGT	CAATGCAACA	ACAAATGTGA	CCCCAGTGCC	TCTGGGAATT	1680
	GTGACCGGCT	GACAGGCGAG	TGTTTGAAGT	GTATCCACAA	CACAGCCGGC	ATCTACTCGG	1740
	ACCAGTGCA	AGCAGGCTAC	TTGCGGGACC	CATTGGCTCC	CAACCCAGCA	GACAAAGTGC	1800
25	GAGCTTGCAA	CTGTAAACCC	ATGGGCTCAG	AGCCTGTAGG	ATGTCGAAGT	GATGGCACCT	1860
	GTGTTTGCAA	GCCAGGATTT	GGTGGCCCCA	ACTGTGAGCA	TGGAGCATTC	AGCTGTCCAG	1920
	CTTGCTATAA	TCAAGTGAAG	ATTGAGATGG	ATCAGTTTAT	GCAGCAGCTT	CAGAGAATGG	1980
	AGGCCCTGAT	TTCAAAGGCT	CAGGGTGGTG	ATGGAGTAGT	ACCTGATACA	GAGCTGGAAG	2040
	GCAGGATGCA	GCAGGCTGAG	CAGGCCCTTC	AGGACATTCT	GAGAGATGCC	CAGATTTCAG	2100
30	AAGGTGCTAG	CAGATCCCTT	GGTCTCCAGT	TGGCCAAGGT	GAGGAGCCAA	GAGAACAGCT	2160
	ACCAGAGCCG	CCTGGATGAC	CTCAAGATGA	CTGTGGAAG	AGTTCCGGCT	CTGGGAAGTC	2220
	AGTACCAGAA	CCGAGTTCTG	GATACCTACA	GGCTCATCAC	TCAGATGCAG	CTGAGCCTGG	2280
	CAGAAAGTGA	AGCTTCCTTG	GGAAACACTA	ACATTCCCTG	CTCAGACCAC	TACGTGGGGC	2340
	CAAAATGGCT	TAAAGTCTG	GCTCAGGAGG	CCACAAGATT	AGCAGAAAGC	CACGTGTGAT	2400
35	CAGCCAGTAA	CATGGAGCAA	CTGACAGGG	AACTGAGGA	CTATTCCAAA	CAAGCCCTCT	2460
	CACTGGTGCG	CAAGGCCCTG	CATGAAGGAG	TGCGAAGCGG	AAGCGGTAGC	CCGGACGGTG	2520
	CTGTGGTGCA	AGGGCTTGTG	GAAAAATTGG	AGAAAAACCA	GTCCCTGGCC	CAGCAGTTGA	2580
	CAAGGGAGGC	CACCTCAAGC	GAAATTGAAG	CAGATAGGTC	TTATCAGCAC	AGTCTCCGCC	2640
	TCCTGGATTG	AGTGTCTCGG	CTTCAGGGAG	TCAGTGATCA	GTCCCTTTCAG	GTGGGAAGAAG	2700
40	CAAAGAGGAT	CAACCAAAA	GCGGATTAC	TCTCAACGCT	GGTAACCAAG	CATATGGATG	2760
	AGTTCAAGCG	TACACAAAAG	AATCTGGGAA	ACTGGAAAGA	AGAAGCACAG	CAGCTCTTAC	2820
	AGAATGGAAG	AAGTGGGAGA	GAGAAATCAG	ATCAGCTGCT	TTCCCGTGCC	AATCTTGCTA	2880
	AAAGCAGAGC	ACAAGAGACA	CTGAGTATGG	GCAATGCCAC	TTTTTATGAA	GTGAGAGCA	2940
45	TCCTTAAAAA	CTCAGAGAG	TTTGACCTGG	AGGTGGACAA	CAGAAAAGCA	GAAGCTGAAG	3000
	AAGCCATGAA	GAGACTCTCC	TACATCAGCC	AGAAGGTTTC	AGATGCCAGT	GACAAAGCCC	3060
	AGCAAGCAGA	AAGAGCCCTG	GGGAGCGCTG	CTGCTGATGC	ACAGAGGGCA	AAGAATGGGG	3120
	CCGGGGAGGC	CCTGGAATTC	TCCAGTGAGA	TTGAACAGGA	GATTGGGAGT	CTGAACCTGG	3180
	AAGCCAAATG	GAGAGCAGAT	GGAGCCTTGG	CCATGGAATA	GGGACTGGCC	TCTCTGAAGA	3240
50	GTGAGATGAG	GGAAAGTGAA	GGAGAGCTGG	AAAGGAAGGA	GCTGGAGTTT	GACACGAATA	3300
	TGGATGCAGT	ACAGATGGTG	ATTACAGAAG	CCCAGAAGGT	TGATACCAGA	GCCAAAGAAC	3360
	CTGGGGTTAC	AATCAAAAGC	ACACTCAACA	CATTAGAAGG	CCTCTGCACT	CTGATGGAGC	3420
	AGCCTCTCAG	TGTAGATGAA	GAGGGGCTGG	TCTTACTGGA	GCAGAAAGCT	TCCCAGGCCA	3480
	AGACCAGAT	CAACAGCCAA	CTGGGGCCCA	TGATGTGAGA	GCTGGAAGAG	AGGGCACGTC	3540
55	AGCAGAGGGG	CCACCTCCAT	TTGCTGGAGA	CAAGCATAGA	TGGGATTCTG	GCTGATGTGA	3600
	GAACACTTGA	GAACTATTAG	GACAACCTGC	CCCCAGGCTG	CTACAATACC	CAGGCTCTTG	3660
	AGCAACAGTG	AAGCTGCTCG	AAATATTCT	CAACTGAGGT	TCTTGGGATA	CAGATCTCAG	3720
	GGCTCGGGAG	CCATGTCATG	TGAGTGGGTG	GGATGGGGAC	ATTTGAACAT	GTTTAATGGG	3780
	TATGCTCAGG	TCAACTGACC	TGACCCCAT	CCTGATCCCA	TGGCCAGGTG	GTGTCCTTAT	3840
60	TGCACCATAC	TCCTTGCTTC	CTGATGCTGG	GCAATGAGGC	AGATAGCACT	GGGTGTGAGA	3900
	ATGATCAAGG	ATCTGGAGCC	CAAAGAATAG	ACTGGATGGA	AAGACAAACT	GCACAGGCAG	3960
	ATGTTTGCTC	CATAATAGTC	GTAAGTGGAG	TCCTGGAATT	TGGACAAGTG	CTGTTGGGAT	4020
	ATAGTCAACT	TATCTTTTGA	GTAATGTGAC	TAAAGGAAAA	AACTTTGACT	TTGCCCAGGC	4080
	ATGAAATTCT	TCCTAATGTC	AGAACAGAGT	GCAACCCAGT	CACACTGTGG	CCAGTAAAT	4140
65	ACTATTGCTC	CATATTGTCC	TCTGCAAGCT	TCTTGCTGAT	CAGAGTTCCT	CCTACTTACA	4200
	ACCCAGGGTG	TGAACATGTT	CTCCATTTTC	AAGCTGGAAG	AAGTGAGCAG	TGTTGGAGTG	4260
	AGGACCTGTA	AGGCAGGCC	ATTGAGAGCT	ATGGTGCTTG	CTGGTGCTTG	CCACCTTCAA	4320
	GTCTCTGACC	TGGGCATGAC	ATCCTTTCTT	TTAATGATGC	CATGGCACT	TAGAGATTGC	4380
	ATTTTATTA	AAGCATTTCC	TACCAGCAA	GCAAAATGTT	GGAAAGTATT	TACTTTTTCG	4440
70	GTTCACAAAGT	GATAGAAAAG	TGTGGCTTGG	GCATTGAAAG	AGGTAATAAT	CTCTAGATT	4500
	ATTAGTCCTA	ATTCATCTCT	ACTTTTCGAA	CACCAAAAT	GATGCGCATC	AATGTATTTT	4560
	ATCTTATTTT	CTCAATCTCC	TCTCTCTTTC	CTCCACCCAT	AATAAGAGAA	TGTTCTCTACT	4620
	CACACTTCCG	CTGGGTACAC	TCCATCCCTC	CATTCTCCT	TCCATCCATC	TTTCCATCCA	4680
	TTACTCTCAT	CCATCCTTCC	AACATATATT	TATTGAGTAC	CTACTGTGTG	CCAGGGGCTG	4740
75	GTGGGACAGT	GGTGACATAG	TCTCTGCCCT	CATAGAGTTG	ATTGTCTAGT	GAGGAAGACA	4800
	AGCATTTTGA	AAAAATAAAT	TTAAACTTAC	AAACTTTGTT	TGTCACAAAT	GGTGTATTAT	4860
	GCAATAACCG	CTGGGTTTGC	AACCTCTTTG	CTCAACAGAA	CATATGTTGC	AAGACCTTCC	4920
	CATGGGGGCA	CTTGAGTTT	GGCAAGGCTG	ACAGAGCTCT	GGGTGTGTGA	CATTTCTTTG	4980
	CATTCCAGCT	GTCACCTCTG	GCCTTTCTAC	AACTGATTGC	AACAGACTGT	TGAGTTATGA	5040
80	TAAACCCAGT	GGGAATTGCT	GGAGGAACCA	GAGGCACTTC	CACCTTGGCT	GGGAAGACTA	5100
	TGGTGCTGCC	TGCTTCTGT	ATTTCTCTTG	ATTTCTCTGA	AAGTGTTTTT	AAATAAGAA	5160
	CAATTGTTAG	ATGCC					

Seq ID NO: 220 Protein sequence:
Protein Accession #: NP_005553

85	1	11	21	31	41	51

WO 02/086443

PCT/US02/12476

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 HMLTDAGCTQ DQRLDLSKCD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYNNLDGDN 180
 PEGCTQCFCY GHSASCRSSA EYSVHKITST FHQDVGWKA VQRNGSPAKL QWSQRHQDVP 240
 SQAQLDPVY FVAPAKPLGN QQVSYGQSLS FDRYDRGGR HPSAHDVILE GAGLRITAPL 300
 MPLGKTLPCG LTKTYTFFRLN EHPNNWSPQ LSYFEYRRL RNLTLALRIRA TYGEYSTGYI 360
 DNVTLISARP VSGAPAPWVE QCICPVGYKG QFCQDCASGY KRDSARLGPF GTCIPNCQCG 420
 GGACDPDTGD CYSGDENPDI ECADCPIGFY NDFHDFRSCK PCPCNHPFSC SVMPEEEVV 480
 CNMCPGVTG ARCELADGY FGDPFGEHGP VRPCQPCQCN NMVDFPSAGN CDRLTGRCLK 540
 CIHNTAGIYC DQCKAGYFGD PLAPNPADKC RACNCPMGS EPVGCRRSDGT CVCKPFGGPG 600
 NCEHGAFSCP ACYNQVKIQM DQFMQQLQRM EALISKAQGG DGVPVDTLE GRMQQAEQAL 660
 QDILRDAQSL EGASRSLGLQ LAKVRSQENS YQSRLLDCLKM TVERVRALGS QYQNRVRDTH 720
 RLITQMLSL AESEASLGNT NIPASDHYVG PNGFKSLAQE ATRLAESHVE SASNMEQLTR 780
 ETEDYSKQAL SLVRKALHEG VSGSGSPDG AVVQGLVEKL EKTSLAQQL TREATQAEIE 840
 ADRSYQHSRL LLDVSRRLQG VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EPKRTQKNLQ 900
 NWKEEAQQLL QNGKSGREKS DQLLSRANLA KSRAQEAALM GNATFYEVES ILKNLREFDL 960
 QVDRKAEAE EAMKRLSYIS QKVSADSDKT QQAERLALSA AADAQRAKNG AGEALISSE 1020
 IEQIGSLNL EANVTADGAL AMEKGSLASLK SEMREVEGEL ERKELEFDN MDVQVMVITE 1080
 AQKVDTRAKN AGVTIQDTLN TLDGLLHMD QPLSVDEEGL VLLQKLSRA KTQINSQLRP 1140
 MMSELEERAR QQRGHLHLE TSIDGILADV KNLENIRDNL PFGCYNTQAL EQQ

Seq ID NO: 221 DNA sequence
 Nucleic Acid Accession #: NM_016529
 Coding sequence: 13-1854

1 11 21 31 41 51
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 AAAGGGGCTG ATAATGTGAT TTTTGAGAGA CTTTCAAAAG ACTCAAAATA TATGGAGGAA 120
 ACATTATGCC ATCTGGAATA CTTTGCCACG GAAGGCTTGC GGCATCTCTG TGTGGCTTAT 180
 CGTGATCTCT CTGAGAAATGA GTATGAGGAG TGGCTGAAAG TCTATCAGGA AGCCAGCACC 240
 ATATTGAAGG ACAGAGCTCA ACGGTTGGAA GAGTGTACG AGATCATTGA GAAGAATTTG 300
 CTGCTACTCT CGAACGACAG CATAGAAGAT CGCCTTCAAG CAGGAGTTCC AGAAACCATC 360
 GCAACACTGT TGAAGGCAGA AATTAAATA TGGGTGTTGA CAGGAGACAA ACAAGAACT 420
 CGGATTAATA TAGGGTATTC CTGCCGATTG GTATCGCAGA ATATGGCCCT TATCCTATTG 480
 AAGGAGGACT CTTTGGATGC CACAAGGSCA GCCATTACT AGCACTGCAC TGACCTTGGG 540
 AATTTGCTGG GCAAGGAAAA TGACGTGGCC CTGATCATCG ATGGCCACAC CCTGAAGTAC 600
 GCGCTCTCTG TCGAAGTCCG GAGGAGTTTC CTGGATTGG CACTCTCGTG CAAAGCGGTC 660
 ATATGCTGCA GAGTGTCTCC TCTGCAGAA TCTGAGATAG TGGATGTGGT GAAGAAGCGG 720
 GTGAAGGCCA TCACCTCGC CATCGGAGAC GCGCCCAACG ATGTCGGGAT GATCCAGACA 780
 GCCCACGTGG GTGTGGGAAT CAGTGGGAAT GAAGGCATGC AGGCCACCAA CAACCTGGAT 840
 TACGCCATCG CACAGTTTTC CTACTTAGAG AAGCTTCTGT TGGTTTATGG AGCCTGGAGC 900
 TACAACCGGG TACCAAGTG CATCTGTATG TGTCTCTATA AGAACGTGGT CCTGTATATT 960
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 TGCACTCGCC TGTACATGT GATTTTCAAC GCTTTCGCGC CCTTCACTCT GGAATCTTT 1080
 GAGAGGTCTT GCATCAGGA GAGCATGCTC AGGTTTCCCC AGCTCTACAA AATCACCAG 1140
 AATGGGAAAG GCTTCAACAC AAAGGTTTTC TGGGGTCACT GCATCAACGC CTTGGTCCAC 1200
 TCCCTCATCT TCTTCTGGTT TCCCATGAAA GCTCTGGAGC ATGATACTGT GTTTGACAGT 1260
 GGTCAATGCTA CCGACTATTT ATTTGTTGGA AATATTGTTT ACACATATGT TGTGTGTTACT 1320
 GTTTGTCTGA AAGCTGTGTT GGAGACCACA GCTTGGACTA AATTCAGTCA TCTGGCTGTC 1380
 TGGGGAAGCA TGCTGACCTG GCTGGTGTTC TTTGGCATCT ACTCGACCAT CTGGCCACC 1440
 ATTCCCATTT CTCCAGATAG GAGAGGACAG GCAACTATGG TCCTGAGCTC CGCACACTTC 1500
 TGGTTGGGAT TATTCTGTAT TCCTACTGCC TGTTTGATTG AAGATGTGGC ATGGAGAGCA 1560
 GCAAGCACA CCGCAAAAGG GACATTGCTG GAGGAGGTGC AGGAGCTGGA AACCAGTCT 1620
 CGAOTCTCTG GAAAAGCGGT GCTGCGGAT AGCAATGGAA AGAGGCTGAA CGAGCGCGAC 1680
 CGCCTGATCA AGAGGCTGGG CCGGAAGACG CCCCAGACGC TGTTCGGGGC CAGCTCCCTG 1740
 CAGCAGGGCG TCCCGATGCG GTATGCTTTT TCTCAAGAAG AACACGGAGC TGTAGTCAG 1800
 GAAGAAGTCA TCCGTCTTGA TGACACCACC AAAAAGAAAT CCAGGAAGAA ATAAGACATG 1860
 AATTTTCTCT ACTGATCTTA GGAAAGAGAT TCAGTTTGTG GCACCCAGTG TTAACACATC 1920
 TTTGTACAGG AAGACTGGCG TCCAAGGCCA AAACACCAGG AAACACATTT CTGTGGCCTT 1980
 AGTTAAGCAG TTTGTTAGTT ACATATTTCC TCGCAACCT GGAGTGCAGA CCACAGGGGA 2040
 AGCTATCTTT GCCCTCCCAA CTCGTCTGCA GTGCTTAGCC TAACTTTTGT TTATGTCGTT 2100
 ATGAAGCATT CAACGTGTCT CTGTGAGGTC TCAAAATAAA AACATTATGT TTCACCAATA 2160
 AGAAAAAAA AAAAAAA

Seq ID NO: 222 Protein sequence:
 Protein Accession #: NP_057613

1 11 21 31 41 51
 MSVIVRTPSG RLRLYCKGAD NVIPERLSKD SKYMEETLCH LEYFATEGLR TLCVAYADLS 60
 ENEYEWLKV YQEASTILKD RAQRLEECYE IIEKNLLLLG ATAIEDRLQA GVPETIATLL 120
 KAEIKIWLVT GDKQETAINI GYSCRLVSQN MALILLKEDS LDATRAAITQ HCTDLGNLLG 180
 KENDVALIID GHTLKYALSF EVRRSFLDLA LSCKAVICCR VSPLQKSEIV DVVKRVRKAI 240
 TLAIGDGAND VGMITQAHVG VGISGNEGMO ATNNSDYAIA QFSYLEKLLL VHGAWSYNRV 300
 TKCILYCFYK NUVLYIIEIW FAFVNGFSQO ILFERWCIGL YNVIPTALPP FTLLGIFERS 360
 TQESMLRFPQ LYKITQNGEK FNTKVFVGHG INALVHSLIL FWFPMKALEH DTVFDSGHAT 420
 DYLFVGNIVY TYVVVTVCLK AGLETTAWTK FSHLAVNGSM LTLWVFFGIY STIWPTIPIA 480
 PDMRGQATMV LSSAHFWLGL FLVPTACLIE DVAWRAAKHT CKKTLLEEVQ ELETKSRVLG 540
 KAVLRDSNGK RLNERDLRIK RLGRKTPPTL FRGSSLLQGV PHGYAFSQEE HGAVSQEEVI 600
 RAYDTTKKKS RKK

Seq ID NO: 223 DNA sequence
 Nucleic Acid Accession #: BC017001
 Coding sequence: 1-394

1 11 21 31 41 51

5
10
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25
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40
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AACGCTGGGC AGGSCCGGCG CGGGTCGGGG GGGCCCCGAG GGGCCCGGGC CGAGCGGCGG 60
CGCGCAGGGC GGCAGCATCC ACTCGGGCCG CATCGCCGCG GTGCACAAAG TGCCGCTGAG 120
CGTGCTCATC CGGCCGCTGC CGTCCGTGTT GGACCCCGCC AAGGTGCAGA GCCTCGTGGA 180
CACGATCCGG GAGGACCCAG ACACGCTGCC CCCCATCGAT GTCTCTGGA TCAAGGGGCG 240
CCAGGGAGGT GACTACTTCT ACTCCTTTGG GGGCTGCCAC CGTACGCGG CCTACCAGCA 300
ACTGCAGCGA GAGACCATCC CGCCCAAGCT TGTCCAGTCC ACTCTCTCAG ACCTAAGGGT 360
GTACCTGGGA GCATCCACAC CAGACTTGCA GTAGCAGCCT CTTTGGCACC TGCTGCCACC 420
TTCAGAGGCC CAGAAGACAC ACCTGGCCTC CAGCAGGCTG GGCATGCAAG AAGGGATAGC 480
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AGGATCATGG CCTTACCCTT GAAGCATTAC CGAGAAGGAG AACAGAGATG GGCTTGAAGA 660
GCCACGTGCT GCCGGCTCCA AATTCCTAAG GACAGGATC CCTCTGCATT TTTGTCTATG 720
TAACCTCTTA TATGGACTAC ATTCACTGTC AAGGAAAGGA AAACCTTGAT TGCAGTGGTT 780
TAAACAAACA GAAGATTGTT TTTCCACATA GCATGGATTG TGGAGATGGG TGGCTAATGG 840
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CAGTGTCTGT TACTTCATGG TCCCAAGATG GCTGCTGTAT CCCCAGAAT CATGTCTGCG 960
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ATCAGAAAGT AAAACCTCGT CAGAAGTCTG TTTCTGCTC TCTCCCTCTG CATATCTTCA 1080
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ACAGCAGGGA ACAGAAATGT CATGGCTGAA TAGACCAATC AAGAGAGAAA TGCAGAATTG 1200
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TGTACCAATT AGCTTTTGT GTGTAACAAA CCATCCCAAA ACTTGGCAGC TAGAAACAAA 1320
CCCTGATTTA TCCACACATC CTATGGGTG GCAATTTGGG CTGGGCTCAA CAGGGCAGTT 1380
CTGCTGCTCA CACCTGGGAT CCTCATGGA GCTAAGTCA GCTGTACCT CAGCTGGGCC 1440
TGGATGGTCT AGGATAGCCT TACTCACTTG CCTGGCAGGT GACAGGCTGT TGGCTGGAAT 1500
TGCTTGGTTC TCCTCCATGT GGCCTCTCCA GCAGGCTAGC TCAGGCTTAT TCACATGATG 1560
GCTTCAGATG TCCAAAGAGA GTGAGAGTAG AAGCTGAAGG ACTTCTTGAG TTCTTGGCCT 1620
GGAACCTGGA CTAGGACAGT GTCACTTCTG CTAAGTTCTT TTGGTCAGAG CAAATCACAA 1680
GGCTTTACCC AGATTCAAGG GATGAGAAAC AGACTACATG TCTTGATGAG GGAACCCACA 1740
AAGAGCTTGT GGCCATTTT CACCTATCAC AAATAATTTT GGATGGGTAT TTATTGGAT 1800
AAAGGTATT CCCTCTTCCC CTTTCTCTC TGTCTCATG GGCCTCACTC TGCCAAAGTTG 1860
GAAGGCACCT AGACATTGTC CTGGCCCTCA GGGTCTAGGG GAAGAGGTGT TGGGGCAGGA 1920
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CTCGGCACCT TTAAGCCTCA GTTCTCCAG TTCAATAATA AGGACAAGAG CTTTCCCAT 2160
GCATTCTCTT TCCCGGGGAA AGTTGACTGA GGTGACCAAT AATAGAATTG AAAAGGGAGA 2220
GTGTCTTCAG TCGAATGTGG CATCCTGGAT TGGGTCTTGG AACAAAAACA GGACATTAGT 2280
GGGAAATATG GAAATCTGAA AAAAGTCTGA ATTTTAGTTA ATATACCAAT TTCAGTCTCT 2340
TGGTTTGTAG AGATGTACCA TGGTGATGTA AGATGTTGAC CTTGGGGTAG GCTGGGTGAA 2400
GGGTATACAG GAACCTTTG TACTATCTCT GCAACTTCTC TGTAATCTA GTATCATTC 2460
AAAATAAAG TTTATTTAAT TTAATAAATA AAAAAAATA AA

Seq ID NO: 224 Protein sequence:
Protein Accession #: AAH17001.1

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55

1 11 21 31 41 51
TLGRAGAGRG APEGPGPSGG AQGSIHSGR IAAVHNVPLS VLIRPLPSVL DPAKVQSLVD 60
TIREDPDSVP PIDVLWIKGA QGGDYFYSFG GCHRYAAYQQ LQRETIPAKL VQSTLSDLRV 120
YLGASTPDLQ

Seq ID NO: 225 DNA sequence
Nucleic Acid Accession #: NM_021048
Coding sequence: 1..1110

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1 11 21 31 41 51
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TCCACTTCCA CCAGCTCCTC TTTTCCATCC TCTTTTCCCT CCTCCTCCTC TTCTCCTCC 180
TCCTCTGCT ATCCTTAAT ACCAAGCACC CCAGAGGAGG TTTCTGCTGA TGATGAGACA 240
CCAAATCTAG CCCAGATGTC TCAGATAGCC TGCTCCTCCC CCTCGTCTGT TGCTTCCCTT 300
CCATTAGATC AATCTGATGA GGGCTCCAGC AGCCAAAAGG AGGAGAGTCC AAGCACCCTA 360
CAGGTCTCTG CAGACAGTGA GTCTTTACCC AGAAGTGAGA TAGATGAAAA GGTGACTGAT 420
TTGGTGCACT TTCTGCTCTT CAAGTATCAA ATGAAGGAGC CGATCACAAA GGCAGAAATA 480
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GAGTGCACTG TGCTGGTCTT TGGCATTGAT GTAAAGGAAG TGGATCCAC TGGCCACTCC 600
TTTGTCTCTG TCACCTCCCT GGGCCTCACC TATGATGGGA TGCTGATGA TGTCAGAGC 660
ATGCCCAAGA CTGGCATTCT CATACTTATC CTAAGCATAA TCTTCATAGA GGGCTACTGC 720
ACCCCTGAGG AGGTCACTG GGAAGCACTG AATATGATGG GGCTGTATGA TGGGATGGAG 780
CACCCTCATTT ATGGGGAGCC CAGGAAGCTG CTCACCCAAG ATTGGGTGCA GGAATACTAC 840
CTGGAGTACC GGCAGGTGCC TGGCAGTGAT CCGTGCACGG ATGAGTTTCT GTGGGGTCCA 900
AGGGCTCATG CTGAAATGAG GAAGATGAGT CTCCTGAAAT TTTTGGCCAA GGTAAATGGG 960
AGTGATCCAA GATCCTTCCC ACTGTGGTAT GAGGAGGCTT TGAAGATGA GGAAGAGAGA 1020
GCCCAGGACA GAATTGCCAC CACAGATGAT ACTACTGCCA TGGCCAGTGC AAGTTCTAGC 1080
GCTACAGGTA GCTTCTCCTA CCCTGAATAA

Seq ID NO: 226 Protein sequence:
Protein Accession #: NP_066386

85

1 11 21 31 41 51
MPRAPKRQRC MPEEDLQSQS ETQGLEGAQA PLAVEEDASS STSTSSSFPS SFPSSSSSSS 60

WO 02/086443

PCT/US02/12476

SSCYPLIPST PEEVSADDET PNPPQSAQIA CSSPSVVASL PLDQSDGESS SQKEESPSTL 120
QVLFDSESLP RSEIDEKVTD LVQPLLFKYQ MKEPITKAEI LESVIKNYED HFPLLFSEAS 180
ECMLLVFGID VKEVDPTGHS FVLVTSGLLT YDGMLSDVQS MPKTGILILI LSIFIEGYC 240
TPBEVIWEAL NMMGLYDME HLIYGEPRKL LTQDWQENY LEYRQVPGSD PARYEPLWGP 300
RAHAIRKMS LLKFLAKVNG SDPRSFLWY EEALKDEBER AQDRIATTDD TTAMASASSS 360
ATGSFSYPE

Seq ID NO: 227 DNA sequence

Nucleic Acid Accession #: NM_005025.1

Coding sequence: 82-1314

1 11 21 31 41 51
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TATAATCGTC TTAGAGCCAC TGGTGAAGAT GAAATATTTC TCTTCTCTCC ATTGAGTATT 240
GCTCTTGCAA TGGGAATGAT GGAAGTGGG GCCCAAGGAT CTACCCAGAA AGAAATCCGC 300
CACTCAATGG GATATGACAG CCTAAAAAAT GGTGAAGAA TTTCTTTCTT GAAGGAGTTT 360
TCAAAACATG TAACGTCTAA AGAGAGCCAA TATGTGATGA AAATTGCCAA TTCCCTGTTT 420
GTGCAAAATG GATTTTCAGT CAATGAGGAG TTTTGTGAAA TGATGAAAA ATATTTTAAT 480
GCAGCAGTAA ATCATGTGGA CTTCAGTCAA AATGTAGCCG TGGCCAACTA CATCAATAAG 540
TGGGTGGAGA ATAACACAAA CAATCTGGTG AAAGATTGGG TATCCCCAAG GGATTTTGAT 600
GCTGCCACTT ATCTGGCCCT CATTAAATGCT GTCTATTTC AAGGGAACTG GAAGTCGAG 660
TTTAGGCTG AAAATACTAG AACCTTTTCT TTCACATAAG ATGATGAAA TGAGTCCAA 720
ATTCCAATG TGTATCAGC AGGAGAATT TATTATGGGG AATTAGTGA TGGCTCCAAT 780
GAAGCTGGTG GTATCTACCA AGTCCTAGAA ATACCATATG AAGGAGATGA AATAAGCATG 840
ATGCTGGTGC TGTCCAGACA GGAAGTTCCT CTGCTACTC TGGAGCCATT AGTCAAAGCA 900
CAGCTGGTGT AAGAAATGGC AAACCTCTGTG AAGAAGCAA AAGTAGAAGT ATACCTGCC 960
AGGTTTCCAG TGAACAGGA AATTGATTTA AAAGATGTTT TGAAGGCTCT TGAATAAAT 1020
GAAATTTTCA TCAAAGATG AAATTTGACA GGCCTCTCTG ATAATAAGGA GATTTTCTT 1080
TCCAAAGCAA TTCACAAGTC CTTCCTAGAG GTTAATGAAG AAGGCTCAGA AGCTGCTGCT 1140
GTCTCAGGAA TGATTGCAAT TAGTAGGATG GCTGTGCTGT ATCTCAAGT TATTGTGAC 1200
CATCCATTTT TCTTTCTTAT CAGAAACAGG AGAACTGGTA CAATCTATT CATGGGACGA 1260
GTGATGCATC CTGAAACAA GAACACAAGT GGACATGAT TCGAAGAACT TTAAGTTACT 1320
TTATTTGAAT AACAGGAAA ACAGTAACTA AGCACATTAT GTTTGCAAT GGTATATATT 1380
TAGGATTTGT GTTTTACAGT ATATCTTAAG ATAATATTTA AAATAGTTCC AGATAAAAC 1440
AATATATGTA AATTATAAGT AACCTGTCAA GGAATGTTAT CAGTATTAAG CTAATGGTCC 1500
TGTTATGTCA TGTGTTTGT GTGCTGTTGT TTAATAATAA AGTACCTATT GAACATGTG

Seq ID NO: 228 Protein sequence:

Protein Accession #: NP_005016.1

1 11 21 31 41 51
| | | | | |
MAFLGLFSL VLQSMATGAT FPPEAIADLS VNMYNRLRAT GEDENILFSP LSIALAMGMM 60
ELGAQGSTQK EIRHSMGYDS LKNGEESFSL KEFENMVTAK ESQVYMKIAN SLFVQNGFHV 120
NEEFLLQMKK YPNAAVNHVD FSNVAVANY INKVENNTN NLVKDLVSPR DFDAATYLAL 180
INAVYFKGNW KSQRPENTR TFSPTKDES EVQIPMMYQQ GEFYGEFSD GSNEAGGIYQ 240
VLEIPYEGDE ISMMLVLBRQ BVPLATLEPL VKAQLVEEWA NSVKKQKVEV YLPRFTVEQE 300
IDLKDLVKAL GITETFIKDA NLGSLDNKE IFLSKAIHKS FLEVNEEGSE AAASVGMIAI 360
SRMAVLPQV IVDHFFFLI RNRRTGTILF MGRVMHPETM NTSGHDFEEL

Seq ID NO: 229 DNA sequence

Nucleic Acid Accession #: NM_003695

Coding sequence: 12-398

1 11 21 31 41 51
| | | | | |
CGACATCAGA GATGAGGACA GCATTGTGTC TCCTTGACGC CCTGGCTGTG GCTACAGGGC 60
CAGCCCTTAC CTTGCGCTGC CAGTGTGCA CCAGCTCCAG CAAGTCAAG CATTCTGTGG 120
TCTGCCCGGC CAGCTCTGCG TTCTGCAAGA CCACGAACAC AGTGGAGCCT CTGAGGGGGA 180
ATCTGGTGAA GAAGGACTGT GCGGAGTCGT GCACACCCAG CTACACCTCG CAAGGCCAGG 240
TCAGCAGCGG CACCAGCTCC ACCCAGTGCT GCCAGGAGGA CCTGTGCAAT GAGAAGCTGC 300
ACAACGCTGC ACCCACCCTG ACCGCCCTCG CCCACAGTGC CCTCAGCCTG GGGCTGGCCC 360
TGAGCCTCCT GGCCTGATC TTAGCCCCCA GCCTGTGACC TTCCCCCAG GGAAGGCCCC 420
TCATGCCTTT CCTTCCCTTT CTCTGGGGAT TCCACACCTC TCTTCCCCAG CCGGCAACGG 480
GGGTGCCAGG AGCCCCAGG TGAGGGCTTC CCCGAAAGTC TGGGACCAGG TCCAGGTGGG 540
CATGGAATGC TGATGACTTG GAGCAGGCC CACAGACCCC ACAGAGGATG AAGCCACCCC 600
ACAGAGGATG CAGCCCCAG CTGCATGGA GGTGGAGGAC AGAAGCCCTG TGGATCCCCG 660
GATTTACAC TCTTCTGTT TTGTTGCCGT TTATTTTGTA CTCAAATCTC TACATGGAGA 720
TAAATGATTT AAACC

Seq ID NO: 230 Protein sequence:

Protein Accession #: NP_003686

1 11 21 31 41 51
| | | | | |
MRTALLLLAA LAVATGPALT LRCHVCTSSS NCKHSVVCFA SSRFCKTTNT VEPLRGNLVK 60
KDCAESCTPS YTLGQVBSG TSSTQCCQED LCNEKLHNAA PTRTALAHS LSLGLALSLL 120
AVILAPSL

Seq ID NO: 231 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 126-752

	1	11	21	31	41	51	
	CGGGGCGAGGT	GGCTCATGCT	CGGGAGCGTG	GTTGAGCGGC	TGGCGCGGTT	GTCTCGGAGC	60
5	AGGGGCGCAG	GAATFCTGAT	GTGAAACTAA	CAGTCTGTGA	GCCCTGGAAC	CTCCACTCAG	120
	AGAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCCT	GGGTATAGAA	180
	GTGTGAGGGA	GAGAACACAG	ACTTCTGGGA	CGCACAGAGA	CGGTGAAGAT	TCCAAGTTCA	240
	GGAGAACTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
	TCCTCTTGA	TGCCTCCATG	CATTCTCAGC	TCAGAACTCT	GGATGAGGAG	CATCCCAAGG	360
10	GAAAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	AAACACCAGC	420
	ACCCAGTGGA	CAATGCTGGG	CTTTTTCCT	GTATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
	CCCGTGTGGC	CCACAAGAAG	GGGAGGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
	AAGTTGGGCC	AGAGCTGCT	TCCCTGCGAA	GGTTGTGTG	GATCTTCTGC	CGCACCAGGC	660
15	TCATCCTGTC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAAAAT	720
	TTCAGGATGG	CTGTATTCTG	CGGTGAGAAT	GAGAGAGTCA	AGCTGGGCGA	AATCTCTCGC	780
	CAAGAGTTCA	GGCTTCCTTT	GGAGACTGCT	CCATCAGTGC	CGAGGTGTGT	GGGAACAGGC	840
	TTCACTGCAC	CGCCATCTTA	CTGAGTTGCT	TCACGTGAGG	AAAAGGGGGC	TTTGGCCCTG	900
	TGACTCAGT	CCACATTTTG	GATTGCATAC	TGGAAAAGAA	GCCAACTCTC	TTGCTAGTAA	960
20	ACCAGCAACC	CGGCTGTATA	CAGTGGTGAC	CCAAGCAATG	GATATAAACC	TAAAAATCTG	1020
	AGGGAGGGGA	GAGGTGGAAT	ACAGTAGTTC	TTGGAATCTG	AAGTCTCCTA	TTTGAATCAG	1080
	TTATTTCCCTG	GAGCTTGGCA	AAAATCTGAT	TGGTGGGGAT	CTCCTAGGAC	CTAGTGGACA	1140
	TCGTGTATTA	ATTTAATCTC	AGGAAAAACA	AGAAATTAAC	CCAGAGAGAG	TCTGGGTTTT	1200
	GGAAATTCAG	GAGCTACCT	CCAGACCGTG	GTGCTGGGCC	TCCATTTTIG	TCTGTCAATC	1260
25	AGCTCTGACT	TACAGCTGCA	GTCACCTTTG	CTATAAGGCA	CCTGGGTAGA	AGGGTGGATG	1320
	GGCTTCACAT	CAATTTTTTT	CTTCCTTTAG	GGTGGGGGAT	TGGTTTGGCT	TTCTTTTGT	1380
	GTGTTTTTTT	TGTTATTTTT	TGTCAAGATT	GATTTTTAGA	TGCAAGGACT	TGAAAAGACC	1440
	CAGAAGGATG	CCACCAGTTT	TTCCTTGAGG	CCTAGGATTT	TTTATCTGT	CCCGAGCAGA	1500
	GGTAATTCCT	CACAACCTAG	TGCACCACTA	GCACCAAGCA	TTTTGAGCAG	AGTACCTCTT	1560
30	TGGGAGCGTT	TTCGTTTTGT	TTTGTTTTTA	ATTCTCTTTC	CTTAGCAGCA	AGGTCTTTTT	1620
	TCTTAGAGAA	TCTACTCCGT	TGCAGAATCA	TTGCAACCTC	AGGAGCCCTC	ACTGATTGAG	1680
	TGCTGTACAG	CTGATATACT	ACTTTGGACT	CTGGAAACAG	ATATGGGTTC	TATTTCTCTAT	1740
	TTCTACTGTG	TGTCGTTAAA	CAACCGTCGG	AGACCAGATG	ACCTGTTAGA	TGGCTAGTCC	1800
35	TGTATAACTC	GACTCTGTAT	GTTTCAATGT	ATGTTACTGC	AATGCTTCAC	CTGCTGTACA	1860
	GTGTTTGTGA	GATGCTCTTT	GAAGATGGTA	CTTTTATATT	T		

Seq ID NO: 232 Protein sequence:
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
40	MKDDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFR	TRPLECQDAL	ETAARAEGLS	60
	LDASMSHSQLR	ILDEHPHKGK	YHGLSALKP	IRTSKHQHP	VDNAGLFSM	TFSWLSLAR	120
	VAHKKGELSM	EDVWSLSKHE	SSDVNCRLE	RLWQBELNEV	GFDAASLRRV	VWIFCRTRLI	180
45	LSIVCLMITQ	LAGFSGPNFQ	DGCILRSE				

Seq ID NO: 233 DNA sequence
Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51	
50	TTTTAATGGT	GCTCATATAT	ACTGTATTTT	TTGTTGTTTA	GTTTACTTTA	TTGAGAGTGT	60
	CACAACATGA	ATCACATAAT	CATGATTTTT	TTTTTTTACT	TTTACTCCCC	AAATATATCA	120
	TGTTTCTTAG	ATCGTAGTCA	TTGAGAAGTC	CCAATAACTC	TAAACTTTTG	AGTTATAACG	180
	TAGTAACACT	CTCTTTCATC	TTTGTGTTAG	CTCTGTAGTC	TAACTCTGGA	TTTAAATTTT	240
55	TTTGTTTCCA	AAGTCAACAT	TGAATTATTC	TTAGATACTT	TAAGCCACTG	AATTCAGTTC	300
	TGTTTGACTG	AAAGCAAAAC	AACGTGACAG	TTTATTTTCA	AACACTAACT	TCTTGATATT	360
	TGTTTATGTT	ATATCTTTTT	ATTAATATAT	TATTTTGACT	AAGCTTTTCA	AAAAATTTTG	420
	AAGCTATTTT	AATCATCAAG	TATGGAAAAC	AAATTACTAT	TGCATTTTCC	TATATATGCA	480
60	TATATATGAG	ATTAACCAAG	ATTGTATCAT	TTTGGCCTTA	ATGCTCTGGT	ATAAAAGATA	540
	ATTAGCTTAC	TATAGTATTA	ATAAATTTTT	CAGTTGGTTT	GGGCAAAATT	AAACCTGAAA	600
	AATAGGTTAA	AAAGTAGTTA	CAAATTAAC	TTACTAATTT	ATACCTGATT	TTTTTCTTGT	660
	AATTAAGATA	CATTTTAAAT	GAGCTTTATA	ATACCTTAAA	AAGTTGGTTC	TAATTTAAAA	720
	TATGAAAGCT	CTGGCTATCA	TCCTGGGATA	GTAATTTCTA	ATTATATAGT	ATTTCAAAC	780
65	TATATATTTT	TTAGTTCTCT	TGAGATAACT	AATTTCTAAT	TATATATGTT	TCAAAAACCA	840
	TATCCGTGAT	TTTTTTTTAAG	AATTGTTTTA	TAAATAGGTC	ATAAGATACA	AGGTCTGCAT	900
	TAGAAGACCC	ACTCTTACTA	GGTCCCTTAA	GGATCTGCCA	TAGATTTTTT	TTTTTTTTTT	960
	TTTTTTTTTAG	GTAGTTTAAA	GCAAGCACTG	ATACCAGTGG	GAGTTGGTCT	TGATCTAGGA	1020
	GATTCGTGTA	AGCATCCAAA	AACAATGCCT	AATTTTCAGT	CTTAGGTTAT	GGCTTGTGAC	1080
70	TCCAGATAAA	AGATGGAGAA	TACCTCATGT	ACTGTGACTT	GAAAATGAAT	TCTTAAATTT	1140
	CTTAGGCTCT	CTCCATGTAT	CTTCTTAAG	GAAAAGTTTC	TGAGTGTGAT	CTCTCTTTTG	1200
	CCATAGTATC	AAGTGGAGGG	TAGTTCAGAA	AAGTTAATAG	GAAATCTTTT	GTGACAGCAG	1260
	ACTATAATAG	AAGTTTGAGT	AATATTTTAA	TAAATTTATA	TAATTCAAAT	GATAAAAATG	1320
	TATCAATGTT	ATCCAAATGAT	TTTTATTAAA	AAATTACCTT	ATTATTAGAA	CTGTGCCAT	1380
75	TACATAAAAA	GTGCTCATGT	ATTGGAATTT	TAAATAATTT	ATTTAAATCA	AGACCACCAT	1440
	AAGTCATTAA	TAATTTAATA	ATTGTTTTTA	ATCAGTGGTT	TTCAACCCCTC	ACTTCATATT	1500
	AGAATCATCT	GAGGACTTTT	AATATGGAAT	CCACCTCATA	ACAATTAAGT	CTAAATTTCT	1560
	GGAGATGGA	GCCATGCTTG	TTTTTCCAAA	AGCTCTTTGA	GTGATTCTAA	TTTGTAGTCA	1620
	GAGTTGAAGA	CCACTGCTCT	AAATTAGTGC	AGGAAAATGC	TTTTATTCTC	CCCATGTTAA	1680
80	CTTTTAAAC	TAGTAATGTA	CCCAGTTAAG	TTTTGATGGT	TAAATTTCCA	CTAAAGAAC	1740
	TATTTCTTCA	ATAACTAGCA	TTTATTACAT	GAAATTTAAG	AGTTTAAAGT	CCATCAAAT	1800
	AGCCCTTGTC	TAAAGATTAT	ATTCTTCTC	TATAACTTCA	AAATAGATAT	TTCAATCAAA	1860
	CTGTTTCAGT	GAGAAAACAT	AATGGATTTT	TTTTTTTTTC	CTCTGGAGCT	GCCGTTCAG	1920
	TGAGATGGAG	GAGGTGGGCA	CATTAAAGGT	CAGTTCACTA	ACCTATGGTT	CAGAGTTCTG	1980
	ATCATATGGA	AGTTTGGAAA	AGAGAGCTTA	TCACAGGTTT	GTATGCTGGT	GAATGGATAG	2040
85	TTTTAATCT	CACCTGCTCA	AAAGAGAATC	AGCTCTCCAG	CAGTTCTAGA	AAAGCTTTGA	2100
	CAATCCCCAA	GGGGCAGTGT	TACCTTACTC	CTTCACTGCT	TCTTAGAAGG	TAGAATTAA	2160
	TTTCTGGAAT	TGCACCTACA	TGTTTTCTTA	TTAACATTCA	GAATTGGGAA	TATTAATTTT	2220

TCCAGTGGAGT AGTTTTCTGA AATTGGTAAC TTGGAGAGTA AAATAACGTA TTTTGCTTTT 2280
 CAATTTTGTG TTTGTTTACT TTTATGTAAA AATTGTGATAT GTGAATTACA CAGTTCTAAT 2340
 AAAACCTCAT GCCTTTTTCAT TACATCTAAT TTGAACCTCTC AACTTCAGTG CCAGAAGTGC 2400
 TTTAAAGATG CTTTAATGAA AAGTATTAAG AAAATATATA GATTTGTATG TCAGTTTATA 2460
 CTTCAGAAAT CCATATATTT GTCATATTTA TTTTCTTAGA AACCTCCTAA TTGGATAACT 2520
 AGATGGTATT TAAAATGAAT GCCCAAAAAT ATCTTGTAAC TTTGTCCAAA AGTTTATCTG 2580
 TTGGAAGCCG CCAGCCATTC ATGTAGAGAG TTTATAAGAA AATAATTTAA AATTGTATGC 2640
 ATTTTATATT ACTATGGTAT CTGTGTACCA TATTCTAAG TATTCAATTAT TAAATTGGTA 2700
 CTTCTTAAAA CCATAACCTG GCTTGCCTTT TAGTGTAAAC CACAAAATCC AACATTGTAT 2760
 ATAGAGATTC TTCTTTTATG AAGAAGAGCT GACGTAATTT ATTACCAAGT CATCTGCACA 2820
 AAGACATTAA CATAAGTCTC TGAGCAGTGA TACATTTTCA AACATGAAGA GTGACAAACA 2880
 CCACATTAAA CAACCCAGGC AACACTCAGA CTTGGCACTT TCCTACGAAT CCATCCTATA 2940
 TGTGCCTGGT ATGCCTCTCT GCATAACTTA CACGAATCGT CCTCCCTACT TGTCTACGCT 3000
 CCTTCATCAA GCACTTGCCA ACACATTAC CTCTAACTTG TACAACCTTA CCAACTCACC 3060
 ACAACATCTG CAACTCTACC CTATCAACTG CCAACCTAAA GACCCCAAC ACAACACAAC 3120
 CCCCAAACAC AAAACGACTA AATCATACC ACCACACAG CCACACACA CACACCAACC 3180
 CACACAACCA ACACACCACG ACCAAACACC CCACCAACAA CAAGCTAACA ACCACAAACA 3240
 GACAACACAT CACATACACT CACTACCCCC CCATACCTCC ACCCACCA

Seq ID NO: 234 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 27-281

1 11 21 31 41 51
 AGCAGGAGGA GAGCTGGCGG GAAGACATGC ACCCCTTGAA GACCCAGAGA GAGGCCGTCT 60
 GTCTACCGGG TAGCAGTTAC ATCAGACTGA GACACTTCCT GTTTACAGGA GACTATAAAA 120
 TTCCTGCCCC GTGCTCATTT GGGGCTGAGC CCATTTTAGG CCTCAGCCCA TCTGCACCCA 180
 GGGCGCTCACT GAAACAGTGT GTTGCTCCAC ACCGCTTGT TTTGCTTGT GGGCGCTCT 240
 CAGGGTTCCG ACCAATCCAA GAGCCTTGCA GAAAGCATTA ACGTGCTTT CTCTTTGGCA 300
 GAGTTTTTCT TTGCTCTGAT CTTGGAGACA TCCCTCTGCC TAGTGGAAC ATAAGGAATA 360
 CAGAAAGAAT GCAAGGAGAT AGACCAACGT GAGATTCTCC TTCATGCACT CAAGAGAAAG 420
 ATGTTGAGAG AAGAGCTAGT CTTTCAGGCT GGGCTGGTGA CCTGAGAAAG AATGTCAGC 480
 TTTCTTCTC CACTTGGCAT ATCAAGAGCC AGGCGTGGAA GACTAAAAA GGAATGTGT 540
 ATAAAACTG TTCAGCGGTT CGCCACAAAG AAGTGGTAAA GTAGCAAAA TGGGGATGGA 600
 GATGCCAGGA GGAAGATGC CAGGGGTAAA GTGGGAAAAT GGGAACTGA AGCCAGGAGG 660
 TCAAGCCAA GCAACAGGTG TTCTGTTTTT CATCACAGAA CTAATAAGTG GTGCTGAGGA 720
 CTCAAACCCG GGAAGGCCCA CTCTAGAACC CATGCTGGTC ATCCATATCC CCAAGGCCCT 780
 GGTGAGAAAC CAGCTAAGCA GATGGCTTGG GTCATCAGGA CGTCCATTAC ATCCAAAGGA 840
 AGACAGCTG TGACGTTTCA AAAGCAAAAG TCCCTACCA GCCAGTGAAG CTACCTGATT 900
 TCTCAGTATC TTACGCCAG TGACACGATC TACCTCAAA ACTTAAAAA AAAAGGGAAA 960
 CATAAACACA TAACAGCAGC AGCAATAATT AAAGATGAGA TGAGAACAAT TAAGAAAAA 1020
 GGAAGGTTCT CCTGTGACTG TTTTATTTTT AGGGAAACAG AGAGGAAGAA GAATGATTTT 1080
 TCTTTTGATG ACTCTATATC CAACTCTGAG GTTTGATTAA AGAAATGACC TTGAACCACA 1140
 CCAAGAAAAA ATAAAGACA ATTTCCAGTA AGTATGCCAG TTCGAATTA TGATTACTT 1200
 TTTATTTTAA CTCTGGAATC AGCAGAGATT TACATGCATT ACGATGATTA ACATCTGAAA 1260
 TTTGACCTTG AATAATCTT TACATTGTAA ATTCTTAATG ATCAAAACA GGTCTCTCAGT 1320
 GATTAAAAA TATTAGTAAT TAATTATTAA AGGAGAATAA TTGCAATATC AACATTCTTA 1380
 AAATCTCAAG GCTTTTAAAG CATTTGTACA AATGACTGGA CATTTTTTAA ATTTGAAAAA 1440
 AAAAAAAGC CCTCCATCTG ATTCTCATTT TCATTGTGAG TGCAACAAAC AAAAAAGGTAT 1500
 GCATCTCTC TCTGCGGAG CACTGTCTCG CAAGCTAGAA ATTCTCACGA CTACCTTTGA 1560
 TCCCATCAAA GCCAAAGAAA GAAAAGAAA TTGTCTCTGA CAGATATATG ACATTAAAAA 1620
 ATAATCCC

Seq ID NO: 235 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MHPLKTQREA VCLPRSSYIR LRHFLFTGDY KIPAPCSFGA DAILGLSPSA PRRSLKQCV 60
 PHRLVLLVGA LSGFRPIQEP CRKH

Seq ID NO: 236 DNA sequence
 Nucleic Acid Accession #: NM_002075
 Coding sequence: 406..1428

1 11 21 31 41 51
 CCACAATAGG GGCAGACCTG TCCATCCTTC TCTGTGGGTC CCCTGTACCT TTCTCCCCCA 60
 ACAGGATCAG ACCCAGAGGC AGCTGGTTGG GGTTTGTGCA GAAGAAGGAT TATCCAGATC 120
 AGTCCCTTCT AATCTCAGCT CCTGCCTGTA CCCTCCCACT CTACCCAAAC CCTCTTCCCC 180
 ACCACCTTGA GCTGAGGAGC ACAGTTTGAG GCCCCCCCAA CCCCCCGCCG GTCCGGGGCCA 240
 GGCCAGGCCA GGCCAGCTCC TCTGGCAGCA GAGCCTGGGC AGGTGACGGG CGGGCGCGGG 300
 CGTCGCAGCT GAGGGAGTAA GGAGGCTCCC AGGAACCGGA GCTGGAACCC CGGCCGAGGT 360
 CCAGCCAGAG CCCAAGAGCC AGAGTGACCC CTCGACCTGT CAGCCATGGG GGAGATGGAG 420
 CAACTGCGTC AGGAAGCGGA GCAGCTCAAG AAGCAGATTG CAGATGCCAG GAAAGCCTGT 480
 GCTGACGTTA TCTGCGCAGA GCTGGTGTCT GGCCTAGAGG TGGTGGGAGC AGTCCAGATG 540
 CGGACGCGGC GGACGTTAAG GGGACACCTG GCCAAGATT ACGCCATGCA CTGGGCCACT 600
 GATTCTAAGC TGCTGGTAAG TGCCCTCGAA GATGGGAAGC TGATCGTGTG GGACAGCTAC 660
 ACCACCAACA AGGTGCACGC CATCCCACTG CGCTCCTCCT GGGTCATGAC CTGTGCCTAT 720
 GCGCCATCAG GGAATTTTGT GGCACTGTGG GGGCTGGACA ACATGTGTTC CATCTACAA 780
 CTCAAATCCC GTGAGGGCAA TGTCAAGGTC AGCCGGGAGC TTTCTGCTCA CACAGTTAT 840
 CTCTCCTGCT GCCGCTTCTT GGATGACAAC AATATTGTGA CCAGCTCGGG GGACACCAG 900
 TGTGCCTTGT GGGACATTGA GACTGGGCAG CAGAAGACTG TATTTGTGGG ACACACGGGT 960
 GACTGCATGA GCCTGGCTGT GTCTCCTGAC TTCAATCTCT TCATTTCCGG GGCCTGTGAT 1020
 GCCAGTGCCA AGCTCTGGGA TGTGCGAGAG GGGACCTGCC GTCAGACTTT CACTGSCCAG 1080

5
10
15

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GAGTCGGACA TCAACGCCAT CTGTTTCTTC CCCAATGGAG AGGCCATCTG CACGGGCTCG 1140
GATGACGCTT OCTGCCGCTT GTTTGACCTG CCGGCAGACC AGGAGCTGAT CTGCTTCTCC 1200
CACGAGAGCA TCATCTGCGG CATCACGTCC GTGGCCTTCT CCCTCAGTGG CCGCTACTA 1260
TTCGCTGGCT ACGACGACTT CAACTGCAAT GTCTGGGACT CCATGAAGTC TGAGCGTGTG 1320
GGCATCCTCT CTGGCCACGA TAACAGGGTG AGCTGCCTGG GAGTCACAGC TGACGGGATG 1380
GCTGTGGCCA CAGGTTCTGT GGAACAGCTT CTCAAAAATCT GGAACAGTGG AGGCTGGAGA 1440
AAGGGAGATG GAAGGCACTG AACACACTCA GCAGCCCCCT CCGCGACCCC ATCTCATTCA 1500
GGTGTCTCTT TCTATATTCG GGGTGCCATT CCCACTAAGC TTTCTCCTTT GAGGGCAGTG 1560
GGGAGCATGG GACTGTGCCT TTGGGAGGCA GCATCAGGGA CACAGGGGCA AAGAACTGCC 1620
CCATCTCCTC CCATGGCCTT CCCTCCCCAC AGTCTCTACA GCCTCTCCTT TAATGAGCAA 1680
GGACAACCTG CCCCTCCCCA GCCCTTTGCA GGCCCGAGCAG ACTTGAGTCT GAGGCCCCAG 1740
GCCCTAGGAT TCCTCCCCCA GAGCCACTAC CTTTGTCCAG GCCTGGGTGG TATAGGGCGT 1800
TTGGCCCTGT GACTATGGCT CTGGCACCAC TAGGGTCTCT GCCCTCTTCT TATTATGCT 1860
TTCTCCTTTT TCTACCTTTT TTTCTCTCTT AAGACACCTG CAATAAAGTG TAGCACCTCG 1920
GT

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Seq ID NO: 237 Protein sequence:
Protein Accession #: NP_002066

20
25

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1 11 21 31 41 51
MGE MEQLRQE AEQLKKQIAD ARKACADVTL AELVSGLEV GRVQMRTRRT LRHGLAKIYA 60
MHWATDSKLL VSASQDGLKI VWDSYTTNKV HAIPLRSSWV MTCAYAPSGN FVACGGGLDNM 120
CSLYNLKSR E GNVKVSREL S AHTGYLSCCR FLDDNNIVTS SGDTCALWD IETGQKTVF 180
VGHTGDCMSL AVSPDFNLFI SGACDASAKL WDVREGTCRQ TFTGHESDIN AICFPNGEA 240
ICTGSDAS C RLFDLRADQE LICFSHESII CGITSVAPSL SGRLLFAGYD DFN CNVWDSM 300
KSERVIGILS HDNRVSCLG V TADGMAVATG SWDSFLKIWN

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30
Seq ID NO: 238 DNA sequence
Nucleic Acid Accession #: CAT cluster

35
40
45
50

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1 11 21 31 41 51
TCCCAATGTG TNGAACCTAC CATAAATTCT TTTCTTACNG GACAATCTTA TNCTAANCAA 60
TACCATTTCG TTTTAAGGCA GATAATCTCT CAAGTTTTCT AATGATATCT GAAACTATTA 120
ACTGATTCCTG TGAATTATGA AATCTGAAAA GGAATTGGAA GTTGCTAAAA ATCTATCATT 180
TGCAATGACC AGTGTGAAGC ACAGTGGAAAT GAGAATGCGT GCCCTGACAC CAAAGAAAAA 240
TAAGTGACTG GAAAGCTGAA GAATCACCAG CTTCAGTGAC ATGGAAACCCA GTGATTGTAT 300
TTTTGACGAG TATCGGGTGA CTTTGAGGTG GTCAAGAAAC CACACTTTAA GAACAATGTC 360
CAAAAAGGGG AAAAAAAGA GCAACCAAAG AAAAAAATC CATAAAATTG CACAGAAGAA 420
AAGAAAAGAA AATAAAATAC ACAATATGGA CGATGGAGAA AAACAGTTAC ATTTCTTTAT 480
GGATCAAGAA GTTTGTGTAC ACATAATCTC ATTTTGAGAT ATATAACTAT TTTTGTCTTT 540
CAGAAAGTAA TCAAAATATT TCAAAATGCT GTCTTATGAA ACTACAATAT TCTCAGAGAT 600
TAGAAAAGT TTTCTGTAAA AGTCAGATAG TAAATATTTT AGGTTTTCGA GTGTCTTTTG 660
CAACTACTCA ACTTTCCTAC TGTAGCACA GAGTAGCTGT GGTACTGTGC AAATAAATTG 720
CTTGTGTTCC AATAAAGCTT CATTTACAAA AACATGCCAT GGGCCATATT TGGCCTGTAC 780
ACTGTTGTTT GCCAAGTCTT AATATAGTTG CTTAGCAAGT ATTGTGAGCT ATTTGAGGAA 840
GACATGAAAG TTCATTGGGT TGCTAAAAAG TATGTAGAAA TTCAAAGGAA AATTAAAAAT 900
TAGGCTAAGT TATAATACAC TGTTTTAACA ATTGTAAAT GTAAAGAGAA TTTACAAATA 960
AAAAATCCAA ATAAAA

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Seq ID NO: 239 DNA sequence
Nucleic Acid Accession #: NM_001786.1
Coding sequence: 130-1023

55
60
65
70
75
80

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1 11 21 31 41 51
GGGGGGGGGG GGCACCTGGC TTCAAAGCTG GCTCTTGAA ATTGAGCGGA GAGCGACGCG 60
GTTGTTGTAG CTGCCGCTGC GGCCGCCGCG GAATAATAAG CCGGGATCTA CCATACCCAT 120
TGACTAACTA TGGAGAGATTA TACCAAAATA GAGAAAATTG GAGAAGGTAC CTATGGAGTT 180
GTGTATAAGG GTAGACACAA AACTACAGGT CAAAGTGGTAG CCATGAAAAA AATCAGACTA 240
GAAAGTGAAG AGGAAGGGGT TCCTAGTACT GCAATTCGGG AAATTTCTCT ATTAAAGGAA 300
CTTCGTATC CAAATATAGT CAGTCTTCAG GATGTGCTTA TGCAGGATTC CAGTTTATAT 360
CTCATCTTTG AGTTTCTTTC CATGGATCTG AAGAAATACT TGGATTCTAT CCCTCCTGGT 420
CAGTACATGG ATTCTTCACT TGTAAAGAGT TATTTATACC AAATCCTACA GGGGATTGTG 480
TTTTGTCACT CTAGAAGAGT TCTTCACAGA GACTTAAAC CTCAAAATCT CTTGATTGAT 540
GACAAAGGAA CAATTAAACT GGCTGATTTT GGCCTTGCCA GAGCTTTTGG AATACCTATC 600
AGAGTATATA CACATGAGGT AGTAACACTC TGGTACAGAT CTCCAGAAGT ATTGCTGGGG 660
TCAGCTCGTT ACTCAACTCC AGTTGACATT TGGAGTATAG GCACCATATT TGCTGAACTA 720
GCAACTAAGA AACCACTTTT CCATGGGGAT TCAGAAATTG ATCAACTCTT CAGGATTTTC 780
AGAGCTTTGG GCACTCCCAA TAATGAAGTG TGGCCAGAAG TGGAATCTTT ACAGGACTAT 840
AAGAATACAT TTCCCAAATG GAAACCAGGA AGCCTAGCAT CCCATGTCAA AAACCTGGAT 900
GAAAATGGCT TGGATTGTCT CTCGAAAATG TTAATCTATG ATCCAGCCAA ACGAATTCT 960
GGCAAAATGG CACTGAATCA TCCATATTTT AATGATTGGA ACAATCAGAT TAAGAAGATG 1020
TAGCTTTCTG ACAAAGATTT TCCATATGTT ATGTCAACAG ATAGTTGTGT TTTTATTTGT 1080
AACTCTTGTC TATTTTGTG TATATATAT TTTCTTGTTA TCAAACTTCA GCTGTACTTC 1140
GTCTTCTAAT TTCAAATAA TAACTTAAAA ATGTAAATAT TCTATATGAA TTTAAATATA 1200
ATTCTGTAAA TGTGAAAAA AAAAAA AAAA

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Seq ID NO: 240 Protein sequence:
Protein Accession #: NP_001777.1

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1 11 21 31 41 51
MEDYTKIEKI GEGTYGVVYK GRHKTTGQVV AMKKIRLESE EEGVPSTAIR EISLLKELRH 60
PNIVSLQDVL MQDSRLYLIF EFLSMDLKKY LDSIPPQYIM DSSLVKSXYL QILQGIVFCH 120

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SRRVLHRDLK PQNLLIDDKG TIKLADFLGA RAFGIPIRVY THEVVTLYWR SPEVLLGSAR 180
 YSTPVDIWSI GTIFAEALATK KPLPHGDSEI DQLFRIFRAL GTPMNEVWPE VESLQDYKNT 240
 FPKWKPGSLA SHVKNLDENG LDLLSKMLIY DPAKRISGKM ALNHPYFNDL DNQIKKM

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Seq ID NO: 241 DNA sequence
 Nucleic Acid Accession #: NM_033379.1
 Coding sequence: 132-854

10 1 11 21 31 41 51
 CGCCCGCGCG CGGGCTCAAC TTTGTAGAGC GAGGGGCCAA CTTGGCAGAG CGCGCGGCCA 60
 GCTTTGCAGA GAGCGCCCTC CAGGGACTAT GCGTGCGGGG ACACGGGATC TACCCATACC 120
 ATTGACTAAC TAGGGAAGAT TATACCAAAA TAGAGAAAAA TGGAGAAGGT ACCTATGGAG 180
 15 TTGTGTATAA GGGTAGACAC AAAACTACAG GTCAAGTGGT AGCCATGAAA AAAATCAGAC 240
 TAGAAAGTGA AGAGGAAGGG GTTCTAGTA CTGCAATTCG GGAAATTTCT CTATTAAAGG 300
 AACTTCGTCA TCCAAATATA GTCAGTCTTC AGGATGTGCT TATGCAGGAT TCCAGGTTAT 360
 ATCTCATCTT TGAGTTTCTT TCCATGGATC TGAAGAAATA CTGGATTCT ATCCCTCCTG 420
 GTCAGTACAT GGAATCTTCA CTGTTAAGG TAGTAACACT CTGGTACAGA TCTCCAGAAG 480
 20 TATTGCTGGG GTCAGCTCGT TACTCAACTC CAGTTGACAT TTGGAGTATA GGCACCATAT 540
 TTGCTGAACT AGCAACTAAG AAACCACTTT TCCATGGGGA TTCAGAAAT GATCAACTCT 600
 TCAGGATTTT CAGAGCTTTG GGCACCTCCA ATAATGAAGT GTGGCCAGAA GTGGAATCTT 660
 TACAGGACTA TAGAATATCA TTTCCCAAT GGAACACAGG AAGCCTAGCA TCCCATGTCA 720
 AAAACTTGGG TGAATAATGGC TTGGATTTGC TCTCGAAAAT GTTAATCTAT GATCCAGCCA 780
 25 AACGAATTC TGCAAAATG GCACTGAATC ATCCATATTT TAATGATTTG GACAAATCAGA 840
 TTAAGAAGAT TAGACTTTCT GACAAAAGT TTCCATATGT TATGTCAACA GATAGTTGTG 900
 TTTTATTGT TAACCTCTGT CTATTTTGT CTTATATATA TTTCTTGTG ATCAAACTTC 960
 AGCTGTACTT CGTCTTCTAA TTTCAAAAT ATAACCTAAA AATGTAAATA TTCTATATGA 1020
 ATTTAAATAT AATTCTGTAA ATGTGAAAAA AAAAAA

30

Seq ID NO: 242 Protein sequence:
 Protein Accession #: NP_203698.1

35 1 11 21 31 41 51
 MEDYTKIEKI GEGTYGVVYK GRHKTGQVV AMKKIRLESE EEGVPSTAIR EISLLKELRH 60
 PNIVSLQDVL MQDSRLYLIF EPLSMDLKKY LDSIPPGQYM DSSLVKVVTI WYRSPEVLLG 120
 SARYSTPVDI WSIGTIFAEL ATKKPLPHGD SEIDQLFRIF RALGTPNNEV WPEVESLQDY 180
 KNTFPKWKPG SLASHVKNLND ENGLDLLSKM LIYDPAKRIS GKMALNHPFY NDLDNQIKKM

40

Seq ID NO: 243 DNA sequence
 Nucleic Acid Accession #: AF101051.1
 Coding sequence: 221-856

45 1 11 21 31 41 51
 GAGCAACCTC AGCTTCTAGT ATCCAGACTC CAGCGCGGCC CGGGGCGCGG ACCCCAACCC 60
 CGACCCAGAG CTCTCTCCAG GCGCGCGCAG CGAGCAGGGC TCCCGCGCTT AACTTCCTCC 120
 GCGGGGCCCC GCGACCTTCG GGAGTCCGGG TTGCCACCTT GCAAACTCTC CGCCTCTGCG 180
 50 ACCTGCCACC CCTGAGCCAG CGCGGGCGCC CGAGCGAGTC ATGGCCAAAG CGGGGCTGCA 240
 GCTGTGTGGG TCCATTCTCG CCTTCTGGG ATGGATCGGC GCCATCGTCA GCACCTGCCCT 300
 GCCCCAGTGG AGGATTTACT CCTATGCCGG CGACAACATC GTGACCGCCC AGGCCATGTA 360
 CGAGGGGCTG TGGATGTCTT CGGTGTGCGA GAGCACCGGG CAGATCCAGT GCAAAGTCTT 420
 55 TGACTCTCTG CTGAATCTGA GCAGCACATT GCAAGCAACC CGTGCCCTGA TGGTGGTTGG 480
 CATCTCTCTG GAGTGAATAG CAATCTTTGT GGCCACCGTT GGCATGAAGT GTATGAAGTG 540
 CTTGGAAGAG GATGAGGTGC AGAAGATGAG GATGGCTGTC ATTGGGGGTG CGATATTTCT 600
 TCTTGCAAGT CTGGCTATTT TAGTTGCCAC AGCATGGTAT GGCAATAGAA TCGTTCAGAA 660
 ATTCTATGAC CCTATGACCC CAGTCAATGC CAGGTACGAA TTTGGTCAGG CTCCTCTCAC 720
 60 TGGCTGGGCT GCTGCTTCTC TCTGCCTTCT GGGAGGTGCC CTACTTTGCT GTTCTGTGCC 780
 CCGAAAAACA ACCTCTTACC CAACACCAAG GCCCTATCCA AAACCTGCAC CTTCAGCGG 840
 GAAAGACTAC GTGTGACACA GAGGCAAAAG GAGAAAAATCA TGTGAAACA AACCGAAAAT 900
 GGACATTGAG ATACTATCAT TAACATTAGG ACCTTAGAAT TTTGGGTATT GTAATCTGAA 960
 GTATGGTATT ACAAAACAAA CAAACAAACA AAAAACCCAT GTGTTAAAT ACTCAGTGCT 1020
 65 AAACATGGCT TAATCTTATT TTATCTTCTT TCCTCAATAT AGGAGGGAAG ATTTTACCAT 1080
 TTGTATTACT GCTTCCCAT TTAGTAATCAT ACTCAATGG GGGAGGGGTG GCTCCTTAAA 1140
 TATATATAGA TATGTATATA TACATGTTTT TCTATTAAAA ATAGACAGTA AAATACTATT 1200
 CTCATTATGT TGATACTAGC ATACTTAAAA TATCTCTAAA ATAGGTAAAT GTATTTAATT 1260
 CCATATTGAT GAAGATGTTT ATTGGTATAT TTTCTTTTTC GTCCTTATAT ACATATGTAA 1320
 70 CAGTCAAATA TCATTTACTC TTCTTCATTA GCTTTGGGTG CCTTTGCCAC AAGACCTAGC 1380
 CTAATTTACC AAGGATGAAT TCTTTCAATT CTTCATGCGT GCCCTTTTCA TATACTTATT 1440
 TTATTTTTTA CCATAATCTT ATAGCACTTG CATGTTTATT AAGCCCTTAT TTGTTTGTG 1500
 TTTCAATGGT CTCTATCTCC TGAATCTAAC ACATTTTATA GCCTACATTT TAGTTTCTAA 1560
 75 AGCCAAGAAG AATTTATTAC AAATCAGAAC TTTGGAGGCA AATCTTTCTG CATGACCAAA 1620
 GTGATAAATT CCTGTTGACC TTCCACACA ATCCCTGTAC TCTGACCCAT AGCACTCTTG 1680
 TTTGCTTTGA AAATATTTGT CCAATTGAGT AGCTGCATGC TGTCCCCCA GGTGTTGTAA 1740
 CACAACTTTA TTGATTTGAAT TTTTAAGCTA CTTATTCTATA GTTTTATATC CCCCTAACT 1800
 ACCTTTTGTG TCCCATTTCC TTAATTGTAT TGTTTTCCCA AGTGTAAATTA TCATGCGTTT 1860
 TATATCTTCC TAATAAGGTG TGGTCTGTTT GTCTGAACAA AGTGCTAGAC TTTCTGGAGT 1920
 80 GATAATCTGG TGACAAATAT TCTCTCTGTA GCTGTAAGCA AGTCACTTAA TCTTTCTACC 1980
 TCTTTTTTCT ATCTGCCAAA TTGAGATAAT GATACTTAAC CAGTTAGAAG AGSTAGTGTG 2040
 AATATTAATT AGTTTATATT ACTCTCATTC TTTGAACATG AACTATGCCT ATGTAGTGTG 2100
 TTTATTTGCT CAGCTGGCTG AGACACTGAA GAAGTCACTG AACAAAACCT ACACACGTAC 2160
 CTTCACTGTA TTCACTGCCT TCCCTCTCTC ACCAGTCTAT TTCCACTGAA CAAAACCTAC 2220
 85 ACACATACCT TCATGTGGTT CAGTGCCTTC CTCTCTCTAC CAGTCTATTT CCACCTGAAC 2280
 AAACCTACGC ACATACCTTC ATGTGGCTCA GTGCTTCTCT CTCTCTACCA GTCTATTTCC 2340
 ATTCCTTCAG CTGTGTCGA CATGTTTGTG CTCTGTTCCT TTTTAAACAC TGCTCTTACT 2400
 TTTCCAGTCT GTACAGAAAT CTATTTCTACT TGAGCAAGAT GATGTATGGA AAGGGTGTG 2460

GCACTGGTGT CTGGAGACCT GGATTGAGT CTTGGTGCTA TCAATCACCG TCTGTGTTTG 2520
 AGCAAGGCAT TTGGCTGCTG TAAGCTTATT GCTTCATCTG TAAGCGGTGG TTTGTAATTC 2580
 CTGATCTTCC CACCTCACAG TGATGTTGTG GGGATCCAGT GAGATAGAAT ACATGTAAGT 2640
 GTGGTTTGT AAATTGAAAA GTGCTATACT AAGGGAAGA ATTGAGGAAT TAACTGCATA 2700
 CGTTTTGGTG TTGCTTTTCA AATGTTTGA AATAAAAAA TGTTAAGAAA TGGGTTTCTT 2760
 GCCTTAACCA GTCTCTCAAG TGATGAGACA GTGAAGTAAA ATTGAGTGCA CTAACGAAT 2820
 AAGATTCTGA GGAAGTCTTA TCTTCTGCAG TGAGTATGGC CCAATGCTTT CTGTGGCTAA 2880
 ACAGATTGAA TGGGAAGAAA TAAAGCCTA CGTGTTGGTA AATCCACAG CAAGGGAGAT 2940
 TTTTGAATCA TAATACTCA TAAGGTGCTA TCTGTTCACT GATGCCCTCA GAGCTCTTGC 3000
 TGTTAGCTGG CAGCTGACGC TGCTAGGATA GTTAGTTTGG AAATGGTACT TCATAATAAA 3060
 CTACACAAGG AAAGTCAGCC ACCGTGCTCT ATGAGGAATT GGACCTAATA AATTTTAGTG 3120
 TGCCCTCCAA ACCTGAGAAT ATATGCTTTT GGAAGTTAAA ATTTAARTGG CTTTGGCCAC 3180
 ATACATAGAT CTTTCATGATG TGTGAGTGTA ATTCATGTG GATATCAGT ACCAAACATT 3240
 ACAAATAAAT TTTATGGCCC AAAATGACCA ACGAAATGT TACAATAGAA TTTATCCAAT 3300
 TTTGATCTTT TTTATTTCTT CTACCACACC TGGAAACAGA CCAATAGACA TTTTGGGGTT 3360
 TTATAATGGG AATTTGTATA AAGCATTACT CTTTTCAT AAATTGTTT TTAATTTAAA 3420
 AAAAGGAAAA AAAAAAAAAA AAA

Seq ID NO: 244 Protein sequence:
 Protein Accession #: AAD16433.1

1 11 21 31 41 51
 | | | | |
 MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMYEGL WMSCVSQSTG 60
 QIQCKVFDLS LNLSSLTQAT RALMVVGILL GVIAIFVATV GMKCMKLED DEVQKMRMAV 120
 IGGAIPLLAG LAILVATAWY GNRIVQEFYD EMTFVNARYE FGQALPTGWA AASLCLLGGA 180
 LLCCSCPRTK TSYPTPRYP KPAPSSGKDY V

Seq ID NO: 245 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 | | | | |
 TTTTITTTTT TTTTITTTTT TTTTCAAGG AGAGCACAAG GAACITTTAT AATGACTTTC 60
 TTAATGGTTA AATGCTGTTT ACCAAGTGAC CCAGAGGCAG CGTGGTTTAG TGGTTTCAAC 120
 AGCATGGTCC CGAGAGTCTG ACAAACCTCA GTTCAATATCC TTCTTTTGTC TTCACTTAGT 180
 TTTTCTTCTT GAGATTAGT TTCTTCATCG TTAACAATGA GGATATTAT ATGTTTCACA 240
 CAGTTGTAT GAAGAATGCA TATATTAGAA TGCCTGTAGT CTGAGCTACT CAGGAGGCTA 300
 AGGTGGGGAG GTGCTCAAG CCCAGGAAT CAAAGCTGCA ATGCATTATG ATTACAGCTG 360
 TTAATAGCCA CTGCACCTCA GCCTGGGCAA TGTAGTAAGA TCCCATCTCT GGCTGGGAGG 420
 GTCCTACGCC CACGGAGTCT CGCTGATTGC TAGCACAGCA GTCTGAGATC AAACCTGCA

Seq ID NO: 246 DNA sequence
 Nucleic Acid Accession #: XM_058553.2
 Coding sequence: 897-1400

1 11 21 31 41 51
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 TAAATGTATT TAGTCTCAGT GCTCAATAGA AGAGATTTCT AATAGAAAAG GATTCAAAC 120
 GTGAAACCAT TTCTCTTTTA ATGTTTCACA TTCTGTITAC AGATTTGTTC TCTTGTGACT 180
 CTGTTATCCA TAATATGGAC AGTTCTTGAG TCCTAACATT GAGAGGTTTT CCCTTAGTGC 240
 ATAGAGGGAA TGAGTATTAA TTGGAGAAGC TTAAGTATT GCCACTTTAG CACTGAAGAT 300
 TGGGATGAGA GGAGGTGAAA CCTCACTAGA AAAAGGGACA ATGTTAGTGT GGCCCTTCTT 360
 GATCATGTTT AAGAAAAGTC ATGAAAATGG TGAACATAGT TTTCAGGACA TATTGGAAGG 420
 GTTGAGTATA TACTGTCTGT CAAAGACTTC CAGCATTTCC AGGTCCCTAGA GAGGAACAA 480
 ACTGTAACG TGCTCTATCTG TATTTTAAAG AACCCAGGAG GAAAGCTTTA TAATAGAACA 540
 TTATTTCTGT GTTTATGTAT AAGGGGTTTT TTGTTTTTTT AAAGACAGGA TCTCACTCCA 600
 TTGTCACGGC CAAGTGCAAT GGCACGAACC TCATAGCTCC TGGACTTAAG TGATCTGCCT 660
 GCCTTTGGCT CCTGAGTAGC TGGGACTACA GGCATGAGCC CCGATGCTG GCTAAGTTTG 720
 TTTTITGTTT TGTTTGTGTT TTTGTTTTTG GGGGGGGTTG TTTTGTTTTT TGTAGAGACG 780
 TAGTCTTGCT TTGTTGCCAG GCTAGTCTCA AACTCCTGGC TTCAAGTGAT CCTCCTGCCT 840
 CAGCTCCCA GAGTGCTAGG ATTACAGCAC TTGGATTGAG CTCTTTCATT TCCAACATGG 900
 AAGAACTTA CACCGACTCC CTGGACCCTG AGAAGCTATT GCAATGCCCC TATGACAAA 960
 ACCATCAAA CAGGGCTTGC AGGTTTCCTT ATCATCTTAT CAAGTGACAG AAGAATCATC 1020
 CTGATGTTGC AAGCAAATTG GCTACTTGTC CCTTCAATGC TCGCCACCAG GTTCTCTGAG 1080
 CTGAAATTAG TCATCATATC TCAAGCTGTG ATGACAGAAG TTGTATTGAG CAAGATGTTG 1140
 TCAACCAAAC CAGGAGCCTT AGACAAGAGA CTCTGGCTGA GAGCACTTGG CAGTGCCCTC 1200
 CTTGCGATGA AGACTGGGAT AAAGATTGTT GGGAGCAGAC CAGCACCCCA TTTGTCTGGG 1260
 GCACAACCTA CTACTCTGAC AACAACAGCC CTGCGAGCAA CATAGTTACA GAACATAAGA 1320
 ATAACCTGGC TTCAGGCATG CGAGTTCCCA AATCTCTGCC GTATGTTCTG CCATGGAAAA 1380
 ACAATGGAAA TGCACAGTAA CTGAATACCT ATCTCATCAA ATGCCAGACC CTAGAAGACT 1440
 GTTGCTTCTT CTTCTACCAG TGGGTTCTCA TTTTCTCTCT AATCTAATA TAGAATGGTA 1500
 AACTCCCTGT GACTTTCCAA ACTGACAAGC ACACTTTTTT CCTCCCCCTT TGAATCCTCA 1560
 TTTAATGCAA GAACCTCAT ACTCAGAAGC TTCCAATAA ACCTTTGATA CAGATTG

Seq ID NO: 247 Protein sequence:
 Protein Accession #: XP_058553.1

1 11 21 31 41 51
 | | | | |
 MEETYDSDLD PEKLLQCPYD KNHQIRACRF PYHLIKCRKN HPDVASKLAT CPFNARHQVP 60
 RAEISHHSS CDDRSCTEQ VVNQTRSLRQ ETLAESTWQC PPCDEDDWDK LWEQTSTPFV 120
 WGTTHYSNN SPASNIVTEH KVNLAGSMRV PKSLPYVLPW KNNGNAQ

WO 02/086443

Seq ID NO: 248 DNA sequence
Nucleic Acid Accession #: NM_003392
Coding sequence: 758..1855

PCT/US02/12476

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1	11	21	31	41	51	
TTAAGGAAAT	CCGGGCTGCT	CTTCCCCATC	TGGAAGTGGC	TTTCCCCACA	TCGGCTCGTA	60
AACTGATTAT	GAAACATACG	ATGTTAATTC	GGAGCTGCAT	TTCCTCAGCTG	GGCACTCTCG	120
CGCGCTGGTC	CCCCGGGCGT	CGCCCCCCAC	CCCTGCCCCT	TCCCTCCCGC	GTCTTCCCCC	180
CATCTCCAC	CCCCCGCGCT	GGCCACCCCG	CCTCCTTGGC	AGCCTCTGGC	GGCAGCGCGC	240
TCCACTCGCC	TCCCGTGCTC	CTCTCGCCCA	TGGAATTAAT	TCTGGCTCCA	CTTGTGTCTC	300
GGCCACGGTT	GGGAGAGGGA	CGGAGGGTGG	CCGCAGCGGG	TTCTGTAGTG	AATTACCCAG	360
GAGGGAATGA	GCACAGCACC	AACATAGAGAG	GGTTCAGGGG	GTGCGGGAAT	CGAGCGAGCA	420
GGAAGGAGGC	AGCGCTGGC	ACCAAGGGCTT	TGACTCAACA	GAATTGAGAC	ACGTTTGTAA	480
TCGCTGGCGT	GGCCGCGCGA	CAGGATCCCA	GCGAAAATCA	GATTTCCTGG	TGAGGTTGCG	540
TGGGTGGATT	AATTGGGAAA	AAGAACTGCT	CTATATCTTG	CCATCAAAAA	ACTCACGGAG	600
GAGAAGCGCA	GTCAATCAAC	AGTAACTTA	AGAGACCCCT	GATGCTCCCC	TGGTTAACT	660
TGTATGCTTG	AAAATTATCT	GAGAGGGAAT	AAACATCTTT	TCCTTCTTCC	CTCTCCAGAA	720
GTCCATTGGA	ATATTAAGCC	CAGGAGTTGC	TTTGGGGATG	GCTGGAAGTG	CAATGTCTTC	780
CAAGTTCTTC	CGGATGCGCT	TGGCCATATT	TTTCTCTCTC	GCCCAGGTTG	TAATTGAAGC	840
CAATTCTTGG	TGGTGGCTAG	GTATGAATAA	CCCTGTTCAG	ATGTCAGAAG	TATATATTAT	900
AGGAGCACAG	CCTCTCTGCA	GCCAACTGGC	AGGACTTTCT	CAAGGACAGA	AGAAACTGTG	960
CCACTTGTAT	CAGGACCAAC	TGCAGTACAT	CGGAGAAGGC	GCGAAGACAG	GCATCAAAGA	1020
ATGCGAGTAT	CAATTCCGAC	ATCGACGGTG	GAACTGCAGC	ACTGTGGATA	ACACCTCTGT	1080
TTTTGGCAGG	GTGATGCGCA	TAGGCAGCCG	CGAGACGGCC	TTCAATACG	CCGTGAGCGC	1140
AGCAGGGGTG	GTGAACGCCA	TGAGCCGGGC	GTGCCGCGAG	GGCGAGCTGT	CCACTGCGCG	1200
CTGCAGCGCG	CGCCGCGCGC	CCAAGGACCT	CGCCGCGGAC	TGGCTCTGGG	CGCGCTGCGG	1260
CGACAAATC	GACTATGGCT	ACCGCTTTGC	CAAGGAGTTC	GTGGACGCCC	GCGAGCGGGA	1320
GCGCATCCAC	GCCAGGGGCT	CCTACGAGAG	TGCTCGCATC	CTCATGAACC	TGCACAACAA	1380
CGAGGCGCGC	CGCAGGACGG	TGTACAACCT	GGCTGATGTG	GCCTGCAAGT	GCCATGGGGT	1440
GTCCGGCTCA	TGTAGCCTGA	AGACATGCTG	GCTCGAGCTG	GCAGACTTCC	GCAAGGTGGG	1500
TGATGCGCTG	AAGGAGAAGT	ACGACAGCGC	GGCGGCCATG	CGGCTCAACA	GCCGGGGCAA	1560
GTTGGTACAG	GTCAACAGCC	GCTTCAACTC	GCCCACCACA	CAAGACCTGG	TCTACATCGA	1620
CCCCAGCCCT	GACTACTGCG	TGCGCAATGA	GAGCACCAGC	TGCTGGGCA	GCGAGGGCGG	1680
CCTGTGCAAC	AAGAGCTCGG	AGGGCATGGA	TGGCTGCGAG	CTCATGTGCT	GCGCCCGTGG	1740
GTACGACCAG	TTCAAGACCG	TGCAGACGGA	GCGCTGCCAC	TGCAAGTTCC	ACTGGTGCTG	1800
CTACGTCAAG	TGCAAGAAGT	GCACGGAGAT	CGTGGACCAG	TTTGTGTGCA	AGTAGTGGGT	1860
GCCACCCAGC	ACTCAGCCCC	GCTCCCAGGA	CCCGCTTATT	TATAGAAAGT	ACAGTGATTC	1920
TGGTTTTTGG	TTTTTAGAAA	TATTTTTTAT	TTTTCCCCAA	GAATTGCAAC	CGGAACCATTT	1980
TTTTTTCTTG	TACCATCTA	AGAACTCTGT	GGTTATTAT	TAATATTATA	ATTATTATT	2040
GGCAATAATG	GGGGTGGGAA	CCACGAAAAA	TATTTATTTT	GTGGATCTTT	GAAAAGGTAA	2100
TACAAGACTT	CTTTTGGATA	GTATAGAATG	AAGGGGGAAA	TAACACATAC	CCTAATCTAG	2160
CTGTGTGGGA	CATGGTACAC	ATCCAGAAGG	TAAAGAAATA	CATTTTCTTT	TTCTCAAATA	2220
TGCCATCATA	TGGGATGGGT	AGGTTCCAGT	TGAAAGAGGG	TGGTAGAAT	CTATTCAACA	2280
TTCACTTTCT	ATGACCAAAA	TAGATTGTAA	ATTCTCTGGT	GCAAGATAAA	AGGCTCTGGG	2340
AAAACAAAAC	AAAACAAAAC	AAACCTCCCT	TCCCAGCAG	GGCTGCTAGC	TTGCTTTCTG	2400
CATTTTCAAA	ATGATAATTT	ACAATGGAAG	GACAAGAATG	TCATATTCTC	AAGGAAAAAA	2460
GGTATATCAC	ATGCTCAATT	CTCCTCAAT	ATTCCATTG	CAGACAGACC	GTCAATTCT	2520
AATAGCTCAT	GAAATTTGGG	CAGCAGGGAG	GAAAGTCCCC	AGAAATTAAG	AAATTTAAAG	2580
CTCTTATGTC	AAGATTCTGG	TTTGAAGCTG	TTATAAGAA	TGGGATTCCA	GATTTTGTAA	2640
AAGACCCCCA	ATGATTCTGG	ACACTAGATT	TTTTGTTTGG	GGAGGTTGGC	TTGAACATAA	2700
ATGAATATC	CTGTATTTTC	TAGGGATAC	TTGGTTAGTA	AATTATAATA	GTAGAAATAA	2760
TACATGAATC	CCATTACACG	GTTTCTCAGC	CCAAAGCAAC	AGGTAATTGC	GTGCCATTCA	2820
GCACGTGACC	AGAGCAGACA	ACCTATTTGA	GGAAAAACAG	TGAAATCCAC	CTTCTCTTTC	2880
ACACTGAGCC	CTCTCTGATT	CCTCCGTGTT	GTGATGTGAT	GCTGGCCACG	TTTCCAAACG	2940
GCAGCTCCAC	TGGGTCCCCT	TTGGTTGTAG	GACAGGAAAT	GAAACATTAG	GAGCTCTGCT	3000
TGGAATAACG	TTCACTACTT	AGGGAATTTT	GTTTCTTAAA	ACTTTTATTT	TGAGGAGCAG	3060
TAGTTTCTTA	TGTTTTAATG	ACAGAACTTG	GCTAATGGAA	TTCAAGAGG	TGTTGACGG	3120
TATCACTGTT	ATGATCCTGT	GTTTAGATT	TCCACTCATG	CTTCTCTTAT	TGTACTGCAG	3180
GTGTACCTTA	AAACTGTGCC	CAGTGTACTT	GAACAGTTGC	ATTTATAAGG	GGGGAAATGT	3240
GGTTTAATGG	TGCTGATAT	CTCAAAGTCT	TTGTACATA	ACATATATAT	ATATATACAT	3300
ATATATAAAT	ATAAATATAA	ATATATCTCA	TTGCAGCCAG	TGATTTAGAT	TTACAGCTTA	3360
CTCTGGGGTT	ATCTCTCTGT	CTAGAGCATT	GTTGTCTTTC	ACTGCAGTCC	AGTTGGGATT	3420
ATTCCAAAAG	TTTTTTGAGT	CTTGAGCTTG	GGCTGTGGCC	CCGCTGTGAT	CATACCCTGA	3480
GCACAGCAGAA	GCAACCTCGT	TTCTGAGGAA	GAAGCTTGAG	TTCTGACTCA	CTGAAATGCG	3540
TGTTGGGGTTG	AAGATATCTT	TTTTTCTTTT	CTGCCCTACC	CCTTTGTCTC	CAACCTCCAT	3600
TTCTGTTTCA	TTTGTGGAGA	GGGCATTACT	TGTTGTTTAT	AGACATGGAC	GTTAAGAGAT	3660
ATTCAAAACT	CAGAAGCATC	AGCAATGTTT	CTCTTTTCTT	AGTTCAATCT	GCAGAATGGA	3720
AACCCATGCC	TATTAGAAAT	GACAGTACTT	ATTAATTGAG	TCCCTAAGGA	ATATTACAGC	3780
CACATACATG	ATAGCTTTTT	TTTTTTTTTT	TTTTTTTTTA	TAAGGACACC	TCTTTCCAAA	3840
CAGGCCATCA	AATATGTTCT	TATCTCAGAC	TTACGTTGTT	TTAAAAGTTT	GGAAAGATAC	3900
ACATCTTTCT	ATACCCCCCT	TTAGGAGGTT	GGGCTTTTAT	ATCACCTCAG	CCAACCTGCG	3960
CTCTTAATTT	ATTGCATAAT	GATATCCACA	TCAGCCAACT	GTGGCTCTTT	AATTTATTGC	4020
ATAATGATAT	TCACATCCCC	TCAGTTGCCG	TGAATTGTGA	GCAAAAGATC	TTGAAAGCAA	4080
AAAGCACTAA	TTAGTTTAAA	ATGTCACCTT	TTTGGTTTTT	ATTATACAAA	AACCATGAAG	4140
TACTTTTTTT	ATTTGCTAAA	TCAGATTGTT	CCTTTTTAGT	GACTCATGTT	TATGAAGAGA	4200
GTTGAGTTTA	ACAATCCTAG	CTTTTAAAAG	AAACTATTTA	ATGTAAAATA	TTCTACATGT	4260
CATTGAGTGA	TTATGTATAT	CTTCTAGCCT	TTATTCTGTA	CTTTTAATGT	ACATATTTCT	4320
GTCTTGGCGT	ATTGTATAT	TTCACTGGTT	TAAAAAACAA	ACATCGAAAG	GCTTATTCCA	4380
AATGGAAGAT	AGAAATATAA	ATAAAACGTT	ACTTGTAAAA	AAAAAAA		

Seq ID NO: 249 Protein sequence:
Protein Accession #: NP_003383

1 11 21 31 41 51

MAGSAMSSKF FLVALAIFFS FAQVVIEANS WWSLGMNPNV QMSEVYIIGA QPLCSQLAGL 60
 SQGQKLCYL QDQHMQYIGE GAKTGIKECQ YQFRHRRWNC STVDNTSVFG RVMQIGSRET 120
 AFTYAVSAAG VVNAMSRACR EGELSTCGCS RAARPKDLPR DWLWGGCGDN IDVGYRFAKE 180
 FVDARERERI HAKGSYESAR ILMNLHNNEA GRRTVYNLAD VACKCHGVSG SCSLKTCWLQ 240
 LADFRKVGDA LKEKYDSAAA MRLNSRGKLV QVNSRFNSPT TQDLVYIDPS PDYCVRNEST 300
 GSLGTQGRLC NRTSEGMDGC ELMCCGRGYD QFKTVQTERC HCKFWCCYV KCKKCTEIVD 360
 QFVCK

Seq ID NO: 250 DNA sequence
 Nucleic Acid Accession #: NM_014058
 Coding sequence: 56..1324

1 11 21 31 41 51
 | | | | |
 15 TGACTTGGAT GTAGACCTCG ACCTTCACAG GACTCTTCAT TGCTGGTTGG CAATGATGTA 60
 TCGGCCAGAT GTGGTGAGGG CTAGGAAAAG AGTTTGTGGG GAACCTCTGG TTATCGGCCCT 120
 CGTCATCTTC ATATCCCTGA TTGTCTGGC AGTGTGCATT GGACTCACTG TTCATTATGT 180
 GAGATATAAT CAAAAGAAGA CCTACAATTA CTATAGCACA TTGTCAATTA CAACTGACAA 240
 20 ACTATATGCT GAGTTTGGCA GAGAGGCTTC TAACAATTTT ACAGAAATGA GCCAGAGACT 300
 TGAATCAATG GTGAAAATG CATTTTATAA ATCTCCATTA AGGGAAGAAT TTGTCAAGTC 360
 TCAGGTTATC AAGTTCAGTC AACAGAAGCA TGGAGTGTGG GCTCATATGC TGTGTATTGG 420
 TAGATTTTAC TCTACTGAGG ATCCTGAAAC TGTAGATAAA ATTGTTCAC TTGTTTACA 480
 TGAAAAGCTG CAAGATGCTG TAGGACCCCT TAAAGTAGAT CCTCACTCAG TTAATAATTA 540
 25 AAAAATCAAC AAGACAGAAA CAGACAGCTA TCTAAACCAT TGCTGCGGAA CACGAAGAAG 600
 TAAACTCTA GTTCAGAGTC TCAGGATCGT TGGTGGGACA GAAGTAGAAG AGGGTGAATG 660
 GCCCTGGCAG GCTAGCCTCG AGTGGGATGG GAGTCATCGC TGTGGAGCAA CCTTAATTAA 720
 TGCCACATGG CTTGTGAGTG CTGCTCACTG TTTTACAACA TATAAGAACC CTGCCAGATG 780
 GACTGCTTCC TTTGGAGTAA CAATAAAACC TTGAAAATG AAAACGGGTC TCCGGAGAAT 840
 30 AATTGTCCAT GAAAAATACA AACACCCATC ACATGACTAT GATATTTCTC TTGCAGAGCT 900
 TTCTAGCCCT GTTCCCTACA CAAATGCAGT ACATAGAGTT TGTCTCCCTG ATGCATCTTA 960
 TGAGTTTCAA CCAGGTGATG TGATGTTTGT GACAGGATTT GGAGCACTGA AAAATGATGG 1020
 TTACAGTCAA AATCATCTTC GACAAGCACA GGTGACTCTC ATAGACGCTA CAACTTGCAA 1080
 TGAACCTCAA GCTTACAATG ACGCCATAAC TCCTAGAATG TTATGTGCTG GCTCCTAGA 1140
 35 AGGAAAAACA GATGCATGCC AGGGTGACTC TGGAGGACCA CTGGTTAGTT CAGATGCTAG 1200
 AGATATCTGG TACCTTGCTG GAATAGTGAG CTGGGGAGAT GAATGTGCGA AACCACACAA 1260
 GCCTGTGGTT TATCTAGAGT TTACGGCCTT GCGGGACTGG ATTACTTCAA AAACCTGGTAT 1320
 CTAAGAGAGA AAAGCCTCAT GGAACAGATA ACATTTTTTT TTGTTTTTTG GGTGTGGAGG 1380
 40 CCATTTTATG AGATACAGAA TTGGAGAAGA CTTCGAAAAC AGCTAGATTT GACTGATCTC 1440
 AATAAACTGT TTGCTTGATG CAAAAAATAA A

Seq ID NO: 251 Protein sequence:
 Protein Accession #: NP_054777

1 11 21 31 41 51
 | | | | |
 45 MYRPDVVRAR KRVCWEPWVI GLVIFISLIV LAVCIGLTVH YVRYNQKTTY NYYSTLSFTT 60
 DKLYAEPGRE ASNVPTFMSQ RLESWVKNFA YKSPRLREFV KSOVIKFSQQ KHGVLAHMLL 120
 50 ICRFHSTEDP ETVDKIVQLV LHEKLQDAVG PPKVDPHSVK IKKINKTETD SYLNHCCGTR 180
 RSKTLGQSLR IVGGTEVEEG EWPWQASLQW DGSHRGATL INATWLVSAA HCFTTYKNPA 240
 RWTASFVGTI KPSKMKRGLR RIIVHEKYKH PSHDYDISLA ELSSVPVPTN AVHRVCLPDA 300
 SYEFQPGDVM FVTGFALKN DGYSQNHRLQ AQVTLIDATT CNEPQAYNDA ITPRMLCAGS 360
 LEGKTDACQG DSGGPLVSSD ARDIWYLAGI VSWGDECAKP NKPGVYTRVT ALRDWITSKT 420
 GI

Seq ID NO: 252 DNA sequence
 Nucleic Acid Accession #: NM_003504.2
 Coding sequence: 71-1771

1 11 21 31 41 51
 | | | | |
 60 GGCACGAGGC CTGCTGCCGC CGGGCTCTTG GTACCTCAGC GCGAGCGCCA GGCCTCCGGC 60
 CCGCGTGGCT ATGTTCTGTT CCGATTTCOG CAAAGAGTTC TACGAGGTGG TCCAGAGCCA 120
 65 GAGGGTCTTT CTCTTCTGTT CCTCGGACGT GGATGCTCTG TGTGCGTGCA AGATCCTTCA 180
 GGCCTTGTTT CAGTGTGACC ACGTGCAATA TACGCTGGTT CCAGTTTCTG GGTGGCAAGA 240
 ACTTGAAACT GCATTTCTTG AGCATAAAGA ACAGTTTCAT TATTTTATTC TCATAAACTG 300
 TGGAGCTAAT GTAGACCTAT TGGATATTCT TCAACCTGAT GAAGACACTA TATCTTTTGT 360
 GTGTGACACC CATAGCCAGC TCAATGTCGT CAATGTATAC AACGATACCC AGATCAAATT 420
 70 ACTCATTAAA CAAGATGATG ACCTTGAAGT TCCCGCCTAT GAAGACATCT TCAGGGATGA 480
 AGAGGAGGAT GAAGAGCATT CAGGAAATGA CAGTGATGGG TCAGAGCCTT CTGAGAAGCG 540
 CACACGGTTA GAAGAGGAGA TAGTGGAGCA AACCATGCGG AGGAGGCRGC GGCAGAGATG 600
 GGAGGCCCGG AGAAGAGACA TCCTCTTTGA CTACGAGCAG TATGAATATC ATGGGACATC 660
 75 GTCAGCCATG GTGATGTTTG AGCTGGCTTG GATGCTGTCC AAGGACCTGA ATGACATGCT 720
 GTGGTGGGCC ATCGTTGGAC TAACAGACCA GTGGGTGCAA GACAAGATCA CTCAAATGAA 780
 ATACGTGACT GATGTTGGTG TCCTGCAGCG CCACGTTTCC CGCCACAACC ACCGGAACGA 840
 GGATGAGGAG AACACACTCT CCGTGGACTG CACACGGATC TCCTTTGAGT ATGACCTCG 900
 CCTGGTGCTC TACCAGCACT GGTCCCTCCA TGACAGCCTG TGCAACACCA GCTATACGCG 960
 AGCCAGGTTT AAGCTGTGGT CTGTGCATGG ACAGAAGCGG CTCAGGAGT TCCTTGAGA 1020
 80 CATGGGTCTT CCCTGAAGC AGGTGAAGCA GAAATTCCAG GCCATGGACA TCTCCTTGAA 1080
 GGAGAATTTG CGGGAATGA TTGAAGAGTC TGCAAAATAA TTTGGGATGA AGGACATGCG 1140
 CGTGACAGCT TTCAGCATTC ATTTTGGGTT CAAGCACAAG TTTCTGCGCA GCGACGTGGT 1200
 CTTTGCCACC ATGTCTTTGA TGGAGAGCCC CGAGAAGGAT GGCTCAGGGA CAGATCACTT 1260
 CATCCAGGCT CTGACAGCGT TCTCCAGGAG TAACCTGGAC AAGCTGTACC ATGGCCTGGA 1320
 85 ACTGCCAAG AAGCAGCTGC GAGCCACCCA GCAGACCACT GCCAGCTGCC TTTGCACCAA 1380
 CCTCGTCTC TCCAGGGGCG CTTCCTGTA CTGCTCTCTC ATGGAGGGCA CTCAGATGT 1440
 CATGCTGTTT TCTAGGCCGG CATCCCTAAG CCTGCTCAGC AAACACCTGC TCAAGTCTCT 1500
 TGTGTGTTCC ACAAGAACC GCGCTGCAA ACTGCTGCCC CTGGTGATGG CTGCCCCCT 1560

GAGCATGGAG CATGGCACAG TGACCGTGGT GGGCATCCCC CCAGAGACCG ACAGCTCGGA 1620
 CAGGAAGAAC TTTTGGGA GGGCGTTTGA GAAGGCACCG GATCCCGGAT 1680
 GCTGCACAAC CATTTTGACC TCTCAGTAAT TGAGCTGAAA GCTGAGGATC GGAGCAAGTT 1740
 TCTGGACGCA CTATTTCCTC TCTGTCTCTA GGAATTTGAT TCTTCCAGAA TGACCTTCTT 1800
 ATTTATGTAA CTGGCTTTCA TTTAGATTGT AAGTTATGGA CATGATTTGA GATGTAGAAG 1860
 CCATTTTITA TTAATAAAA TGCTTATTTT AGGCTCCGTC CCCAAAAAAA AAAAAAAA 1920
 AAAAAAAA AA

Seq ID NO: 253 Protein sequence:
 Protein Accession #: NP_003495.1

1 11 21 31 41 51
 MFVSDFRKEF YEYVQSQRVL LFVADVDAL CACKILQALF QCDHVQYTLV PVSGWQBLET 60
 AFLEHKEQFH YFILLINGAN VDLLDILQPD EDTIPFVCDT HRPVNVVNVY NDTQIKLLIK 120
 QDDLEVPAY EDIFRDEED EEHSGNDS DG SEPSEKTRRL EEEIVEQTM RRRREWEAR 180
 RRDILFDYEQ YEYHGTSSAM VMFELAWMLS KDLDNMLWNA IVGLTDQWVQ DKITQMKYVT 240
 DVGVLQRHVS RHNHRNDEDE NTLSDVCTRI SFEDYDLRLVL YQHWSLEDSL CNTSYTAARF 300
 KLVSVHGGKR LQEFLLAMGL PLKQVKQKFP AMDISLKENL REMIEESANK FGMKDMRVQT 360
 FSIHFGPKHK FLASDVVFAT MSLMESPEKD GSGTDHFIQA LDSLRSNLN KLYHGLELAK 420
 KQLRATQOTI ASCLCTNLVI SQGPFYLCSL MEGTPDVMLF SRPASLSLLS KHLKSFVCS 480
 TKNRCKLLP LVMAAPLSME HGTVTVVGIP PETDSSDRKN FFGRAFEKAA ESTSSRMLHN 540
 HPDLVIELK AEDRSKFLDA LISLLS

Seq ID NO: 254 DNA sequence
 Nucleic Acid Accession #: NM_022337
 Coding sequence: 48..683

1 11 21 31 41 51
 GGCTGCGCTT CCTGGTCAG GCACGGCAGC TCTGGCCGGC CGCCAGGATG CAGGCCCGCG 60
 ACAAGGAGCA CCTGTACAAG TTGCTGGTGA TTGGCGACCT GGGCGTGGG AAGACCACTA 120
 TCATCAAGCG CTACGTGCAC CAGAACTTCT CCTCGCACTA CCGGGCCACA ATCGGCGTGG 180
 ACTTCGCGCT CAAGGTGCTC CACTGGGACC CGGAGACTGT GGTGCGCCTG CAGCTCTGGG 240
 ATATPGCAGG TCAAGAAAGA TTTGAAACA TGACGAGGGT CTATTACCGA GAAGCTATGG 300
 GTGCAATTTAT TGTCTCGAT GTCAACAGGC CAGCCACATT TGAAGCAGTG GCAAAGTGGG 360
 AAAATGATTT GGAATCCAAG TTAAGTCTCC CTAATGGCAA ACCGCTTCA GTGCTTTTGT 420
 TGGCCAAACA ATGTGACGAG GGAAGGATG TGCTCATGAA CAATGGCCTC AAGATGGACC 480
 AGTTCTGCAA GGAGCAGCGT TTGCTAGGAT GGTTTGAAAC ATCAGCAAAG GAAATATATA 540
 ACATTGATGA AGCTCCAGA TGCTGTGTA AACACATACT TGCAATGAG TGTGACCTAA 600
 TGGAGTCTAT TGAGCCGGAC GTCGTGAAGC CCCATCTCAC ATCAACCAAG GTTGCACGCT 660
 GCTCTGGCTG TGCCAAATCC TAGTAGGCAC CTTTGTGTTG GTCTGTTAGG AATGACCTCA 720
 TTGTTCCACA AATTGTGCTT CTATTTTAC CATTTTGGGT AAACGTCAGG ATAGATATAC 780
 CACATGTGGC AAGCCAAAGA TCTATGCCTC TGTTTTTCAT ATGAGAGAGA AATAGCAAT 840
 GTTCTTCTTA TGCTTCTCTC ACCATCATCA CAGTGTTCAC AAACCTTTGA AAATATTTAG 900
 TCTGTACCAA ACTTCTGTCA TGTAGCTGAC CAAATCTCTG CAGGGCCACA GTCCGCACTG 960
 TTATTTGCTT CTTTAAATCA GCAAAGGCTT CAAGTCTTAA AATAAAGGG GAGAAGAAACA 1020
 AACTAGCTGT CAAGTCAAGG ACTGGCTTTC ACCTTGCCCTT GGTGTCTTTT TCCAGATTTC 1080
 AATATATTCT CTGATGGCCT GACAGGCCTA TTAAGTAGAT GTGATATTTT CTTCACAGAT 1140
 GACCTCCATT TACCTGCTCA CTAAGAGTTG CCTCTGAGTT AGCTCTTTGG AATCGTGAAC 1200
 ACAGGTGTGC TATATTGTCC TTGTCTTAAC TGTCACTTGC CATGGCCTGA ATGTTGGCTT 1260
 AACTGAATAT TGTATGAAA GACATGCCTC CATATGTGCC TTTCTGTTAG CTCTCTTTGA 1320
 CTCAAGCTGT GGGCTCCTC TATACATGCT ATACATGTAA TATATATTAT ATATATTTT 1380
 GCAAGTGAAAC AATAAACAT TAAAGATAA AA

Seq ID NO: 255 Protein sequence:
 Protein Accession #: NP_071732

1 11 21 31 41 51
 MQAPHKEHLY KLVIGDLGV GKTSIIKRYV HQNPSSHRYA TIGVDFALKV LHWDPETVVR 60
 LQLWDIAGQE RFGNMTRVYY REAMGAFIVF DVTRPATFEA VAKWKNLDS KLSLPLNGKPV 120
 SVVLLANKCD QGKDVLMNNG LKMDQFCKEH GPVGFETSA KENINIDEAS RCLVKHILAN 180
 ECDLMESIEP DUVKPHLTST KVASCSCGAK S

Seq ID NO: 256 DNA sequence
 Nucleic Acid Accession #: NM_016321
 Coding sequence: 25..1464

1 11 21 31 41 51
 GGAACCGCCC GCTGCCAGCC CGGCCAGGCA CCCCTGCAGC ATGGCCCTGGA ACACCAACCT 60
 CCGCTGGCGG CTGCGCTGCA CCTGCCTGCT CCTGCAGGTG ATTATGGTGA TTCTCTTCGG 120
 GGTGTTCTGT CGCTACGACT TCGAGGCCGA CGCCCACTGG TGGTCAGAGA GGACGCACAA 180
 GAACTTGAGC GACATGGAGA ACGAATTTCTA CTATCGCTAC CCAAGCTTCC AGGACGTGCA 240
 CGTGAATGTC TTGCTGGGCT TCGGCTTCTC CATGACTTTC CTGCAGCGCT ACGGCTTCAG 300
 CGCCGTGGGC TTCAACTTCC TGTGGCAGC CTTCGGCATC CAGTGGGCGC TGCTCATGCA 360
 GGGCTGGTTC CACTTCTTAC AAGACCGCTA CATCGTCGTG GGCCTTGGG GCAATTCAG 420
 CGCTGACTTC TGGTGGGCTT CTGTCTGCGT GGCCTTGGG GCAATTCAG GTAAAGTCAG 480
 CCCCATTGAC CTGCTCATCA TGACTTTCTT CCAAGTGACC CTCTTCGCTG TGAATGAGTT 540
 CATCTCTCTT AACCTGCTAA AGGTGAAGGA TGCAGGAGGC TCCATGACCA TCCACACATT 600
 TGGCGCTTAC TTTGGGCTCA CAGTGACCGG GATCCTCTAC CGACGCAACC TAGAGCAGAG 660
 CAAGGAGAGA CAGAAATCTG TGTACCACTG GGACCTCTTT GCCATGATTG GCACCTCTT 720
 CCTGTGGATG TACTGGCCCA GCTTCAACTC AGCCATATCC TACCATGGGG ACAGCCAGCA 780
 CCGAGCCGCC ATCAACACCT ACTGCTCTT GGCAGCCTGC GTGCTTACCT CGGTGGCAAT 840

ATCCAGTGCC CTGCACAAGA AGGGCAAGCT GGACATGGTG CACATCCAGA ATGCCACGCT 900
 CGCAGGAGGG GTGGCCGTGG GTACCGCTGC TGAGATGATG CTCATGCCTT ACGGTGCCCT 960
 CATCATCGGC TTCGTCTGCG GCATCATCTC CACCTGGGT TTTGTATACC TGACCCCAT 1020
 CCTGGAGTCC CGGCTGCACA TCCAGGACAC ATGTGGCATT AACAACTCTG ATGGCATTCC 1080
 TGGCATCATA GCGGCGATCG TGGGTGCTGT GACAGCGGCC TCGGCCAGCC TTGAAGTCTA 1140
 TGGAAAAGAA GGGCTTGTC ATTCCTTTGA CTTCCTTGA ACCCTGGCCA TGGCCCTGAT 1260
 AAGAACACAG GGAAGTTTCC AGATTATGG TCTCTTGGT ACCCTGGCCA TGGCCCTGAT 1260
 GGGTGGCATC ATTGTGGGCG TCACTTTGAG ATTACCATC TGGGGACAA CTTCAGATGA 1320
 GAACGTCTTT GAGGATGCGG TCTACTGGGA GATGCCTGAA GGAACAGCA CTGTCTACAT 1380
 CCCTGAGGAC CCCACCTTCA AGCCCTCAGG ACCCTCAGTA CCCTCAGTAC CCATGGTGTG 1440
 CCCACTACCC ATGGCTTCTT CGGTACCCCTT GGTACCCCTAG GCTCCAGGG CAGGTGAGGA 1500
 GCAGGCTCCA CAGACTSTCC TGGGGCCCG AGGAGCTGGT GCTGACCTAG CTAGGGATGC 1560
 AAGAGTGAGC AAGCAGCACC CCCACCTGCT GGCTTGGCCT CAAGGTGCTC CCACCCCTGC 1620
 CCTCCCTCTT ATCCCGGGG GTCTGMCCTGA GAATGGAGAA GGAGAAGCTA CAAAGTGGGC 1680
 ATCCAAGCCG GGTCTGCGCT GCAGAACTTC TGCTCTGCTC TGGGGTCTTG GCCACATTGG 1740
 AGAAAAACAG GCTCAAAGTG GGGCTGGGAC CTGGTGGGTG AACCTGAGCT CTCACAGGAG 1800
 ACAACTTAGC TGCCAGTAC CACCTATGAG GCTCTTCTAC CCCGTGCTC CACCTCGGCC 1860
 AGCATCTCCT ATGCTCCCTG GGTCCCGCAG ACCTCTCTGT GTTGTGTGCG TGGCAGCCTC 1920
 CAGGAATAAA CATTCTTGTG GTCCTTTGTA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 257 Protein sequence:
Protein Accession #: NP_057405

1 11 21 31 41 51
 MAWNTNLRWR LPLTCLLLQV IMVILEGVFV RYDFEADAHW WSEKTHKNLS DMENEFYRY 60
 PSFQDVHVMV FVGFGLMTF LQRYGPSAVG FNFLAAPGI QWALLMQGW HFLQDRYIVV 120
 GVENLINADF CVASVCVAFG AVLKGVSPQI LLIMTFQVIT LFAVNEFILL NLLKVKDAGG 180
 SMTHTTFGAY FGLTVTRILY RNLBQSKER QNSVYQSDLF AMIGTLFLWM YWPSFNSAIS 240
 YHGSQHRRA FVYCSLAAC VLTSSVAISSA LHKKGKLDLV HIQNTATLAG VAVGTAAEMM 300
 LMPYGLIIG INTCGIISTLG FVYLTPLFES RLHIQDTGCI NNHIGIPGII GGIVGAVTAA 360
 SASLEVYKKE GLVHSPDFQG FNGDWTARTQ GKFIQYGLLV TLMALMGGI IVGLILRLPF 420
 WGQPSDENCF EDVAVWEMPE GNSTVYIPED PTFKPSGSPV PSVPMVSPLP MASSVPLVP

Seq ID NO: 258 DNA sequence
Nucleic Acid Accession #: NM_002358.2
Coding sequence: 75..692

1 11 21 31 41 51
 GGGAAAGTGCT GTTGGAGCCG CTGTGGTTGC TGTCCGCGGA GTGGAAGCGC GTGCTTTTGT 60
 TTGTGTCCCT GGCATGCGCG CTGCAGCTCT CCCGGGAGCA GGAATCACC CTGCGCGGGA 120
 GCGCGAAAT CGTGGCCGAG TTCTTCTCAT TCGGCATCAA CAGCATTTTA TATCAGCGTG 180
 GCATATATCC ATCTGAAACC TTTACTCGAG TGCAGAAATA CGGACTCACC TTGCTGTGTA 240
 CTACTGATCT TGAGCTCATA AAATACTTAA ATAATGTGGT GGAACAACTG AAAGATTGGT 300
 TATACAAGTG TTCAGTTCAG AAAGTGGTTG TAGTTATCTC AAATATTGAA AGTGGTGAGG 360
 TCCTGGAAG ATGGCAGTTT GATATTGAGT GTGACAAGAC TGCAAAAGAT GACAGTGAC 420
 CCAGAGAAAA GTCTCAGAAA GCTATCCAGG ATGAAATCCG TTCAGTGATC AGACAGATCA 480
 CAGCTACGGT GACATTCTG CCACTGTGGG AAGTTTCTTG TTCATTGAT CTGCTGATTT 540
 ATACAGACAA AGATTGTGGT GTACCTGAAA AATGGGAAGA GTCGGGACCA CAGTTTATTA 600
 CCAATTCTGA GGAAGTCCCG CTTCGTTTCT TACTACTTAC AATCCACAAA GTAAATAGCA 660
 TGGTGGCCCT CAAAATCTCT GTCAATGACT GAGGATGACA TGAGGAAAAT AATGTAATTG 720
 TAATTTTGAA ATGTGGTTTT CCGTGAATCA GGTCTATCTA AGTTGATATG TTTTATTCTA 780
 TTGGTTAATT TTTACATGGA GAAACCAAAA ATGATACTTA CTGAAGTGTG TGTAATTGTT 840
 CCTTTATTTT TTTGGTACCT ATTGACTTA CCATGGAGTT AACATCATGA ATTTATTGCA 900
 CATTGTCAA AAGGAACCGG GAGGTTTTTT TGTCAACATT GTGATGTATA TTCCTTTGAA 960
 GATAGTAATC GTAGATGGAA AACTTGTGCT TATAAGCTA GATGCTTCC TAAATCAGAT 1020
 GTTTTGGTCA AGTAGTTTGA CTCAGTATAG GTAGGGAGAT ATTTAAGTAT AAAATACAAC 1080
 AAAGGAAGTC TAAATATTCA GAATCTTTGT TAAGGTCCTG AAAGTAACTC ATAATCTATA 1140
 AACAAAGAAA TATTGCTGTA TAGCTCCTTT TGACCTTCAT TTCATGTATA GTTTTCCCTA 1200
 TTGAATCAGT TTCAATTTAT TTGACTTTAA TTTATGTAAC TTGAACCTAT GAAGCAATGG 1260
 ATATTGTGAC TGTTTAATGT TCTGTGATAC AGAACTCTTA AAAATGTTTT TTCATGTGTT 1320
 TTATAAAATC AAGTTTAAAG TGAAAGTGAG GAAATAAAGT TAAGTTTGTG TTAATAAAAA 1380
 AAAAAAAAAA

Seq ID NO: 259 Protein sequence:
Protein Accession #: NP_002349.1

1 11 21 31 41 51
 MALQLSREQG ITRLSARIV AEFFSFGINS ILYQRGIYPS EFTFRVQKYG LTLVTTDLE 60
 LKYLNNVVE QKDWLYKCS VQKLVVVISN IESGEVLERW QFDIECDKTA KDDSAPREKS 120
 QRAIQDEIRS VIRQITATVT FLPLLEVSCS FDLIYTDKD LVVPEKWEEB GPQFITNSEE 180
 VRLRSFTTTI HKVNSMVAYK IPVND

Seq ID NO: 260 DNA sequence
Nucleic Acid Accession #: NM_001211
Coding sequence: 43..3195

1 11 21 31 41 51
 AAAGGCCGTC AGCAGGACGA GGACCTGAGC CAGGAATGCA GGATGGCGGC GGTGAAGAAG 60
 GAAGGGGGTG CTTGAGTGA AGCCATGTCC CTGGAGGGAG ATGAATGGGA ACTGAGTAAA 120
 GAAAATGTAC AACCTTTAAG GCAAGGGCGG ATCATGTCCA CGCTTCAGGG AGCACTGGCA 180
 CAAGAATCTG CCTGTAACAA TACTCTTCAG CAGCAGAAAC GGSCATTGTA ATATGAAATT 240

Seq ID NO: 261 Protein sequence:
Protein Accession #: NP_001202

Seq ID NO: 262 DNA sequence
Nucleic Acid Accession #: NM_003784
Coding sequence: 365..1507

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GTCTACTTAT	CAATAAGCAG	CTGCCTGTGC	AGAGTGCAGG	CTGCACCTTT	GGACAGCCTT	60
TAAAACTGAA	TTCTCAGAAT	TTTAGAACAA	ATTTTGTGCT	AGAAATGCTG	ACTTTGGTTC	120
ATTAGGTAGT	GGTAAACACG	GCTCCCTTCG	AAGCTCTCCT	TCATCACCTT	CCTAAGTGCA	180
TGTACAGGGA	AGCTCTCCTT	CATCACCTTC	CTAAGTGCAT	GGGGGAAAT	ACCTAGGGCT	240
CAACAGTCTT	GAGAAGTGTG	GAAACATTTT	CTTTGTGAGT	GAGAACAGAT	CACCTAGAGA	300
AAGGAAACCA	GATTCCCATC	ACTGCTTCTG	GGTATCAGAT	GCTAGCGCTG	CACTCCATTT	360
TGCAATGGCC	TCCTTGCTG	CAGCAAATGC	AGAGTTTTCG	TTCAACCTGT	TCAGAGAGAT	420
GGATGACAA	CAAGGAAATG	GAAATGTGTT	CTTTTCTCTT	CTGAGCCTCT	TCGCTGCCTT	480
GGCCCTGGTC	CGCTTGGGCG	CTCAAGATGA	CTCCCTCTCT	CAGATTGATA	AGTTGCTTCA	540
TGTTAACACT	GCCTCAGGAT	ATGGAACTC	TTCTAATAGT	CAGTCAGGGC	TCCAGTCTCA	600
ACTGAAAAGA	GTTTTTCTG	ATATAAATGC	ATCCACAAG	GATTATGATC	TCAGCATTGT	660
GAATGGGCTT	TTTGCTGAAA	AAGTGTATGG	CTTTCATAAG	GACTACATTG	AGTGTGCCGA	720
AAAATTATAC	GATGCCAAA	TGGAGCGAGT	TGACTTTACG	AATCATTTAG	AAGACACTAG	780
ACGTAATATT	AATAAGTGGG	TTGAAAATGA	AACACATGGC	AAAATCAAGA	ACGTGATTGG	840
TGAAGGTGGC	ATAAGTTCAT	CTGCTGTAAT	GGTGTGGTGG	AATGCTGTGT	ACTTCAAAGG	900
CAAGTGGCAA	TCAGCCTTCA	CCAAGAGCGA	AACCATAAAT	TGCCATTTC	AATCTCCCAA	960
GTGCTCTGGG	AAGGCAGTCG	CCATGATGCA	TCAGGAACGG	AAGTTCAATT	TGCTGTATT	1020
TGAGGACCCA	TCAATGAAGA	TTCTTGAGCT	CAGATACAA	GGTGGCATAA	ACATGTACGT	1080
TCTGTGCTCT	GAGAAATGAC	TCTCTGAAAT	TGAAAACAAA	CTGACCTTTC	AGAATCTAAT	1140
GGAAATGGAC	AATCCAAGGC	GAATGACCTC	TAAGTATGTT	GAGGTATTTT	TTCTCAGTT	1200
CAAGATAGAG	AAGAATTATG	AAATGAAACA	ATATTGAGA	GCCTAGGGC	TGAAAGATAT	1260
CTTTGATGAA	TCCAAAGCAG	ATCTCTCTGG	GATTGCTTCG	GGGGTCTGTC	TGTATATATC	1320
AAGGATGATG	CACAAATCTT	ACATAGAGGT	CACTGAGGAG	GGCACCGAGG	CTACTGCTGC	1380
CACAGGAAGT	AATATTGTAG	AAAAGCAACT	CCCTCAGTCC	ACGCTGTTTA	GAGCTGACCA	1440
CCCATTCCTA	TTTGTATCA	GGAAGGATGA	CATCATCTTA	TTCAAGTGGA	AAGTTTCTTG	1500
CCCTTGAAAA	TCCAAATGGT	TTCTGTATTA	GCAGTCCCCA	CAACATCAAA	GRACCACCAC	1560
AAGTCAATAG	ATYTGRGTTT	AATTTGAAAA	ATGTGGTGT	TCCTTTGAGT	TTATTTCTTC	1620
CTAAGCATGG	TCAGCAGATG	ACACTGGTGA	CTTGACCTTT	CCTAGACACC	TGGTTGATTG	1680
TCCTGATCCC	TGCTCTTAGC	ATTCTACCAC	CATGTGTCTC	ACCCATTTC	AATTTCATTG	1740
TCCTTTCTTC	CACGCTCATT	TCTATCATT	TCCCCCATGA	CCCGTCTGGA	AATTATGGAG	1800
RGTGCTCAAC	TGGTAAGGAG	AACGTAGAAG	TAGCCCTAGG	GATCCTTTTT	GAACCTCTAC	1860
AGTTATCGCA	GATATTCTAG	CTTCATTGTA	AGCAATCTAG	GAAATAAGCC	CTGCTGCTTT	1920
CTAGAAATAA	GTGTGAAGGA	TAAATTTTCT	TGTTTGACCT	ATGAAAGATT	TAGAGTTTAC	1980
CTTCATATGT	TTGATTTTAA	ATCAGTGTAT	AATCTAGATG	GTAAAAAATG	TGAAATTTGG	2040
ATTAGGGAG	NKLTFFQAL	TTTCATTAAT	GCTTTCAATT	GACAAATTTT	GGCCTTTCTT	2100
TGATAAGACA	ATATGTACAT	GTTTTTTC	ATATTAAAGA	TCTTTTAACT	GTTGGCAGTT	2160
GTATCTTACA	GAATCATATT	TCATATGCTG	TGTAGTTTAT	AAGTTTTTCC	TCTATTTATC	2220
AGAAATAAGA	AATACAACAT	ACCTGTAAA				

Seq ID NO: 263 Protein sequence:
Protein Accession #: NP_003775

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55

1	11	21	31	41	51	
MASLAAANAE	FCFNLFREMD	DNQNGNVFF	SSLSLFAALA	LVRLGAQDD	LSQIDKLLHV	60
NTASGYGNSS	NSQSQLSQL	KRVFSDINAS	HKDYDLSIVN	GLFAEKVYGF	HKDYIECAEK	120
LYDAKVERVD	FTNHLEDTRR	NINKWVENET	HGKIKNVIGE	GGISSAVMV	LVNAVYFKGK	180
WQSAFTKSET	INCHFKSPKC	SGKAVAMMHQ	ERKFNLVSB	DPSMKILELR	YNGGINMYVL	240
LPENDLSEIE	NKLTFFQAL	WTNPRRMTSK	VVEVFPPQFK	IEKNYEMKQY	LRALGLKIDF	300
DESKADLSGI	ASGGRLYISR	MMHKSIVIEV	EEGTATAAT	GSNIVEKQLP	QSTLFRADHP	360
FLFVIRKDDI	ILPSGKVSCP					

Seq ID NO: 264 DNA sequence
Nucleic Acid Accession #: AB052906
Coding sequence: 74-814

60
65
70
75
80
85

1	11	21	31	41	51	
AAAACCTTGA	GGTGATTCAT	CTTCCAGGCT	CTCCTTCCAT	CAAGTCTCTC	CTCCCTAGCG	60
CTCTGGGTCC	TTAATGGCAG	CAGCCGCGCG	TACCAAGATC	CTTCTGTGCC	TCCCGCTTCT	120
GCTCCTGCTG	TCCGGCTGGT	CCCGGCTGG	GCGAGCCGAC	CCTCACTCTC	TTTGCTATGA	180
CATCACCGTC	ATCCCTAAGT	TCAGACCTGG	ACCACGGTGG	TGTGCGGTTC	AAGGCCAGGT	240
GGATGAAAG	ACTTTTCTTC	ACTATGACTG	TGGCAACAAG	ACAGTCAAC	CTGTCACTCC	300
CCTGGGGAAG	AACTAAATG	TCACAACGGC	CTGGAAGCA	CAGAACCAG	TACTGAGAGA	360
GGTGGTGGAC	ATACTTACAG	AGCAACTGCG	TGACATTGAG	CTGGAGAATT	ACACACCCAA	420
GGAACCCCTC	ACCCTGCAGG	CCAGGATGTC	TTGTGAGCAG	AAAGCTGAAG	GACACAGCAG	480
TGGATCTTGG	CAGTTCAGTT	TCGATGGGCA	GATCTTCTCT	CTCTTTGACT	CAGAGAAGAG	540
AATGTGGACA	ACGTTTCATC	CTGGAGCCAG	AAAGATGAAA	GAAAAGTGGG	AGAATGACAA	600
GGTTGTGGCC	ATGTCCTTCC	ATTACTTCTC	AATGGGAGAC	TGTATAGGAT	GGCTTGAGGA	660
CTTCTTGATG	GGCATGGACA	GCACCCCTGA	GCCAAGTGCA	GGAGCACCAC	TGCCCATGTC	720
CTCAGGCACA	ACCAACTCA	GGGCCACAGC	CACCACCTTC	ATCCTTTGCT	GCCTCCTCAT	780
CATCCTCCCC	TGCTTCACTC	TCCTGGCAT	CTGAGGAGAG	TCCTTTAGAG	TGACAGGTTA	840
AAGCTGATAC	CAAAAGGCTC	CTGTGAGCAC	GGTCTTGATC	AAACTCGCCC	TTCTGTCTGG	900
CCAGCTGCCC	ACGACCTACG	GTGTATGTCC	AGTGGCCTCC	AGCAGATCAT	GATGACATCA	960
TGGACCAAT	AGCTCATTC	CTGCCCTGAT	TCCTTTTGCC	AACAATTTTA	CCAGCAGTTA	1020
TACCTAACAT	ATTATGCAAT	TTTCTCTTGG	TGCTACCTGA	TGGAATTCCT	GCACCTTAAG	1080
TTCTGGCTGA	CTAACAAAGA	TATATCATTT	TCTTTCTTCT	CTTTTGTGTT	GGAAAATCAA	1140
GTACTTCTTT	GAATGATGAT	CTCTTCTCTG	CAAATGATAT	TGTCAGTAAA	ATAATCACGT	1200
TAGACTTCAG	ACCTCTGGGG	ATTCTTTCGG	TGTCCTGAAA	GAGAATTTT	AAATTATTTA	1260
ATAAGAAAAA	ATTATATATTA	ATGATTGTTT	CCTTTAGTAA	TTTATTGTTT	TGTACTGATA	1320
TTTAAATAAA	GAGTCTTATT	TCCAAAAAAA	AAAAAAA	A		

Seq ID NO: 265 Protein sequence:
Protein Accession #: BAB61048.1

1 11 21 31 41 51
 5 MAAAAATKIL LCLPLLLLLS GWSRAGRADP HSLCYDITVI PKFRPGPRWC AVQGGVDEKT 60
 FLHYDCGNKT VTPVSPGLKK LNVTTAWKAQ NPVLREVVDI LTEQLRDIQL ENYTPKEPLT 120
 LQARMSCEQK AEGHSSGSQW F5FDGQIFLL FDSEKRMWTT VHPGARKMKE KWENDKVVM 180
 SFHYFSMGDC IGWLEDFLMG MDSTLEPSAG APLAMSSGTT QLRATATTLL LCCLLIILPC 240
 FILPGI

Seq ID NO: 266 DNA sequence
 Nucleic Acid Accession #: XM_084853.1
 Coding sequence: 127-444

1 11 21 31 41 51
 15 ATTGATGATA TATTAAACGA AATCAAATTT GGTGAATATG TGGACACTGG AAAGCTAATC 60
 GACAAGATCA ACTTACCAGA TTCTCTAAAA GTGTACCTTA ACCACAAGCC ACCTTTTGGT 120
 AACACCATGA GTGGCATCCA CAAGAGCTTT GAGGTGCTCG GTTATACCAA CTCCAAGGG 180
 AAAAAGGCCA TTGGAAGAGA GGAATCTCTG AGACTGCTCG TTTACTAAAG TGAGCATATG 240
 20 ACGGAGGAGG AGATGTTGGA TTGCTTTGCT TCACTGTTTG GCCTGAATCC CGAGGGATGG 300
 AAATCCGAGC CTGCAACCTG CTCCGTCAAA GGTTCAAGAA TTGCTCTGA AGAAGAACTT 360
 CCAGACGAAA TCACTGCAGA AATATTGCGG ACTGAAATTC TTGGCTTAAC CATTTCAGAA 420
 GATTCCGGCC AGGATGGTCA GTGAAGTTAC CAGGAATGTT TAAAGCACA AGGACTTTGG 480
 GTGTGTGTGC ATGCACATGT GTGTGTTTTC CATGAGGCAC TGCTTTTAT GCATTTCCCT 540
 25 CCCCCTCTC ATCTTTAGAA CATTTAGACA TTAAAGCAAG TTTCTGGTGA GCAATG

Seq ID NO: 267 Protein sequence:
 Protein Accession #: XP_084853.1

1 11 21 31 41 51
 30 MSGIHKSEFV LGVTNSKGGK AIRREDFLRL LVTKEHMT EEMLDCAFSL FGLNPEGWKS 60
 EPATCSVKGS EICLEELPD EITAEIPATE ILGLTISED GQDQG

Seq ID NO: 268 DNA sequence
 Nucleic Acid Accession #: NM_001898
 Coding sequence: 57-482

1 11 21 31 41 51
 40 GGCTCTCACC CTCCTCTCCT GCAGCTCCAG CTTTGTGCTC TGCTCTGAG GAGACCATGG 60
 CCCAGTATCT GAGTACCCTG CTGCTCCTGC TGGCCACCCT AGCTGTGGCC CTGGCCTGGA 120
 GCCCAAGGA GGAGGATAGG ATAATCCCGG GTGGCATCTA TAACGCAGAC CTCAATGATG 180
 45 AGTGGGTACA GCGTGCCCTT CACTTCGCCA TCAGCGAGTA TAACAAGGCC ACCAAAGATG 240
 ACTACTACAG ACCTCCGCTG CCGGTACTAA GAGCCAGGCA ACAGACCGTT GGGGGGGTGA 300
 ATTACTTCTT CGAGCTAGAG GTGGGCGCGA CCATATGTAC CAAGTCCCGA CCCAACTTGG 360
 ACACCTGTGC CTTCCATGAA CAGCCAGAAC TGCAGAAGAA ACAGTTGTGC TCTTTCGAGA 420
 TCTACGAAGT TCCTTGGGAG AACAGAAGGT CCCTGGTGAA ATCCAGGTGT CAAGAATCCT 480
 50 AGGGATCTGT GCCAGGCCAT TCGCACCAGC CACCACCACC TCCACCCCCC TGTAGTGCTC 540
 CCACCCCTGG ACTGGTGGCC CCCACCCTGC GGGAGGCCCT CCCATGTGCC TGCGCCAAGA 600
 GACAGACAGA GAAGGCTGCA GGAGTCCTTT GTTGCTCAGC AGGGCGCTCT GCCCTCCCTC 660
 CTTCTCTCTT GCTTCTAATA GCCCTGGTAC ATGTATACACA CCCCCCACC TCCTGCAATT 720
 AAACAGTAGC ATCGCC

Seq ID NO: 269 Protein sequence:
 Protein Accession #: NP_001889.1

1 11 21 31 41 51
 60 MAQYLSTLLL LLATLAVALA WSPKEEDRII PGGIYNADLN DEWVQRALHF AISEYNKATK 60
 DDYRRPLRV LRARQQTVGG VNYFFDVEVG RTICTKSQPN LDTCAPEHQ ELQKQLCSF 120
 EIEVFWENR RSLVKSRQS S

Seq ID NO: 270 DNA sequence
 Nucleic Acid Accession #: XM_093210
 Coding sequence: 13-1854

1 11 21 31 41 51
 70 ATGGCAAGCG CCGGAATCTC CTCAGCTGCC GTTTCACAAA AGAGGTACCA GGTCCGCACC 60
 AAACGAGCAC ACAAGCAGCA CCAGGAGCTG CAGAAGAAGG AGGCGGCAGC GATGGACCAG 120
 GGCAGAGGGA ATGGGGAGGG GGCATCTTAC CCTATATCTG AGGTGCGACT GCGGGACGTA 180
 GAGCGGACTG GGCCTTTCCC GTTGGCGCGT GGCCTCAATC AGGACTTCTT GCCCACGTGC 240
 75 GCCTTCAAAA CGGTAAAGAG TGCAACTGAA CGTGTGAGAC ATGGTGCAGA TAGGCTGAGA 300
 GCGCGCGGGA GAGATGCCCA TGAACCTAAG TACCCGAGCA CGCCCTCCAC TTCTACCACC 360
 ACGAGTAACA CGCCCCCCAC GGGACCGCTC TCGAGGTCCC CCAAGCCCAAG GACGCAAGGA 420
 GGAACGCCCC GGGCGCGCGC CAGCAGCGGC GGGCACCAGG CCAATGGCCA CGGAACCTAG 480
 CACTGGCAGT CCGGCTCTCT CACACGCGAG CGGTGCAGTG TGGCCGACGG AGCCTCCCGG 540
 80 GCGGAGGACC CAGCTAGGCC GTCAACCCCGG TTGCTCCACC GGAAGGGGGG ACCAGGCAAA 600
 CTGCCCAAGG CCCCGAGCCC AGGCTCCCTG GCGGAGGCCT CCGCTGGTCC CGCCAGATC 660
 ATGGCGGCCA CAGGCTCCC GAGCCATGGC TTCTGTCTCC GGAACGCCCC GCGCTCCTGG 720
 CTGTCCAGCT AG

Seq ID NO: 271 Protein sequence:
 Protein Accession #: XP_093210

1 11 21 31 41 51

MLRHGEQKRR	RARKKWDFLP	TCAPKTVRAA	TERVRHGADR	LRGGGRDAHE	LKYPDTPSTS	60
TTTSNTAPTQ	PLSRSPKPR	QGGTPRRRPA	AAGTRANGHG	TQHWQSALLT	PQACSVADGA	120
SRAEDPARPS	PRLLPRREGAP	GKLPKAPSPG	SLAEASAGLL	AHVRLQNADA	QVRSISQALP	180
PNSSVGRKEE	RFGAGQQRRA	PAPMATELST	GSRPSSHRRR	AVWPTEPPGP	RTQLEPSRPL	240
LPREGAPGKL	FKAPSPGSLA	EASAGPAQIM	AATRLPSRGP	LSGNGPASWL	SS	

Seq ID NO: 272 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..732

1	11	21	31	41	51	
GGATACTGTG	TCACCTCAAAG	TAATGGGAGG	GAGAGAGAAC	AGGGAGGGTA	GGGATGCTTT	60
TGAAAAAGCT	TTTTTCCCA	CTTTAACTT	GCTTTAGCGT	TAAGAGTACT	TACCAGCTAA	120
TAATGTGGAG	GAAATTATTC	TTTCTCATTC	GAGATTACAG	AATATATCTA	TTCACTCTGA	180
ATACCCACTT	GAAGCCTCTG	TAGAAATGTC	TCGTCCTCCG	GTTGTATTTC	TAAACCTTAC	240
ATGATTTTGT	CTTGTTTCTG	CAGTGAGAAA	TTACATCCAT	AGCAAAGACA	AAAGTCTTTT	300
TAAATTATTT	TTATTTATCT	TTCATATAGT	TCTTACAATT	TCTAAAAAAT	TAACACTCAT	360
TTAGTATCAC	AATTATATGG	AGAGGGTTTT	TTGTATTTT	AAGCATATGT	GGCTTATATA	420
AAAATTGACG	AAGTCATAGG	ACTGTCTATG	ATTGCAGCTC	TGAGAACCAA	TGCTTGAAAC	480
TTAAGCC						

Seq ID NO: 273 Protein sequence:
Protein Accession #: Eos sequence

1	11	21	31	41	51
MGGRENREGR	DAFEKAFFPT	FNLL			

Seq ID NO: 274 DNA sequence
Nucleic Acid Accession #: NM_003976.2
Coding sequence: 299-961

1	11	21	31	41	51	
CTCTGAGCTT	CTCTGAGCCT	TGTTTGCTCA	TCTGGAAAAA	GGGGATTAAA	CCATTACCT	60
CATGGAGTTG	TGAAGAATA	GCTGCAAAGC	ACCTAACACA	TAGTAAGGTT	CCCAGTGCAG	120
CTACTTCTGC	TGGTTGAGT	CTAGCTGTGT	AGGCCCTTGT	TTCTCTACCT	GGAGAAACTG	180
GGGTGGCAGG	CCGGTCCCCC	ACAAAAGATA	ACTCATCTCT	TAATTTGCAA	GCTGCCTCAA	240
CAGGAGGGTG	GGGGAACAGC	TCAACAATGG	CTGATGGGCG	CTCCTGGTGT	TGATAGAGAT	300
GGAACTTGGG	CTTGGAGGCC	TCTCCACGCT	GTCCCACTGC	CCCTGGCCTA	GGCGGCAGCC	360
TGCCCTGTGG	CCCACCTTGG	CCGCTCTGGC	TCTGCTGAGC	AGCGTCGCAG	AGGCCCTCCCT	420
GGGCTCCGCG	CCCCGCAGCC	CTGCCCTCCG	CGAAGGCCCC	CCGCTGTGCC	TGGCGTCCCC	480
CGCCGGCCAC	CTGCCGGGGG	GACGACGGCG	CCGCTGGTGC	AGTGGAGAGG	CCCGGCGGCC	540
GCCGCGCCAG	CCTTCTCGGC	CCGCGCCCCC	GCCGCTGCA	CCCCCATCTG	CTCTTCCCGG	600
CGGGGGCCGC	CGCGCGCGGG	CTGGGGGCCC	GGGCAGCGCG	GCTCGGGCAG	CGGGGGCGCG	660
GGGCTGCCGC	CTGCCCTCGC	AGCTGGTGCC	GGTGCGCGCG	CTCGGCTTGG	GCCACCGCTC	720
CGACGAGCTG	GTGCGTTTCC	GCTTCTGCGC	CGGCTCTGCG	CGCGCGCGCG	GCTCTCCACA	780
CGACCTCAGC	CTGCCCAAGC	TACTGGGCGC	CGGGGCCCTG	CGACCGCCCC	CGGGCTCCCG	840
GCCCGTCAAG	CAGCCCTGCT	GCCGACCCAC	CGGCTACGAA	CGGCTCTCCT	TCATGGACGT	900
CAACAGCAC	TGAGAAACCG	TGGACCGCCT	CTCCGCCACC	GCCTGCGGCT	GCCTGGGCTG	960
AGGGCTCGCT	CCAGGGCTTT	GCAGACTGGA	CCCTTACCGG	TGGCTCTTCC	TGCTGGGAC	1020
CCTCCCGCAG	AGTCCCACTA	GCCAGCGGCC	TCAGCCAGGG	ACGAAGGCCCT	CAAAGCTGAG	1080
AGGCCCTTAC	CGGTGGGTGA	TGGATATCAT	CCCCGAACAG	GTGAAGGGAC	AACTGACTAG	1140
CAGCCCCAGA	GGCCTCACCC	TGCGGATCCC	AGCCTAAAG	ACACCAAGAG	CCTCAGCTAT	1200
GGAGCCCTTC	GCGCTCCAG	CTCAGAGACT	CTGGCACTGG	CCAGGCCCTG	AACCTGGGAG	1260
CCCTCCTCTG	ATGAACACTA	CAGTGGCTGA	GGCATCAGCC	CCGCCCCAGG	CCCTGTAGGG	1320
ACAGCATTTG	AAGGACACAT	ATTGCAGTTG	CTTGGTTGAA	AGTGCCCTGT	CTGGAACCTG	1380
CTGTACTCA	CTCATGGGAG	CTGGCCCC				

Seq ID NO: 275 Protein sequence:
Protein Accession #: NP_003967.1

1	11	21	31	41	51	
MELGLGLST	LSHCPWRRQ	PALWPTLAAL	ALLSSVAEAS	LGSAPRSPAP	REGPPPVLAS	60
PAGHLPGGRT	ARWCSGRARR	PPFPSPRPAP	PPFPAPPSALP	RGGRAARAGG	PGSRARAAGA	120
RGCRRLRSQV	PVRALGLGHR	SDELVRFRFC	SGSCRARRSP	HDLSLASLLG	AGALRPFPFGS	180
RPVSQPCCRP	TRYEAVSFMD	VNSTWRTVDR	LSATACGCLG			

Seq ID NO: 276 DNA sequence
Nucleic Acid Accession #: NM_057091.1
Coding sequence: 783-1445

1	11	21	31	41	51	
ACTGGCCGCT	GAGAGAAGAA	TGGGTGGGAG	CAGAGAGCAG	CTGCTGCAGG	GCAGACAGCC	60
GGACCCCAAA	ATCTGCACGT	ACCAGCAGTC	AGCCGCCCCA	CGCAGGGACC	GGCTTACCCC	120
TGCTCTCCCG	CCCTCACTCA	CTTTCTCCCG	CCCTCGGCCC	GGCTCTCCAG	CTCTCTACTT	180
CGCGTGTCTA	CAAACTCAAC	TCCCGGTTTC	CGTGCTCTCT	CACCGCTCGA	GTTCTCTACT	240
CTCCATATCC	GAGGGGCCCC	TCCAGCATC	TACCCCTCTC	CCAACTCTCG	GGGACCTAGC	300
CAAGCTAGGG	GGGACTGGAT	CCGACGGGTG	GAGCAGCCAG	GTGAGCCCGG	AAAGGTGGGG	360
CGGGCGAGGG	GCGCTCCAG	CCCCACCCCG	GGATCTGGTG	ACGCTGGGGG	TGGAATTTGA	420
CACCGGACGG	CTGCGGGCGC	GGCAGGAGG	CTGCTGAGGG	ATGGAGTTGG	GCCCGGCCCC	480
CAGACAAGGC	CCGGGGGCTC	CGCCAGCAGC	AGGTCCCTCG	GGCCCCAGCC	CTCGCTGCCA	540

CCCGGGCTG GAGCCCCACA CCCGAGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC 600
 TAAAAAGAGC ACTGCCAGGT GTACAGTCCT GGGCATGCGC TGTTTGAGCT TCGGGGGAGA 660
 GCCCAGCACT GGTCCCCGGA AAGGTGCCTA GAAGAACAAG GTGCAGGACC CCGTCTGCC 720
 TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GGGCTCCTG GTGTTGATAG 780
 AGATGGAAT TGGACTTGGG GGCCTCTCCA CGCTGTCCCA CTGCCCTGG CCTAGGCGGC 840
 AGCTTGCCCT GTGGCCCAAC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT 900
 CCTTGGGCTC CGCGCCCCGC AGCCCTGCCC CCCGCGAAGG CCCCCCGCT GTCTGGCGT 960
 CCCCBCGCG CCACCTGCGG GGGGGACGCA CGGCCGCTG GTGCAGTGA AGAGCCCGC 1020
 GGCGCCGCG CCAGCCTTCT CGGCCGCGC CCCCBCGCT TGCACCCCA TCTGCTCTC 1080
 CCGCGGGGG CGCGCGCGG CGGGCTGGGG CCGCGGGCAG CCGCGCTCGG GCAGCGGGG 1140
 CGCGGGGCTG CGCCTGCGC TCGCAGCTGG TGCCTGTCG CGCGCTCGGC CTGGGCCACC 1200
 GCTCOGACGA GCTGGTGCCT TTCCGCTTCT GCAGCGGCTC CTGCGCGC GCAGCTCTC 1260
 CACACGACCT CAGCCTGGCC AGCCTACTGG GCGCCGGGGC CCTGCGACCG CCCCBCGCT 1320
 CCGCGCCCT CAGCCAGCCC TGCTGCGGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG 1380
 AGCTCAACAG CACTTGAGGA ACCGTGGACC GCCTCTCGC CACCGCTGCG GGCTGCTGG 1440
 GCTGAGGCT CGCTCCAGGG CTTTGCAGAG TGGACCTTA CCGTGGCTC TTCTGCTCT 1500
 GGACCCCTCC GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGACGGAAG GCCTCAAAGC 1560
 TGAGAGGCC CTACCGGTGG GTGATGGATA TCATCCCGA ACAGGTGAAG GACAACTGA 1620
 CTAGCAGGCC CAGAGCCCTC ACCCTGCGGA TCCAGCCCTA AAGACACCA GAGACCTCAG 1680
 CTATGGAGCC CTTGAGGCC ACTTCTACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG 1740
 GGACCCCTCC TCTGAGGAC ACTACAGTGG CTGAGGCATC AGCCCCGCC CAGGCCCTGT 1800
 AGGGACAGCA TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGCC TGTGCTGGAA 1860
 CTGGCTGTA CTCATCATG GGAGCTGGCC CC

Seq ID NO: 277 Protein sequence:

Protein Accession #: NP_003967.1

1 11 21 31 41 51
 MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
 PAGHLPGGRT ARWCSGRARR PFPQPSRPAP PFPAPPSALP RGGRAARAGG PGSRARARAAGA 120
 RGCRLRSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPFPFGS 180
 RPSVQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 278 DNA sequence

Nucleic Acid Accession #: NM_057160.1

Coding sequence: 1-714

1 11 21 31 41 51
 ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCTCTCC TCCCCAAGCC 60
 CACCTGGGGT CCTCTTTCT CCCTGAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG 120
 TGGCCCAACC TGGCGCTCT GGCTCTGCTG AGCAGCGTGC CAGAGGCCTC CCTGGGCTCC 180
 GCGCCCGCA GCCCTGCCCC CCGCGAAGGC CCCCBCGCTG TCCTGGCGTC CCCCBCGCGC 240
 CACCTGCGGG GGGGACGCAC GGGCCGCTG TGCAGTGGAA GAGCCCGCGG GCGCCCGCGC 300
 CAGCCTTCTC GGGCGCGGCC CCGCGCGCCT GCACCCCAT CTGCTCTTCC CCGCGGGGGC 360
 CGCGCGGGC GGGCTGGGG CCGGGGACG CGCGCTCGGG CAGCGGGGGC GCGGGGCTGC 420
 CGCCTGCGCT CGCAGCTGGT GCGGTGCGC GCGCTCGGCC TGGGCCACCG CTCGACGAG 480
 CTGGTGGGTT TCCGCTTCTG CAGCGGCTCC TGCCGCGCGC CGCCTCTCC ACACGACCTC 540
 AGCCTGGCCA GCCTACTGGG CGCCGGGGCC CTGCGACCGC CCCCBCGCTC CCGCCCGCTC 600
 AGCCAGCCCT GCTGCCGACC CACGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660
 ACCTGGAGAA CCGTGGACCG CACTCTCGCG ACOCCTGCG GCTGCTGGG CTGAGGGCTC 720
 GCTCCAGGGC TTTGCAGACT GGACCCCTAC CGTGGCTCT TCCTGCTGG GACCTCCCG 780
 CAGAGTCCCA TAGCCAGCG GCCTCAGCCA GGGACGAAGG CCTCAAAGCT GAGAGGCCCC 840
 TACCGGTGGG TGATGGATAT CATCCCCGAA CAGGTGAAGG GACAACCTGAC TAGCAGCCCC 900
 AGAGCCCTCA CCTTGGGAT CCCAGCCTAA AAGACACCAG AGACCTCAGC TATGGAGCCC 960
 TTTGGACCCA CTCTTCACAG ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCCT 1020
 CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCCCGCCC AGGCCCTGTA GGGACAGCAT 1080
 TTGAAGGACA CATATTGCAG TTGCTTGGTT GAAAGTGCT GTGCTGGAAC TGGCCTGTAC 1140
 TCACTCATGG GAGCTGGCCC C

Seq ID NO: 279 Protein sequence:

Protein Accession #: NP_476501.1

1 11 21 31 41 51
 MPGLISARQ FLLEVLPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SSVAEASLGS 60
 APRSPAPREG PFPVLASPAH HLPGRRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG 120
 RAARAGGPGS RARAAGARG RLRSQLVFVR ALGLGHRSD E LVRFRFCSSG CRRARSPHDL 180
 SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG

Seq ID NO: 280 DNA sequence

Nucleic Acid Accession #: NM_057090.1

Coding sequence: 29-715

1 11 21 31 41 51
 CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACCTGGA CTTGGAGGCC TCTCCACGCT 60
 GTCCCACTGC CCTGGCCTA GCGCGCAGGC TCCACTTGGT CTCTCCGCGC AGCCTGCCCT 120
 GTGGCCCAAC CTGGCGGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT CCTTGGGCTC 180
 CGCGCCCGC AGCCCTGCCC CCGCGAAGG CCCCBCGCT GTCTGGCGT CCCCBCGCGC 240
 CCACCTGCGG GGGGACGCA CCGCCGCTG GTGCAGTGA AGAGCCCGCG GCGCGCGGCC 300
 GCAGCCTTCT CGGCCGCGC CCGCGCGGCC TGCACCCCA TCTGCTCTC CCGCGGGGG 360
 CGCGCGGGC GGGCTGGGG GCGCGGGCAG CGCGCTCGG GCAGCGGGGG CGCGGGGCTG 420
 CGCGCTGCGC TCGCAGCTGG TGCCTGTCG CGCGCTCGGC CTGGGCCACC GCTCCGACGA 480
 GCTGGTGCCT TTCCGCTTCT GCAGCGGCTC CTGCGCGCGC GCGCGCTCTC CACACGACCT 540
 CAGCCTGGCC AGCCTACTGG GCGCCGGGGC CTGCGACCG CCCCBCGCT CCGCGCGCT 600
 CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG ACCTCAACAG 660

CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCCTGG GCTGAGGGCT 720
 CGCTCCAGGG CTTTGCAGAC TGGACCCTTA CCGGTGGCTC TTCTGCCTGG GGACCCTCCC 780
 GCAGAGTCCC ACTAGCCAGC GGCTCAGCC AGGGACGAAG GCCTCAAAGC TGAGAGGGCC 840
 CTACCGGTGG GTGATGATA TCATCCCGA ACAGGTGAAG GGACAACTGA CTAGCAGCCC 900
 CAGAGCCCTC ACCCTGGGGA TCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC 960
 CTTGGAGCCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAAACCTG GGACCCTCTC 1020
 TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCGCC CAGGCCCTGT AGGGACAGCA 1080
 TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGCC TGTGCTGGAA CTGGCCTGTA 1140
 CTCATCATG GGAGCTGGCC CC

Seq ID NO: 281 Protein sequence:
Protein Accession #: NP_476431.1

1 11 21 31 41 51
 MELGLGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE 60
 GPPFVLASPA GHLEGGGTAR WSGRARRPP PQPSRPAPPP PAPPSALPRG GRAARAGGPG 120
 SRARAAGARG CRLRSQLVFV RALGLHRSB ELVRFRCSSG SCRRARSPHD LSLASLLGAG 180
 ALRPPPGSRP VSQPCRPTR YEAVSEMDVN STWRTVDRLS ATACGCLG

Seq ID NO: 282 DNA sequence
Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 CTACTGCACC TGCCCTCTGT TTCCTTTGGA AATCTCTTAC CTTTCATTAG GGTTCCTTTC 60
 ATAGCAATTT CTTTGTGTTT TTAAGACTTC TACATTGCTT TTCTTTTAT TATCTGTGCT 120
 CCGTGAACTT TATGAATGCT GCTTAAATAT AATGTCAAAT TATGTTTAT CTGCCTACTC 180
 AGGTAACGTT TTCTTTTGTCT CTCATCTTGG TTTCATATA CTATTTTGTG TTTTGTGTA 240
 GATCTAATCA ATGATCTAGT CAGAAGCTAC TTCACTGGCT AACAGTGATC ATGTTTCATG 300
 GCTAAAAATG AACTTGAATC ACGGAAGTAG TGGTTGGTCC AGTTTGAAAG CTCTTATTAG 360
 TATCTTCTAT CTTGGCTGTA ATAATAGCCA TTATTTGTTA TGCCCTTGTG ATGTAGCAGA 420
 CACTCTTAAG CATTTTATGT GTATTATTCA AATTGCTATT ACTGTTCTTT TTATAGTTGA 480
 GAATCTCAGG ATACCTACAT TTATCACTTT TTCAATATAT ATGTATTTCT TATT

Seq ID NO: 283 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 564-1481

1 11 21 31 41 51
 GAGACTTTTA ATCATCTATC CCTTGTGCTT TACGCAGACC CTACAATACA CTAGAGGCTT 60
 CAAAGAGATC AAAAATTCAC ATGTGTAGAC AAATTAGGTC CCTTAAGATG CCAGGCAAAAC 120
 GAAAGTGCTAC CAAACACAGC AATGACTGTC CTAAGAGTGC GTTCTGGGAT ACACCTGTAA 180
 ACTTGGATCA AGTTCCCTCC CCTCTCCTCA AAATATATCG ACTTGTGCTG AAAGAAATCA 240
 CGACCGATGC TCACAATCTC GACCTCGTAA TTATATAGGG GGTGGTTTTC GTTCTGCGCT 300
 CTTTCCCTGA TTCACTGGCA GGTAAACATAT TTCACTGTACA AAATGAACAG CAACACCACG 360
 GCAAAACAGG GACAGGCCCT CAAAGTTGTC GGTAGGGAGC CAGGACCCCG CCAAGTGGCGT 420
 GGGGAGACAC CGTACTAAAC AAGCTTGCAA ACAGCAGGCA CCTTCTCTGC ACTGAGGAGG 480
 AAGGGCTGSC TAAGGGAGGC CGGGGCGGAG GAAGCCAAGC TCTGCAGGCC CTGACAAAGT 540
 CCTCCCGGCC TCCACGGGTC GCCATGGCAA CGCGGGGTCT GTGCTGGCCG GGAATGGCCG 600
 GCCTGGCGCG CGCAGGGGCC GCTGGGAAAG CGCGTCCCGC CCGCGGCTCC GCCAGTTTGA 660
 ACTTGGCGGG CAGATGTGGG CGCGCGGGGC GCTGGGGGCC TACTTTTCCC TCTTCTACG 720
 CCGGTTTCTC TGCTGACTGC AGACCCAGGT CTCGGCCCTC CTGGAATCCC TGCTCAGTCC 780
 CTATGACGGG CGCACGTGGG CAGGGGCTGG AGGTGGTGGC CTCGCGTCCG CCGCGCTGC 840
 CGCTGAGCTG CAGCAATTC ACCAGGTGCG TGTGTCTCTC CCTTGGCCAC CAGAGCTTCC 900
 AGTTTGACGA GGACGAGGCT GACGGGGAGG ATGAGGAAGA CGTGGATGAT GAGGAAGAGC 960
 TGGATGAAGA TGCCCATGAT TCAGAGGCCA AAGTGGCGAG CTTGAGAGGA ATGGAGTTAC 1020
 AGGGGTGGCG CAGCACTCAG GTTGAATCAG AAAATAACCA AGAAGAACAG AAACAGGTGC 1080
 GCTTACCGA AAGCCGCTCG ACACCATGGG AGGTGTGTTT TATTGGCAAA GAAAAAGAA 1140
 AACGTGACCG GCTGCAACTG AAAGCTCTAG AGGAATTAAT TCAACAATA GAAAAAGAA 1200
 AAGAAATGGA AGAACGTGAA AAAAGAAAGA TAATTGCTGA AGAAAAGCAC AAGGAATGGG 1260
 TTCAGAAAAA GAATGAGCAA AAAAGAAAG AAAGAGAACA AAAAATTAAT AAAGAAATGG 1320
 AGGAAAAAGC AGCAAGAGAA CTGGAGAAAG AATACTTGCA AGAAAAGCA AAAGAAAAAT 1380
 ATCAAGATG GTTAAAGAAA AAAATGCTG AAGAATGTGA GAGGAAGAG AAAGAAAAAG 1440
 AAAACAACAG CAAGCTGAAA TACAGGAGAA AAAGGAAATA GCAGAAAAA AGTTTCAAGA 1500
 ATGGTTGGAA AATGCGAAAC ATAAACCTCG TCCAGCTGCA AAGAGCTATG GTTATGCCAA 1560
 TGGAAAACTT ACAGGTTTTT ACAGTGGAAA TTCCTATCCA GAACCGAGCT TTTATAATCC 1620
 AATTCCGTGG AAACCAATTC ATATGCCACC TCCCAAGAA GCTAAGGATC TATCAGGAAG 1680
 GAAGAGTAAA AGACCTGTGA TAAGTCAGCC ACACAAGTCA TCATCTCTGG TAATTCATAA 1740
 AGCCAGGAGC AATCTTTGCC TTGAACTCT GTGCAGAATA CAAAGATAGC GTATGTGGAA 1800
 AATAACATGC TTTTATCTGG AGCTATTTAA TTTAAAAATC AGAAATTGTT TTTTACTGCT 1860
 CAGTCAATAA CTCACACTT AATGTGATTA TTGACAAATA GCAATTTTTC CATTTGTATA 1920
 TGGAGTCTCT AGAGTTGAGG AAGATATTT CTGGATTTTG GTTTTATAA ACTTTTAAAG 1980
 GTTGATCTTG GCATGTTGTT TTGCAGAATA AGTGGCTGAA TATGTAAGAA TTGTTTGT 2040
 ATTTAGCTTG TATTAAAGT ACACGTGAAT ACCAATAAAA CTACAAATT TTCTTG

Seq ID NO: 284 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
 MATRGLCWPG LAGLARAGPA GKARPRRGS SLNLAGQMW AGRWGPTFPF SYAGFSADCR 60
 PRSRPSSDSC SVPMTGARGQ GLEVVRSPP PLPLSCSNST RSLSPGLHQ SFQFDEDDGD 120
 GDEEDVDDE EDVDEADHS EAKVASLRGM ELQGCSTQV ESENNQSEK QVRLPESRLT 180
 PWEVWFIGKE KEERDRQLK ALEELNQOLE KRKEMEEREK RKI IAEKHK EHVQKQNEK 240
 RKEREQRINK EMEKAARKEL EKEYLQEKAK EKYQEWLKKK NABECERKK EKQNSKLKY 300

RRKRR

Seq ID NO: 285 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1-1746

	1	11	21	31	41	51	
10	ATGCCACTGA	AGCATTATCT	CCTTTTGCTG	GTGGGCTGCC	AAGCCTGGGG	TGCAGGGTTG	60
	GCCTACCATG	GCTGCCCTAG	CGAGTGTACC	TGCTCCAGGG	CCTCCCAGGT	GGAGTGCACC	120
	GGGGCAGCA	TGTGGGGGT	GCCCACCCCT	CTGCCCTGGA	ACGCCATGAG	CCTGCAGATC	180
	CTCAACACGC	ACATCACTGA	ACTCAATGAG	TCGCCGTTC	TCAATATCTC	AGCCCTCATC	240
	GCCCTGAGGA	TTGAGAAGAA	TGAGCTGTCT	CGCATCACGC	CTGGGGCCTT	CCGAAACCTG	300
15	GGCTCGCTGC	GCTATCTCAG	CCTCGCCAAC	AACAAGCTGC	AGGTTCTGCC	CATCGGCCTC	360
	TTCCAGGGCC	TGGACAGCCT	TGAGTCTCTC	CTTCTGTCCA	GTAACCAAGT	GTTCAGATC	420
	CAGCGGGCCC	ACTTCTCCCA	CTGCAGCAAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACCAC	480
	CTGGAATACA	TCCCTGACGG	AGCCTTCGAC	CACCTGGTAG	GACTCACGAA	GCTCAATCTG	540
	GGCAAGAATA	GCTCAACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
20	GTCTTCCGGC	TGATAGAGAA	CAGGCTCACG	GATATCCCCA	TGGGCACTTT	TGATGGGCTT	660
	GTAAACCTGC	AGGAACCTGC	TCTACAGCAG	AACCAAGATT	GACTGTCTCT	CCCTGGTCTC	720
	TTCCACAACA	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACAACCACAT	CTCCAGCTG	780
	CCACCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTCGGG	CCCATGCCCA	ACCTGCGGGA	GCTTTGGCTC	900
25	TATGACAACC	TGCTCTCTTC	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	AGCCTGATTC	TTAGCCGCAA	TCAGATCAGC	TTCTCTCTCC	CGGGTGCCCT	CAACGGGCTA	1020
	AGCGAGCTTC	GGGAGCTGTC	CTCCACACCC	AACGCACTGC	AGGACCTGGA	CGGGAATGTC	1080
	TTCCGCATGT	TGGCCAACCT	GCAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
	CCAGGGAATA	TCTTCGCCAA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAACCTG	1200
30	CTGGAGAACT	TCGCCCTCGG	CATCTTCGAT	CACCTGGGGA	AACTGTGTGA	GCTGCGGCTC	1260
	TATGACAATC	CCTGGAGGTG	TGACTCAGAC	ATCCTTCCGC	TCCGCAACTG	GCTCTGCTCT	1320
	AACCAAGCTA	GGTAGGGGAC	GGCACTGTGA	CCTGTGTGTT	TCAGCCAGCA	CAATGTCCGA	1380
	GGCCAGTCCC	TCATTATCAT	CAATGTCAAC	GTGCTGTGTC	CAAGCGTCCA	TGTCCCTGAG	1440
	GTGCGTAGTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
35	TCGGTCTCTT	TCAACCATGA	GCTAACCAAG	CCTGTGGGAG	ACTACACTGA	TCTGACTACC	1560
	ATTGAGGTCA	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCAGAG	CGGGCTGGCC	1620
	ATTGCCGCTC	TGTAAATTGG	CATTGTGCGC	CTGGCTGCTC	CCCTGGCTGC	CTGCGTCCGC	1680
	TGTTGCTGCT	GCAAGAAAGG	GAGCCAAGCT	GTCCGTGATG	AGATGAAGGC	ACCCAATGAG	1740
	TGTTAAAGAG	CAGGGCTGGA	GCAGGGCTGG	GGATATGATG	GACTGGAGGA	CCTGGGAATT	1800
40	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGAATGCT	CTTCTGGGCC	1860
	TAGATAAAG	GTGTGCCTAC	CTCTCTCTGA	CTTGCTCTGAT	TCTCCGCTAG	AGAAGCAGGT	1920
	CGTGCCGGAC	CTCTCTACAA	TCAGGAAGAT	AGATCCAAC	GGCCATGGCA	AAAGCCCTGG	1980
	GGATTTCGGA	TTCATACCCC	TGGGCTTCCT	TCGAGAGGGC	TCTTCTCTCA	AATCCTCCCC	2040
	ACCTGTCTCT	CAAGAACAGC	CTTCCCTGCG	CCCAGGCCCC	CTCCGGCCCT	CTGTAGACTC	2100
45	AGTTAGTCCA	CAGCCTGCTC	ACTTCGTGGG	AATAGTTCTC	CGCTGAGATA	GCCCCCTCTG	2160
	CCTAAGTATT	ATGAAGTTTG	ATTTCCTCTC	TTTTGTTTCT	CTTGTTTTGT	CTATGCTCTG	2220
	ACCCAGCTCA	TCCCTCTTAA	TGAAGTTTCT	CCCTCTGATT	TTCTGCTCCT	GAAGGAGGCG	2280
	TGAGTTCTCT	CCTCAAGGAA	GACTTCAAAC	CATTTAACTG	GTTTCTTAAG	AGCCGTCAAT	2340
	CAGCCTGGTT	TGGGGGATGC	TATGAAGAG	AGAAGGAAAA	TCATGCCGCT	CAGTTCTCTG	2400
50	AGACAGAAGA	GCCGTCTACA	GTGTCTCACT	TGTGATTTT	ATCTGGAAAA	GGAAGAAACA	2460
	CCCCAGCACA	GCAAGCTCAG	CCTTTATAGG	AAGGATATTT	CCAAACTGCA	AACCTTGGCT	2520
	TGAAAAGTTT	ATGCCCTTAA	GGAATGAAAT	CATGTAGAAAT	TTTGGACTTC	TAAAAACATC	2580
	AAAATCAGCT	TATTAATACG	GGATAGAGAA	AGAAATCTGG	TGCTTGGGGG	TCCCTGTGTT	2640
	CACCCCTAGA	GTTTGTTTTA	AAATTTTAA	TTGAAGCATG	TGAAGTGTAC	STGCAGAAAA	2700
55	GTGGGAACAT	GATAGTGTAT	GGCTTGGTGG	ATTTTCACAA	ACTGAACATA	CCTGTGTAAT	2760
	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCCTGGGC	TTTTCCCGAG	2820
	GGAGATGGGG	TGCTCTGAGG	ATGGACTTAC	CTGGGACCTG	CCCCCATGCA	GCCAGGACCG	2880
	TCCCCCACA	GTCAGCCTGT	GCAAGGCCCC	CGTGGCCAGG	GGTGGAGGAG	AAATATGTGG	2940
	TGTGGACAGG	ATGGGAGACT	GTGGCCTGAA	CAGGAGATT	TATTATATCT	GGAGACCTCG	3000
60	AGAGACCCCT	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
	GTCCGTGCAG	CCACACCTCT	TCCCTGCGCA	GCAAGTTGTC	TGCGGCTCAT	CGGAGGCCCC	3120
	TCCGCTGGA	GCCTCTATAG	GACGTGATAT	GCCTGTATCT	GTTTTTAATT	TTCAATCTTC	3180
	ACTTAGGGGA	AGTGAAATCG	CTCAGAGATG	AGATCCTTTA	ATTGAAAACG	AAGTGTAAAG	3240
	GAAATCTAGT	TCTTTCTAAT	GTGGTAAAA	TCTCCATCAA	CATCACAGTC	AGCTGGCAGC	3300
65	TGAATCTCAG	AATCTCACTT	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCACTCTG	3360
	GTCTGGGGGC	TCCCTGGAGC	TCCTCTGCG	TGTGGTCTGG	TTAGAGATTG	AGTTGTTTGC	3420
	TCCAGGGTTA	TCTCCTCCT	CGAGTCACAG	TCACACGAAT	ACCTGCCCTT	TCTGGCTTTC	3480
	CTGCTATACA	CATATTCACT	TGGCGCTCAA	GAAGTTAGGC	TCATGGCAAC	GTGTGCTTTT	3540
	CTCTGGACCA	CTGGCCCACT	TTACAGTGAA	ATGGAGAAAT	TCAGTCTTCC	ACGTCTGCCC	3600
70	AGGAAGAAG	TTAGCTGAC	TCCACGGGGA	TCTGGAATC	CACGACCAAT	CCCGATCGGC	3660
	TCTTATTAGC	TCCCGCTCC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
	TGCGCTCTTA	TAGCTCCCC	GCTCCACAAG	ACACCTGTGA	TCTGGAATC	TACCACCAAT	3780
	CCCGATCGGC	TCTTATTAGC	TCCCGCTCC	ACAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCAGC	TGCTGACAG	TTTTCCCTTC	CAGTTCTCTG	ACAAAAAGTG	TCCAGAGGGC	3900
75	TGTTTGCAAA	CAGTGTGCA	CTTTGTAGCT	TTTCACCCCT	TGTCCAGGGG	AATCTAGGAG	3960
	AGATGAGGCC	CGTCAGAGTC	AAGAGATGTC	ATCCCCCAG	GGTCTCCAAG	GCATTTCCAC	4020
	ACTATTGGTG	GACCTGTGAG	GACATGCACC	AAGGCTTGCC	AGAGCCAAAC	GGAAGTGAGC	4080
	CCAGAGCATG	GCAATAGAGC	ATCACCCGCT	GATGGTGGCC	TGCTGTGCTT	GGTGCCAAAC	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTTTGGCCAC	AGACCTGTCT	4200
80	GGTGCTCCTG	TGAGTGGCCT	CCAGATGTCT	TTGTGCATAG	GCACAAGTGG	GCCAGGGCTG	4260
	GAGGGAGGTT	GGAAACCTCA	TCATCCGGTG	GGCCCTGCCA	ATCTTAACCC	AGAACCTCTA	4320
	GGTATTCTCT	GCAATAGCCA	TGACATTGGA	GCACCTTCTT	CTCCAGCCAG	AGGCTGACCT	4380
	GAGGGGCACT	GTCTCTCAGT	GACACCAACC	AGGAGCACCC	TAGGTGAGGG	GTGAGGGCCC	4440
	CCTTATGTGA	ACCTCTTGGC	TCTTCTTCTT	TCCCATCAGA	GTGGTTGGAT	GGAGCCATTG	4500
85	GCCTCCTTTT	CTTCAGCCGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGGG	GTCTCCTTTC	CAACAGGATG	ATGCATTGTC	TCAATCTCTA	4620
	GGGCTGGAAT	GAGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGGTACAGA	GTTCACTTTT	4680
	CCTCTCTGTT	TACAGCTCCT	TGACAGTCCC	ACGCCCATCT	GGAGTGGGAG	CTGGAGGTTA	4740

GTGTTGGAGA AGAAACAACA AAGCCAATT AGAACCCTA TTTTAAAAA GTGCTTACTG 4800
 TGCACAGATA CTCTTCAAGC ACTGGACGTG GATTCTCTCT CTAGCCCTCA GCACCCCTGC 4860
 GGTAGGAGTG CCGCCTCTAC CCACTTGTGA TGGGGTACAG AGGCACTTGC TCTTCTGCAT 4920
 GGTGTTCAAT AGGCTGGGAG TTTTATTAT CTCTTCAAAC TTTGTACAAG AGCTCATGGC 4980
 TTGTCTTGGG CTCTCGTCAT TAAACCAAAG GAAATGGAAG CCATTCCCCT GTTGTCTCTC 5040
 TTAGTCTTGG TCATCAGAAC CTCCTTGGT ACCATATAGA TCAAAAGCTT TGTAAACCACA 5100
 GGAATAAATA AACTCTTCCA TCCCTTAAAG AATAGAATAG TTTGTCCCTC TCATGGGAAT 5160
 TGGGCTGTAT GTATATTGTT CTCTCTCTCT AGAATTTAGA GATACAAGAG TTCTACTTAG 5220
 AACTTTTCAT GGACACAATT TCCACAACCT TTCAGATGCT GATGTAGAGC TATTGGGAAA 5280
 GAACCTCCAA ACTCAGGAAG TTTGCAGAGA GCAGACAGCT AGAGATAACT CGGGACCCAG 5340
 AGTTGGTCGA CAGATGTAG ATGTATCCTA GCTTTTAGCC ATAAACCACT CAAAGATTCA 5400
 GCCCCAGAT CCCACAGTCA GAACTGAATC TGCCTTGTG GGAAGCCAGC AGTGGCCTTG 5460
 GGAAGGAAGC CATGGCTGTG GTTCAGAGAG GGTGGGCTGG CAAGCCACTT CCGGGGAAAA 5520
 CTCCTTCCGC CCAAGGTTTC TTCTTCTCT AAGGAGAGAT TGTCTCACC AACCCGCTGC 5580
 CTTATGCTG CTTCAAAGC TAGATCATGT TTGCTTGTCT TAGAGAAATTA CTGCAAAATCA 5640
 GCCCCAGTGC TTGCGCATGC ATTTACAGAT TTCTAGGCC TCAGGGTTT GTAGAGTGTG 5700
 AGCCCTGGTG GGCAGGGTTG GGGGGTCTGT CTTCTGCTGG ATGCTGCTTG TAATCCATT 5760
 GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 286 Protein sequence:
 Protein Accession #: NP_570843.1

1 11 21 31 41 51
 MPLKHYLLLL VGCQAWGAGL AYHGPCSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI 60
 LNMTHITELNE SPFFNLISALI ALRIEKNELS RITPGAFLNL GSLRYLSLAN NKLQVLPGL 120
 FQGLDSLESL LLSSNQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFL HLVLTKLNL 180
 GGNLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQQ NQIGLLSPGL 240
 FHNHNLQRL YLSNNHISQL PPSIPMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRELWL 300
 YDNHISSELD NVFSNLRQLQ PLLLSRNQIS FISPAGFNL TELRELSHT NALQDLQDNV 360
 FRMLANLQNI SLQNNRRLQL PGNIPANVNG LMAIQLQNNQ LENLPLGIFD HLKLCLELRL 420
 YDNFWRCDSD ILPLRNWLLL NQPRLGTDV PVCFSANVR GQSLIIINVN VAVPSVHVPE 480
 VPSYPETPWY PDTSPYDPT SVSSTTELS PVEDYDLTT IQVTDDRSVW GMTQAQSGLA 540
 IAAIVIGIVA LACSLAACVG CCCCCKRSQA VLMQMKAPNE C

Seq ID NO: 287 DNA sequence
 Nucleic Acid Accession #: NM_002362
 Coding sequence: 1..954

1 11 21 31 41 51
 ATGTCTTCTG AGCAGAAGAG TCAGCACTGC AAGCCTGAGG AAGGCGTTGA GGCCCAAGAA 60
 GAGGCCCTGG GCCTGGTGGG TGCACAGGCT CCTACTACTG AGGAGCAGGA GGCTGCTGTC 120
 TCCTCTCTCT CTCTCTTGGT CCTGGCACC CTGGAGGAAG TGCCTGCTGC TGAGTCAGCA 180
 GGTCTCTCCC AGAGTCTCTA GGGAGCCTCT GCCTTACCCTA CTACCATCAG CTCTACTTGC 240
 TGGAGGCAAC CCAATGAGGG TTCCAGCAGC CAAGAAGAGG AGGGGCCAAG CACCTGCCT 300
 GACGCAGAGT CCTTGTTCGG AGAAGCACTC AGTAACAAGG TGGATGAGTT GGCTCATTTT 360
 CTGCTCCGCA AGTATCGAGC CAAGGAGCTG GTCACAAAGG CAGAAATGCT GGAGAGAGTC 420
 ATCAAAAATT ACAAGCGCTG CTCTCTGTG ATCTTCGGCA AAGCCTCCGA GTCCCTGAAG 480
 ATGATCTTTG GCATTGACGT GAAGGAAAGT GACCCCGCCA GCAACACCTA CACCTTGTG 540
 ACCTGCGCTG GCCTTTCTTA TGATGGCCTG CTGGGTAATA ATCAGATCTT TCCCAAGACA 600
 GGCCTTCTGA TAATCGTCTT GGGCACAATT GCAATGGAGG GCGACAGCGC CTCTGAGGAG 660
 GAAATCTGGG AGGAGCTGGG TGTGATGGG GTGTATGATG GGAGGGAGCA CACTGTCTAT 720
 GGGGAGCCCA GGAAACTGCT CACCCAAAGT TGGGTGCAGG AAAACTACCT GGAGTACCGG 780
 CAGGTACCCG GCAGTAATCC TGCAGCTAT GAGTTCCTGT GGGGTCCAAG GGCTCTGGCT 840
 GAAACCACTG ATGTGAAAGT CCTGGAGCAT GTGGTCAGGG TCAATGCAAG AGTTGCGATT 900
 GCCTACCCAT CCCTGCGTGA AGCAGCTTTT TTAGAGGAGG AAGAGGGAGT CTGA

Seq ID NO: 288 Protein sequence:
 Protein Accession #: NP_002353.1

1 11 21 31 41 51
 MSSEQKSQHC KPEEGVEAQE EALGLVGAQA PTTEEQEAHV SSSSPLVPFT LEEVPAEESA 60
 GPPQSPQAS ALPTTISFTC WRQPNEGSSS QEEEGPSTSP DAESLFREAL SNKVDELAFH 120
 LLRKYRAKEL VTKAEMLELV IKNYKRCPPV IFGKASESLK MIFGIDVKEV DPASNTYTLV 180
 TCLGLSYDGL LGNNQIPFKT GLLIIVLGTI AMEGDSASEE EIWEELGVMG VYDGREHTVY 240
 GEPRKLLTD WVQENYLEYR QVPGSNPARY EFLWGPRALA ETSYVKVLEH VVRVNAVRI 300
 AYPSLREAL LEEEEGV

Seq ID NO: 289 DNA sequence
 Nucleic Acid Accession #: NM_002362
 Coding sequence: 46..1344

1 11 21 31 41 51
 CGGCGGCCGC GCCCTGGTTG GGTCCCCACT GCTCTGGGG GCGCCATGGA CGAGGCCGTG 60
 GGCGACCTGA AGCAGGCGCT TCCTGTGTG GCCAGTCCG CAACGGTCCA CGTGGAGGTG 120
 CATCAGCGCG GCAGCAGCAC TGCAAGAAA GAAGACATAA ACCTGAGTGT TAGAAAGCTA 180
 CTCACACAGC ATAATATTGT GTTGTGTGAT TACACATGGA CTGAGTTTGA TGAACCTTTT 240
 TTGACCAAGC ATGTGCAATC TGTGTCTATT ATTGACACAG AATTAAAGGT TAAAGACTCA 300
 CAGCCCATCG ATTTGAGTGC ATGCACTGTT GCACTTCACA TTTTCCAGCT GAATGAAGAT 360
 GGCCCCAGCA GTGAAATCT GGAGGAAGAG ACAGAAAACA TAATTGCAGC AAATCACTGG 420
 GTTCTACCTG CAGCTGAATT CCATGGGCTT TGGGACAGCT TGGTATACGA TGTGGAAGTC 480
 AAATCCCATC TCCTCGATTA TGTGATGACA ACTTTACTGT TTTGAGACAA GAACGTCAAC 540

AGCAACCTCA TCACCTGGAA CCGG3TGGTG CTGCTCCAGG GTCCTCCTGG CACTGGAAAA 600
 ACATCCCTGT GTAAAGCGTT AGCCACAGAA TTGACAATTA GACTTTCAGG CAGGTACCGA 660
 TATGGCCAAAT TAAATGAAAT AAACAGCCAC AGCCTCTTTT CTAAAGTGGT TTCGGAAAGT 720
 GGCAAGCTGG TAACCAAGAT GTTTCAGAGG ATTCAAGGAT TGATTGATGA TAAAGACGCC 780
 CTGGTGTTCG TGCTGATTGA TGAGGTGGAG AGTCTCACAG CCGCCCCGAA TGCCCTGCAGG 840
 GCGGGCACCG AGCCATCAGA TGCCATCCGC GTGGTCAATG CTGTCTTGAC CCAAATTGAT 900
 CAGATTAAAA GGCATTCCAA TGTGTGATT CTGACCACTT CTAACATCAC CGAGAAGATC 960
 GACGTGGCCT TCGTGGACAG GGTGACATC AAGCAGTACA TTGGGCCACC CTCTGCAGCA 1020
 GCCATCTTCA AAATCTACCT CTCTTGTGTT GAAGAACTGA TGAAGTGTCA GATCATATAC 1080
 CCTCGCCAGC AGCTGCTGAG CCTCCGAGAG CTAGAGATGA TTGGCTTCAT TGAACAACAC 1140
 GTGTCAAAAT TGAGCCTTCT TTTGAATGAC ATTTCAAGGA AGAGCGAGGG CCTCAGCGGC 1200
 CGGGTCTCTGA GAAAACCTCC CTTTCTGGCT CATGCGCTGT ATGTCCAGGC CCCCACCGTC 1260
 ACCATAGAGG GGTTCCTCCA GGCCTGTGCT CTGGCAGTGG ACAAGCAGTT TGAAGAGAGA 1320
 AAGAAGCTTG CAGCTTACAT CTGATCCTGG GCTTCCCAT CTGGTGTCTT TCCCATGGAG 1380
 AACACACAA CAGTAAGTGA GGTGCCCCA CACAGCCGTC TCCAGGGAA TCCCTTCTGC 1440
 AAACCAACG TACTTACATG TTTGAAGTAG AAAGCCACCA AGGCCAGGCT TTGTTAAAG 1500
 AAGTGTATTC TATTTATGTT GTTTTAAAT GCATCTGAG AGACAACAT CTGTGCTATT 1560
 TCACTGTTTG TAAAGATAAA TTCAGATTGT TTGTCTCCTT GTGAAGAAC ATCGAAACCT 1620
 GTTGTGTTCC AGCCACACCC CAGTGGATGG GATGCATAAT GCCAGCAAGT TTTGTTTAA 1680
 AGCAAAAAAG GAAGATTAT GCAGGTGTTA TAGAAGCCAG AAGAGAACT GTGTCAACCT 1740
 AAAGAAGCAT ATAATCAAG CATTAAAAAT GCACACATTA CTCCAGGTGG AAGGTGGCAA 1800
 TTGCTTTCTG ATATCAGCTC GTTTGATTTA GTGCAAAAA GTTTTCAAGA CTATTTAATG 1860
 GATGTAAAAA AGCCTATTTC TACATTATAC CAATGAGAAA AAAAATGGTC GGTAAAGTGT 1920
 TCTTTCATAA TAAATAATCA AGACATGGTC CCATTGTCAG GAAAAGTGCA GACTCTGAGT 1980
 GTTCCAGGGA AACACATGCT GGACATCCCT TGTAACCCGG TATGGGCGCC CTGCTATGTC 2040
 TGGGATGTTT CTGCCACCGG TTTTGTGTTG GCAATAACGT TATCACATTT CTAATGAGGA 2100
 TTCACATTAA TATAATATAA AATAAATAGG TCAGTTACTG GTCTCTTTCT GCCGAATGTT 2160
 ATGTTTTGCT TTTATCTCAC AGTAAATATA ATATAATTAA AAA

Seq ID NO: 290 Protein sequence:
 Protein Accession #: NP_004228

1 11 21 31 41 51
 MDEAVGLDLK ALPCVAESPT VHVVEVHQRGS STAKKEDINL SVRKLNLNRHN IVFGDYTWTE 60
 FDEPFLTRNV QSVSIIDTEL KVKDSQPIDL SACTVALHIF QLNEDGPSSE NLEEEETENII 120
 AANHWWLPAA EPHGLWDSLV YDVEVKSHLL DVMVMTLLFS DKNVNSNLIT WNRVVLHGP 180
 PGTGKTSCLK ALAQKLTIRL SSRVRYGQLI EINSLSLFSK WFSBSGKLVT KMFQKIQDLI 240
 DDKDALVPVL IDEVESLTAA RNACRAGTEP SDAIRVNVAV LTQIDQIKRH SNVILTTSN 300
 ITEKIDVAFV DRADLKQYIG PPSAAAIFKI YLSCLLELMK CQIYPRQQL LTLRELEMIG 360
 FIENNVSKLS LLLNDISRKS EGLSGRVLRL LPFLAHALYV QAPTVTITIEGF LQALSIAVDK 420
 QPEERKKLAA YI

Seq ID NO: 291 DNA sequence
 Nucleic Acid Accession #: NM_002658.1
 Coding sequence: 77-1372

1 11 21 31 41 51
 GTCCCCGCGC GCGCGTCGCG CCCTCCTGCC GCAGGCCACC GAGGCGCGCG CCGTCTAGCG 60
 CCCCACCTTC GCCACATGA GAGCCCTGCT GCGCGCGCTG CTTCTCTGCG TCCTGGTCGT 120
 GAGCGACTCC AAAGCGAGCA ATGAACCTCA TCAAGTTCCA TCGAACTGTG ACTGTCTAAA 180
 TGGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCAACATT CACTGGTGCA ACTGCCCAA 240
 GAAATTGCGA GGGCAGCACT GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG 300
 TCACTTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CCGCCCTGCC TGCCCTGGAA 360
 CTCTGCCACT TCCCTTCAGC AAACGTACCA TGCCCAAGA TCTGATGCTC TTCAGCTGGG 420
 CCTGGGGAAA CATAATTACT GCAGGAACCC AGACAACCGG AGGCGACCTT GGTGCTATGT 480
 GCAGGTGGGC TTAAGCCGCG TTGTCCAAGA GTGCATGGTG CATGACTGCG CAGATGGAAA 540
 AAAGCCCTCC TCTCTCCAG AAGAATTAAA ATTTCACTGT GGGCAAAAAG CTCTGAGGCC 600
 CCGCTTTAAG ATTATTGGGG GAGAATTAC CACCATCGAG AACCAGCCCT GGTTCGCGC 660
 CATCTACAGG AGGCACCGGG GGGGCTCTGT CACCTACGTG TGTGGAGGCA GCCTCATCAG 720
 CCCTGCTCGG GTGATCAGCG CCACACACTG CTTCAATTGAT TACCCAAAGA AGGAGGACTA 780
 CATCGTCTAC CTGGGTGCTC CAAGGCTTAA CTCCAACAG CAAGGGGAGA TGAAGTTTGA 840
 GGTGGAAAC CTATCTCTAC ACAAGGACTA CAGCGCTGAC ACGCTTGCTC ACCACAACGA 900
 CATTGCTTTG CTGAAGATCC GTTCCAAGGA GGGCAGGTGT GCGCAGCCAT CCGGACTAT 960
 ACAGACCATC TGCTGCCCC CGATGTATAA CGATCCCCAG TTTGGCACA GCTGTGAGAT 1020
 CACTGGCTTT GGAAGAGAGA ATTCTACCGA CTATCTCTAT CCGGAGCAGC TGAAGATGAC 1080
 TGTGTGAAG CTGATTTCCC ACCGGGAGTG TCAGCAGCCC CACTACTACG GCTCTGAAAT 1140
 CACCACCAA ATGCTATGTG CTGCTGACCC CCAATGGAAG ACAGATTCTT GCCAGGAGGA 1200
 CTCAGGGGGA CCCCTCGTCT GTTCCCTCCA AGGCCGATG ACTTTGACTG GAATTGTGAG 1260
 CTGGGGCCGT GGATGTGCCC TGAAGGACAA GCCAGGCGTC TACACGAGAG TCTCACACTT 1320
 CTTACCTTGG ATCCGAGTC ACACCAAGGA AGAGAATGCG CTGGCCCTCT GAGGGTCCCC 1380
 AGGGAGGAAA CGGGCACCA CCGCTTTCTT GCTGGTTGTC ATTTTTCAG TAGAGTCATC 1440
 TCCATCAGCT GTAAGAGAG ACTGGGAAGA TAGGCTCTGC ACAGATGGAT TTGCTGTGG 1500
 CACCACCAAG GTGAACGACA ATAGCTTTAC CCTCACGGAT AGGCCTGGGT GCTGGCTGCC 1560
 CAGACCTCT GGCAGGATG GAGGGGTGGT CTTGACTCAA CATGTTACTG ACCAGCAACT 1620
 TGCTTTTTC TGACCTGAAG CCTGCAGGAG TTAAGAAAGG CAGGGCATCT CCGTGTGATG 1680
 GGCTCGAAGG GAGAGCCAGC TCCCCGAGC GGTGGGCATT TGTGAGGCC ATGGTTGAGA 1740
 AATGAATAAT TTCCCAATTA GGAAGGTAA GCAGCTGAGG TCTCTGAGG GAGCTTAGCC 1800
 AATGTGGGAG CAGCGGTTT GGGAGCAGAG ACCTAACGA CTTCAAGGCA GGGCTCTGAT 1860
 ATTCCATGAA TGTATCAGGA AATATATATG TGTGTGTATG TTTGCACACT TGTGTGTGG 1920
 GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTCTCTT 1980
 AAATCTGTG GACTGTGATG CCACACAGAG TGGTCTTTCT GGAGAGGTTA TAGGCTACTC 2040
 CTGGGGCCTC TTGGGTCCCC CACGTGACAG TGCTCTGGGA TGACTTATT CTGCAGCATG 2100
 ACCTGTGACC AGCACTGTCT CAGTTTCACT TTCACATAGA TGTCCCTTTC TTGGCCAGTT 2160
 ATCCCTTCCT TTAGCCCTAG TTATCCCAAT CCTCACTGGG TGGGGTGAGG ACCACTCCTT 2220
 AACTGAATA TTTATATTTC ACTATTTTAA TTTATATTTT TGTAATTTTA AATAAAGTG 2280

ATCAATAAAA TGTGATTTTT CTGA

Seq ID NO: 292 Protein sequence:

Protein Accession #: NP_002649.1

1	11	21	31	41	51	
MRALLARLLL	CVLVVSDDSKG	SNELHQVPSN	CDCLNGGTCV	SNKYFSNIHW	CNCPKKFGGQ	60
HCEIDKSKTC	YEGNGHFYRG	KASTDTMGRP	CLPWN SATVL	QQTYHAHRSD	ALQLGLGKH	120
YCRNPDNRRL	PWCYVQVGLK	PLVQECMVHD	CADGKKPSSP	PEELKFQCGQ	KTLRPRPKII	180
GGFEFTIENQ	PWFAAIYRRH	RGSSTYVCCG	GSLISPCWVI	SATHCFIDYP	KKEDYIVVLG	240
RSRLNSNTQG	EMKFEVENLI	LHKDYSADTL	AHHNDIALLK	IRSKEGRCQA	PSRTIQTICL	300
PSMYNDPQFG	TSCEITGFGK	ENSTDYLYPE	QLKMTVVVKLI	SHRECCQPHY	YGSEVTTKML	360
CAADPQWKTD	SCQGDSSGGL	VCSLQGRMTL	TGIVSWGRGC	ALKDKPGVYT	RVSHFLPWIR	420
SHTKEENGLA	L					

Seq ID NO: 293 DNA sequence

Nucleic Acid Accession #: NM_001498

Coding sequence: 93...2006

1	11	21	31	41	51	
GGCAGGAGGC	TGAGTGTCGG	TCTCGCGCCC	GGAAGCGGGC	GACCGCCGTC	AGCCCGGAGG	60
AGGAGGAGGA	GGAGGAGGAG	GAGGGGGCGG	CCATGGGGCT	GCTGTCCAG	GGCTCGCGCG	120
TGAGCTGGGA	GGAAACCAAG	CGCCATGCCG	ACCCAGTGCG	GCGGCACGGG	ATCCTCCAGT	180
TCCTGCACAT	CTACACGCC	GTCAAGGACC	GGCACAAGGA	CGTTCTCAAG	TGGGGCGATG	240
AGGTGGAATA	CATGTTGGTA	TCTTTTGATC	ATGAAAATAA	AAAAGTCCGG	TTGGTCTGT	300
CTGGGGAGAA	AGTTCTTGAA	ACTCTGCAAG	AGAAGGGGGA	AAGGACAAAC	CCAAACCATC	360
CTACCCCTTG	GAGACCGAG	TATGGGAGTT	ACATGATTGA	AGGGACACCA	GGACAGCCCT	420
ACGAGGAAAC	ATTCTCCGAG	TTCAATACAG	TTGAGGCCAA	CATGCGAAAA	CGCCGGAAGG	480
AGGCTACTTC	TATATTAGAA	GAAAATCAGG	CTCTTTGCAC	AATAACTTCA	TTTCCAGAT	540
TAGGCTGTCT	TGGGTTCCAA	CTGCCCAGG	TCAAACCCAA	CCCAGTGGAA	GGAGGAGCTT	600
CCAAGTCCCT	CTTCTTTCCA	GATGAAGCAA	TAAACAAGCA	CCCTCGCTTC	AGTACCTTAA	660
CAAGAAATAT	CCGACATAGG	AGAGGAGAAA	AGGTTGTGAT	CAATGTACCA	ATATTTAAGG	720
ACAAGAAATC	ACCATCTCCA	TTTATAGAAA	CATTACTGTA	GGATGATGAA	GCTTCAAGGG	780
CTTCTAAGCC	GGATCATATT	TACATGGATG	CCATGGGATT	TGGAATGGGC	AATTGCTGTC	840
TCCAGGTGAC	ATTCACAGCC	TGCAGTATAT	CTGAGGCCAG	ATACCTTTAT	GATCAGTTGG	900
CTACTATCTG	TCCAAATGTT	ATGGCTTTGA	GTGCTGCATC	TCCCTTTTAC	CGAGGCTATG	960
GTGCAGACAT	TGATTGTGCG	TGGGGAGTGA	TTTCTGCATC	TGTAGATGAT	AGAACTCGGG	1020
AGGAGCGAGG	ACTGGAGCCA	TTGAAGAAC	ATAACTATAG	GATCAGTAAA	TCCCGATATG	1080
ACTCAATAGA	CAGCTATTTA	TCTAAGTGTG	GTGAGAAATA	TAATGACATC	GACTTGACGA	1140
TAGATAAAGA	GATCTACGAA	CAGCTGTTGC	AGGAAGGCAT	TGATCATCTC	CTGGCCGAGC	1200
ATGTTGCTCA	TCTCTTTATT	AGAGACCCAC	TGACACTGTT	TGAAGAGAAA	ATACACCTGG	1260
ATGATGCTAA	TGAGTCTGAC	CATTTTGAGA	ATATTCACTC	CACAAATTGG	CAGACCAATG	1320
GATTTAAGCA	CCCTCTCCCA	AACCTAGACA	TTGGATGGAG	AGTAGAATTT	CGACCCATGG	1380
AGGTGCAATT	AACAGACTTT	GAGAACTCTG	CCTATGTGGT	GTTTGTGGTA	CTGCTCACCA	1440
GAGTGATCCT	TTCTACAAA	TTGGATTTTC	TCATTCCACT	GTCAAAGGTT	GATGAGAAAC	1500
TGAAGGTAGC	ACAGAAAAGA	GATGCTGTCT	TGCAGGGAAT	GTTTTATTTC	AGGAAAGATA	1560
TTTGCAAGAG	TGGCAATGCA	GTGGTGGATG	GTGTGGGCAA	GGCCCAAGAC	AGCACGGAGC	1620
TCGCTGCAGA	GGGTACACAC	CTCATGAGCA	TAGACACCAT	CATCAATGGG	AAGGAAGGTG	1680
TGTTTCTCTG	ACTGATCCCA	ATTCTGAACT	CTTACCTTGA	AAACATGGAA	GTGGATGTGG	1740
ACACCCAGATG	TAGTATTCTG	AACTACCTAA	AGCTAATTAA	GAAGAGAGCA	TCTGGAGAAC	1800
TAATGACAGT	TGCCAGATGG	ATGAGGGAGT	TTATCGCAA	CCATCCTGAC	TACAAGCAAG	1860
ACAGTGTGAT	AAGTATGAAA	ATGAATTATA	GCCTTATTTT	GAAGTGTAAC	CAAAATGCAA	1920
ATGAATTATG	TGAATGCGCA	GAGTTACTTG	GATCAGCATT	TAGGAAAGTA	AAATATAGTG	1980
GAAAGTAAAC	TGACTCATCC	AAC TAGACAT	TCTACAGAAA	GAAAAATGCA	TTATTGACGA	2040
ACTGGCTACA	TGACCATGCC	TCTCAGCCCG	TGTGTATAAT	ATGAAGACCA	AATGATAGAA	2100
CTGTACTGTT	TTCTGGGCCA	GTGAGCCAGA	AATTGATTAA	GGCTTTCTTT	GGTAGGTAAA	2160
CTTAGAGTTT	ATACAGTGTA	CATGTACATA	GTAAGATATT	TTTGATTAAAC	AATGTATTTT	2220
AATAACATAT	CTAAAGTCAT	CATGAACCTG	CTTGATACAT	TTTAAATTCT	TACTCTGGAG	2280
CAACCTACTG	TCTAAGCAGT	TTTGTAATG	TACTGGTAAT	TGTACAATAC	TTGCATTCCA	2340
GAGTTAAAT	GTTTACTGTA	AATTTTGTG	CTTTTAAAGA	CTACCTGGGA	CCTGATTAT	2400
TGAAATTTT	CTCTTAAAA	ACATTTTCTC	TGTTAATTT	TCCTTTGTCA	TTTCCTTTGT	2460
TGTTTACATT	AAATCATTG	AATCCATTGA	AAGTGCTTCA	AGGGTAATCT	TGGGTTTCTA	2520
GCACCTTATC	TATGATGTTT	CTTTTGCAAT	TGGAATAATC	ACTTGGTCAC	CTTGCCCCAA	2580
GCTTTCCCT	CTGAATAAAT	ACCCATTGAA	CTCTGAAAAA	AAAAAATAAA	AAAA	

Seq ID NO: 294 Protein sequence:

Protein Accession #: NP_001489

1	11	21	31	41	51	
MGLLSQGSPL	SWEETKRHAD	HVRRHGILQF	LHIYHAVKDR	HKDVLKWGDE	VEYMLVSFDH	60
ENKKVRLVL	GEKVLTLQE	KGERTNPNHP	TLWRPEYGSY	MIETPGQPHY	GGTMSEFNTV	120
ENAMRKRRKE	ATSLILEENQA	LCTITSFPRL	GCPGFTLPEV	KPNPVEGGAS	KSLFFFPDEAI	180
NKHPREFTLT	RNIHRRRGEK	VVINVPFKD	KNTSPFFIET	FTEDDEASRA	SKPDHIYMDA	240
MGFGMGNCCL	QVTFQACIS	EARYLYDQLA	TICPIVMALS	AASPFYRGYV	SDIDCRWGI	300
SASVDDRTRE	ERGLEPLKNN	NYRISKSRID	SIDSYLSKOG	EKYNDIDLTI	DKEIYEQLLQ	360
EGIDHLLAQH	VAHLEFIRPL	TLFEEKIHLD	DANESDHFPN	IQSTNWTQMR	FKPPFPNSDI	420
GWRVEFRPME	VQLTDFENSA	VYVFPVLLTR	VILSYKLDLF	IPLSKVDENM	KVAQKRDAVL	480
QGMFYFRKDI	CKGNAVDVG	CGKAQNSTEL	AAEYTLMSI	DTIINGKEGV	FPGILIPILNS	540
YLENMEVDVD	TRCSILNLK	LIKKRASGEL	MTVARWMMREF	IANHPDYKQD	SVITDEMNYN	600
LILKCNQIAN	ELCEPELLG	SAFKRVKYS	SKTDSSN			

WO 02/086443

PCT/US02/12476

Seq ID NO: 295 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-816

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
      GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
10     CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
      GGGAGGGCGC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
      GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
      CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
      AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT 420
      ATGACAGGAC ATGCTATTCC ACCCAGCCAA TTGGATTCTC AGATTGATGA CTTCACTGGT 480
15     TTCAGCAAGG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT 540
      ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCCAAAGC 600
      CAACGAGAAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA 660
      CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGACCTAC TGCAGTCAGG 720
      AAGCGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT 780
20     AAGCACCTTA AGAAGAAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT 840
      CACACCCCAA CCGATAAAAC TCATTAAATG TTGAGGAGAG AAAAGGATCA GATTGCTGTT 900
      TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACCGA ATCAAAATAGC 960
      CTTCCAGAGG CTAAGAAATT TCTGTTAGTA AAAGATGTTT TTTTCCCAA AGCATTTTAT 1020
      TTGAAAGGAT AACTTGTGTT TTGGTTATTT TGTATTCCCA CCGTGTCTGG TAGATATTAT 1080
25     TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A

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Seq ID NO: 296 Protein sequence:
Protein Accession #: Eos sequence

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30     1      11      21      31      41      51
      |      |      |      |      |      |
      MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIIAGS AMSKEKKLMT 60
      GHAIPPSQLD SQIDDFTFPS KDRMMQKPGS NAPVGGNVTS SFGDDLECR ETASSPKSQR 120
35     EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR FFSIIKEAA RCMRRDFVKH 180
      LKKKLKRLM

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Seq ID NO: 297 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-816

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40     1      11      21      31      41      51
      |      |      |      |      |      |
      AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
      GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
45     CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
      GGGAGGGCGC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
      GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
      CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
      AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT 420
      ATGACAGGAC ATGCTATTCC ACCCAGCCAA TTGGATTCTC AGATTGATGA CTTCACTGGT 480
      TTCAGCAAGG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT 540
      ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCCAAAGC 600
      CAACAAGAAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA 660
      CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGACCTAC TGCAGTCAGG 720
      AAGCGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT 780
50     AAGCACCTTA AGAAGAAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT 840
      CACACCCCAA CCGATAAAAC TCATTAAATG TTGAGGAGAG AAAAGGATCA GATTGCTGTT 900
      TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACCGA ATCAAACTGGC 960
      CTTCCAGAGG CTAAGAAATT TCTGTTAGTA AAAGATGTTT TTTTCCCAA AGCGTTTAT 1020
      TTGAAAGGAT AACTTGTGTT TTGGTTATTT TGTATTCCCA CCGTGTCTGG TAGATATTAT 1080
60     TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A

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Seq ID NO: 298 Protein sequence:
Protein Accession #: Eos sequence

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65     1      11      21      31      41      51
      |      |      |      |      |      |
      MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIIAGS AMSKEKKLMT 60
      GHAIPPSQLD SQIDDFTFPS KDRMMQKPGS NAPVGGNVTS SFGDDLECR ETASSPKSQ 120
70     EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR FFSIIKEAA RCMRRDFVKH 180
      LKKKLKRLM

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Seq ID NO: 299 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-816

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75     1      11      21      31      41      51
      |      |      |      |      |      |
      AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
      GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
80     CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
      GGGAGGGCGC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
      GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
      CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
      AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA 420
      TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCCTGGTT 480
85

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WO 02/086443

PCT/US02/12476

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TCAGCAAGA TAGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA 540
CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAGCC 600
AACAGAAAT TAATGCTGAT ATAAAACGTA AATTAGTGAA GGAACCTCGA TCGTTGGAC 660
AAAAATATGA AAAATCTTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA 720
AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA 780
AGCACCTTAA GAAGAAACTG AAACGTATGA TTTGAGAATA CTTGTCCCTG GAGGATTATC 840
ACACCCCAAA TGCATAATCT CATTAATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT 900
TCTACAATGG AGCAGGATAT TGCTGAAGTC TCCTGGCATA TGTTACCGAA TCAACTGGCC 960
TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAA GCGTTTTATT 1020
TGAAAGGATA ACTTGTGTTT TGGTTATTTT GTATTCCAC CTGTGCTGGT AGATATTATT 1080
AACCCATTAG GTAAATACTA TTACAGTCGT GGTTCCTGCA

Seq ID NO: 300 Protein sequence:
Protein Accession #: Eos sequence

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1 11 21 31 41 51
MTDKTEKVV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKAKKLMT 60
GHAIPPSQLD SQIDDFTFPS KDRMMQKPGS NAPVGGNVTS SFGDDLECR ETASSPKSQ 120
EINADIKRL VKELRCVQKQ YEKIFEMLEG VQGPTAVRKR PFESIIEKAA RCMRRDPVKH 180
LKKLKRMI

Seq ID NO: 301 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-812

1 11 21 31 41 51
AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCACAGTGC 120
CCTAGGGGGC ACATTTCCTCA CACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
GGGAGGCGCC ACACTTCAC TGCCATTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAGCTTA 420
TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCCTGGTT 480
TCAGCAAAAG TGGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAATGTTA 540
CCAGCAATTT CTCTGGAGAT GACCTAGAAT GCAGAGGAAT AGCCTCCTCT CCCAAAGCC 600
AACAGAAAT TAATGCTGAT ATAAAATGTC AAGTAGTGAA GGAATCCGA TGCCTTGGAC 660
AATATGAAAA AATCTTCGAA ATGCTTGAAG GAGTGCAAGG ACCTACTGCA GTCAGGAAAC 720
GATTTTTTGA ATCCATCATC AAGGAAGCAG CAAGATGTAT GAGACGAGAC TTTGTTAAGC 780
ACCCTAAGAA GAAATCTGAA CGTATGATTT GAGAATACTT GTCCCTGGAG GATTATCACA 840
CCCAAAATGC ATAACTCAT TAATGATTGA GGAGAGAAAA GGATCAGATT ACTGTTTCT 900
ACAATGGAGC AGGATATTGC TGAAGTCTCC TGGCATATGT TACCGAATCA ACTGGCCTTC 960
CAGAGGCTAA GAAATTTCTG TTAGTAAAAG ATGTTCTTTT TCCCAAAGCG TTTTATTGTA 1020
AAGGATAACT TGTGTTTGGG TTATTTTGTG TTCCACCTG TGCTGGTAGA TATTATTAA 1080
CCATTAGGTA AATACTATTA CAGTCGTGGT TTCTGCA

Seq ID NO: 302 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
MTDKTEKVV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT 60
GHAIPPSQLD SQIDDFTFPS KDGMMQKPGS NAPVGGNVTS NFSGDDLECR GIASSPKSQ 120
EINADIKCQV VKELRCVQKQ EKIFEMLEGV QGPTAVRKR PFESIIEAAR CMRRDPVKHL 180
KKKLKRMI

Seq ID NO: 303 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

1 11 21 31 41 51
AGTGTTCGGC TGGGACAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTTCC ATCCCCCTTG 60
GGCCAAACAG GATCGGTGCT TCTGGTGAGA CGTCTCCCCA TGCACATCAC TCCAGATGTC 120
CCTAGGGGGC ACATTTCCTCA CACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
GGGAGGCGCC ACACTTCAC TGCCATTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA 420
TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCCTGGTT 480
TCAGCAAAAG TAGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA 540
CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAGCC 600
AACAGAAAT TAATGCTGAT ATAAAACGTA AATTAGTGAA GGAACCTCGA TCGTTGGAC 660
AAAAATATGA AAAATCTTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA 720
AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA 780
AGCACCTTAA GAAGAAACTG AAACGTATGA TTTGAGAATA CTTGTCCCTG GAGGATTATC 840
ACACCCCAAA TGCATAATCT CGTTAATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT 900
TCTACAATGG AGCAGGATAT TGCTGAAGTC TCCTGGCATA TGTTACCGAA TCAACTGGCC 960
TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAA GCGTTTTATT 1020
TGAAAGGATA ACTTGTGTTT TGGTTATTTT GTATTCCAC CTGTGCTGGT AGATATTATT 1080
AACCCATTAG GTAAATACTA TTACAGTCGT GGTTCCTGCA

Seq ID NO: 304 Protein sequence:
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
	MTDKTEKVVAV	DPETVFKRPR	ECDSPSYQKR	QRMALLARKQ	GAGDSLIAGS	AMSKAKKLMT	60
	GHAIPPSQLD	SQIDDPFGFS	KDRMMQKPGS	NAPVGNVTS	SFSGDDLECR	ETASSPKSQQ	120
5	ENADIKRKL	VKELRCVQK	YEKIFEMLEG	VQGPTAVRKR	FFESIKEAA	RCMRRDFVKH	180
	LKKKLKRLMI						

Seq ID NO: 305 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 87-689

	1	11	21	31	41	51	
	CGTGGAGGCA	GCTAGCGCGA	GGCTGGGGAG	CGCTGAGCCG	CGCGTCGTGC	CCTGCGCTGC	60
	CCAGACTAGC	GAACAATACA	GTCAGGATGG	CTAAAGGTGA	CCCCAAGAAA	CCAAAGGGCA	120
	AGATGTCCGC	TATGCGCTTC	TTTGTGCAGA	CATGCAGAGA	AGAACATAAG	AAGAAAAACC	180
	CAGAGGTCCC	TGTCAATTTT	GCGGAATTTT	CCAAGAAGTG	CTCTGAGAGG	TGGAAGACGA	240
	TGTCCGGGAA	AGAGAAATCT	AAATTTGATG	AAATGGCAAA	GGCAGATAAA	GTGCGCTATG	300
	ATCGGGAAT	GAAGGATTAAT	GGACCAAGTA	AGGGAGGCAA	GAAGAAGAG	GATCCTAATG	360
20	CTCCCAAAAG	GCCACCGTCT	GGATCTCTCC	TGTTCTGTTC	AGAATTCGCG	CCCAAGATCA	420
	AATCCACAAA	CCCCGGCATC	TCTATTGGAG	ACGTGGCAAA	AAAGCTGGGT	GAGATGTGGA	480
	ATAATTAAAA	TGACAGTGAA	AAGCAGCCTT	ACATCACTAA	GGCGGCAAG	CTGAAGGAGA	540
	AGTATGAGAA	GGATGTGCTT	GACTATAAGT	CGAAAGGAAA	GTTTGATGGT	GCAAAGGGTC	600
	CTGCTAAAGT	TGCCCGGAAA	AAGGTGGAAG	AGGAAGATGA	AGAAGAGGAG	GAGGAAGAAG	660
25	AGGAGGAGGA	GGAGGAGGAG	GATGAATAAA	GAAACTGTIT	ATCTGTCTCC	TTGTGAATAC	720
	TTAGAGTAGG	GGAGGCGCGT	AATTGACACA	TCTCTTATTT	GAGAAGTGTC	TGTTGCCCTC	780
	ATTAGGTTTA	ATTACAAAAT	TTGATCACGA	TCATATTGTA	GTCTCTCAAA	GTGCTCTAGA	840
	AATTGTCACT	GGTTTACATG	AAGTGGCCAT	GGGTGTCTGG	AGCACCCCTG	AACTGTATCA	900
	AAGTTGTACA	TTTTCACATG	CATTTTAAAA	ATGAAAAGGC	ACTCTCGTGT	TCTCCTCACT	960
30	CTGTGCACAT	TGCTGTTGGT	GTGACAAGGC	ATTTAAAGAT	GTTTCTGGCA	TTTTCTTTTT	1020
	ATTTGTAAAG	TGTTGGTAAAC	TATGGTTATT	GGCTAGAAAT	CCTGAGTTTT	CAACTGTATA	1080
	TATCTATAGT	TTGTAATAAG	AACAAAACAA	CCGAGACAAA	CCCTTGATGC	TCCTTGCTCG	1140
	GGCTTGAGGC	TGTGGGGGAG	ATGCCCTTTG	GGAGAGGCTG	TAGCTCAGGG	CGTGCACTGT	1200
	GAGGCTGGAC	CTGTGTGACTC	TGCAGGGGGC	ATCCATTTAG	CTTCAGGTGT	TCTTGTCTCT	1260
35	GTATATAGTG	ACATAGCACT	CTGCTGCCAT	CTTAGCTGTG	GACAAAGGGG	GGTCAGCTGG	1320
	CATGAGAAAT	TTTTTTTATT	TAAAGTGGGT	AGTTTAAAA	CTGTTTGTGT	TTAAACAAAC	1380
	TATAGAACTC	TTCAATGTCA	GCAAAACAAA	GAGTCACTGC	ATCAATGAAA	GTTCAAGAAC	1440
	CTCCTGTACT	TAAACACGAT	TCGCAACGTT	CTGTTATTTT	TTTTGTATGT	TTAGAATGCT	1500
	GAAATATTTT	TGAAGTTAAA	TAAACAGTAT	TACATTTTAA	AAACTCTTCT	CTATTATAAC	1560
40	AGTCAATTTT	TGACTCACAG	CAGTGAACAA	ACCCCCACTC	CATTGTATTT	GGAGACTGGC	1620
	CTCCCTATAA	ATGTGGTAGC	TTCTTTTATT	ACTCAGTGGC	CAGCTCACTT	AGGGCTGAGA	1680
	TGAAGGAGAG	GGCTACTTGA	AGCTACTGTG	TGATTTTGT	TGTGCTGTAG	TGGCATTTCAG	1740
	ATGAAGTCTG	GAGGAGTTAG	GAGAACGACA	TAGGCAAGGT	TCAGCAGCCT	TCCAAGGTAT	1800
	AGGAAGGTGG	GTGATTAGGA	CTGAGGCTAT	CTAGGTTTAA	CTTTTGTCCC	ACCTCCACCC	1860
45	CCTATTTTGT	GGGGCCCAAT	GCATTGCTAA	ACAGCAATTT	CAGAGTGTAT	GGTGTGTCAA	1920
	AAATTAAGGC	TTTATTGTGT	TTCTCTTTCA	CCCCTACCCC	CCGTGCTCCT	GGCACATATC	1980
	ACATTATTTG	TGGTGCCCAA	CATTGCGGCT	CTTGAGCCTG	CTGCTGGTCT	CCTGGATGCC	2040
	AGTGAGGGTA	TGTGGGATGG	GGTGGTGGGG	TAGGGGACGG	TATCCTTTTT	TTGCTCTTAC	2100
	TTGGAAACAC	CAAAACACCC	AAGGAAGATG	ATAGGCTCCA	TCITGGGCCA	CCTGAGCTAT	2160
50	AGGGCAGGCT	AATGGAATCA	ACCATTCTG	AGCACTAAAT	GTATCATGAA	AAGTTGAATG	2220
	GCCTGTCTAT	TAATTTAGCT	CATTCAGTGG	AAATGTAGAT	TGATGTTCAA	TGTTAAACTG	2280
	GAAGGAGCTT	GGTTTGTGTG	TCAGTGGTTA	TATTAGTGGG	TAGTGTAAAC	TTTATCCAG	2340
	GTGCGGTGTA	GGGGAGATGG	CCACAGTAGC	AAGTGGTGAC	ACTAAATACC	ATTTTGAAGG	2400
	CTGATGTGTA	TATACATCAT	TACTGTCCGT	AGCAATGAAG	GATACAGTAC	TGTGTGTGG	2460
55	GTGAGTGTGG	CTAATTGCCA	GCATTAAATAT	TTGGGTGTGT	ATGTTTGAGG	CTATGAACA	2520
	CGCAGGAGTG	TTTTTGTGCT	ATTAATTTTA	AGAGAAAGCA	GCTTTTCTCT	AAAATTCACT	2580
	GTTGAGAAAC	TTGCATGTCT	GGAGGCGGTG	TCCTCTCCGC	CCTGTCCGGT	CCTGGATGAG	2640
	TACGAGTTAT	GGTCACGCTG	ACAGCCTGAT	CTCTTATGTG	TTCATAGCCA	TTGCTCTCC	2700
	CATCAGAACT	GTTTGTCTGT	AATGTGTCTC	TCTAGTTCTA	GAAATGACC	ACTAATTTAA	2760
60	AAAACCTCGT	TGTGAGGTTT	GCCAGAGGCG	ACTTGTCTCA	GAAATTCCTC	TCCTGCTTCA	2820
	GGCATGTCTC	TGTCAGTTGG	CATTCTAAGC	TAAAGCTTTA	GCTTCCCAAT	TCGTGATGTG	2880
	CTAGGCCAAG	ATTCGGGAGC	TGTTGCCAGC	CTCGTCAAAT	ATGGAAGAGA	AACAACCTGC	2940
	GGTCAAAAGG	GAGTGATTGG	TTAAGTGGTG	CGCGTCTATC	TCATAACTAG	ATGTACCAAC	3000
	CAGGGAAGGG	CCAAGGATGG	AAAGGGGTAA	CTTTTGTGCT	TCCAAGTAG	CTAAGCAGAA	3060
65	TGTGGGGAGC	AGTTTAGCCA	GATGATCTTT	GATTAGGCAA	ACATTGAGTT	TTAAAGAGGC	3120
	TGTCAAGTTG	AGGCCACTTG	GTCCATTAGC	TGGGGCAGCA	AGATCACTAC	TCAACGTTTT	3180
	CACACTGTGG	CAAGATTGCT	CTTCTAGTGG	ATAATGCCCC	TAGTTTCTCT	GAGATGATGT	3240
	AAGTGGCATG	ATGTTACCTA	AGGCTTAGGC	TTAGCTTGAT	TTCTGGGCCC	ACTGTCTGTG	3300
	TTCTTAAGAT	GCCAACCTGT	TGCTTTTTTT	TTTTTTTTCC	CCCATTTAAA	AGGATAGTAC	3360
70	CTACTCCCTC	TAACCACTCT	ACCCATTCT	TGAATGACAT	TTTATCCTTC	GGAAAGAACA	3420
	AGGCTGTGAT	GTAGTGACTA	TTGTCTGTGT	CTCCGTGTGT	TGCTGTCTCT	TGTCACAAAT	3480
	GTATTTGGGG	ACGTTGGATG	CATTCATTTT	CTGTAATAAA	G		

Seq ID NO: 306 Protein sequence:

Protein Accession #: NP_005333.1

	1	11	21	31	41	51	
	MAKGDPPKKP	GRMSAYAFV	QTCREBHKKK	NPEVPVNFAB	FSKKCSERNK	TMSGKEKSKP	60
	DEMAKADKVR	YDREMKDYGP	AKGGKKKKDP	NAPKRPSPGF	FLFCSEFRPK	IKSTNPGISG	120
80	GDVAKKLGE	WNLNDSBKQ	PYITKAAKLE	EYKEDVADY	KSKGKFGAK	GPAKVARKKV	180
	EEEEEEEEEE	EEEEEEEEEE					

Seq ID NO: 307 DNA sequence

Nucleic Acid Accession #: NM_022342

Coding sequence: 1..2178

	1	11	21	31	41	51	
	MAKGDPPKKP	GRMSAYAFV	QTCREBHKKK	NPEVPVNFAB	FSKKCSERNK	TMSGKEKSKP	60
	DEMAKADKVR	YDREMKDYGP	AKGGKKKKDP	NAPKRPSPGF	FLFCSEFRPK	IKSTNPGISG	120
85	GDVAKKLGE	WNLNDSBKQ	PYITKAAKLE	EYKEDVADY	KSKGKFGAK	GPAKVARKKV	180
	EEEEEEEEEE	EEEEEEEEEE					

	1	11	21	31	41	51	
5	ATGGGTACTA	GGAAAAAAGT	TCATGCATTT	GTCCGTGTCA	AACCCACCGA	TGACTTTTGT	60
	CATGAAATGA	TCAGATACGG	AGATGACAAA	AGAAGCATTG	ATATTCACAT	AAAAAAGAC	120
	ATTCGGAGAG	GAGTTGTCAA	TAACCAACAG	ACAGACTGGT	CGTTTAAGTT	GGATGGAGTT	180
	TTCACGATG	CCTCCACGGA	CTTGGTTTAT	GAGACAGTTG	CAAAGGATGT	GGTTTCTCAG	240
	CCCTCGATG	GCTATAATGG	CACCATCATG	TGTTATGGGC	AGACGGGAGC	TGGCAAGACA	300
10	ACACCATGA	TGGGGGCAAC	TGAGAATTAC	AAGCACCGGG	GGATCCTCCC	TCGTGCCCTG	360
	AGCAGGTTT	TTAGGATGAT	CGAAGAACGC	CCCACACATG	CCATCACTGT	GCGTGTTTCC	420
	ACTTGGAAA	TCTATAATGA	GAGCCTGTTT	GATCTCCTGT	CCACTCTGCC	CTATGTTGGA	480
	CCTCAGTCA	CACCAATGAC	CATCGTGAAA	AACCTCAAG	GAGTCTTCAT	TAAGGGCTTG	540
	CAGTTTACC	TCACAAGTCA	GGAGGAGGAT	GCATTGAGCC	TCCPTTTTGA	GGGTGAGACC	600
15	ACAGGATTA	TAGCTTCCCA	CACATGAAC	AAAAACTCTT	CCAGATCACA	CTGCATTTTC	660
	CCATCTACT	TAGAGGCCCA	TTCCCGGACC	TTATCAGAGG	AAAAGTACAT	CACCTTCCAA	720
	TTAACTTGG	TGGATCTGGC	AGGCTCAGAG	AGGCTGGGGA	AGTCTGGGTC	TGAGGGCCAA	780
	TCCTGAAGG	AAGCCACCTA	CATCAACAAA	TCGCTCTCAT	TCCTGGAGCA	GGCCATCATT	840
	CCCTTGGGG	ACCAGAAAGC	GGACCAACATC	CCCTTTCGGC	AGTGCAAGCT	CACCCACGCT	900
20	TGAAGGACT	CGTTAGGGGG	AAACTGCAAT	ATGGTCTCTG	TGACAAACAT	CTATGGAGAA	960
	CTGCCAGAT	TAGAAGAAAC	GCTATCTTCA	CTGAGATTTG	CCAGCAGGAT	GAAGCTAGTC	1020
	CCACTGAGC	TGCCATCTCA	TGAAGAGTAT	GATGCTGAGA	GAATGGTCAA	GAACCTGGAG	1080
	AGGAAGTAG	CACACTCTCA	GCAGGAGCTG	GCTATCCATG	ACAGCCTGAC	CAACCGCACC	1140
	TTGTGACCT	ATGAGCCCAT	GGATGAAATC	CAGATTGCTG	AGATCAACTC	CCAGGTGCGG	1200
25	GGTACCTGG	AGGGGACACT	GGACGAGATC	GACATAATCA	GCCTTAGACA	GATCAAGGAG	1260
	GTGTTCAACC	AGTTCCGGGT	GGTCTGAGC	CAACAGGAAC	AGGAAGTGGA	GTCCACTTTG	1320
	GCAGGAAGT	ACACCTCTAT	TGACAGGAAT	GACTTTGCAG	CCATTTCTGC	TATCCAGAA	1380
	CGGGGCTTG	TGGATGTTGA	TGGCCACCTA	GTGGGTGAGC	CTGAAGGACA	AAACTTTGGA	1440
	TCGGAGTCG	CCCCTTTCTC	TACCAAACTT	GGGAAGAAAG	CCAAGTCCAA	GAAGACATTC	1500
30	AAGAGCCAC	TCAGAGCCGA	CACCCACCC	TCCAAACCCG	TGGCCCTTGA	GGAGTTTAA	1560
	ATGAGCAAG	GTAGTGAGAT	CAACCGAATT	TTCAAAGAAA	ACAATCCAT	CTTGAATGAA	1620
	GGAGGAAAA	GGGCCAGCGA	GACCAACAG	CACATCAATG	CCATCAAGCG	GGAGATTGAT	1680
	TGACCAAGG	AGGCCCTGAA	TTTCCAGAAG	TCACTACGGG	AGAAGCAAGG	CAAGTACGAA	1740
	ACAAGGGGC	TGATGATCAT	CGATGAGGAA	GAATTCCTGC	TGATCCTCAA	GCTCAAAGAC	1800
35	TCAAGAAGC	AGTACCGCAG	CGAGTACCAG	GACCTGCGTG	ACCTCAGGGC	TGAGATCCAG	1860
	ATTGCCAGC	ACCTAGTGGG	TCACTGTGCG	CACCGCCTGC	TCATGGAATT	TGACATCTGG	1920
	ACAATGAGT	CTTTTGTGAT	CCCTGAGGAC	ATGCAGATGG	CACTGAAGCC	AGGCCGCAGC	1980
	TCCGGCCAG	GCATGCTCCC	TGTGAACAGG	ATTGTGCTC	TGGGAGAAGA	TGACCAGGAC	2040
	AATTGAGCC	AGCTGCAGCA	GAGGGTGCTT	CCTGAGGGCC	CTGATTCCAT	CTCCTTCTAC	2100
40	ATGCCAAAG	TCAAGATAGA	GCAGAAAGCAT	AATTACTTGA	AAACCATGAT	GGGCTCCAG	2160
	AGGCACATA	GAATAATG					

Seq ID NO: 308 Protein sequence:
Protein Accession #: NP_071737

45	1	11	21	31	41	51	
	MGTRKKVHAF	VRVKPTDDFA	HEMIRYDDDK	RSIDIHLKID	IRRGVVNNQ	TWSFKLDGV	60
	LHDASQDLVY	ETVAKDVVSQ	ALDGYNGTIM	CYQGTGAGKT	YTMGATENY	KHRGILPRAL	120
50	QQVFRMIER	PTHAITVRVS	YLEIYNESLF	DLLSTLPYVG	PSVTPMTIVE	NPQGVPIKGL	180
	SVHLTSQED	AFSLPFEGET	NRIIASHTMN	KNSSRSHCIF	TIYLEAHSRT	LSEKYITSK	240
	INLVDLAGE	RLGKSGEGG	VLKEATYINK	SLSFLEQAI	ALGDQKRDI	PFRQCKLTHA	300
	LKDSLGGNC	MVLVTNLYGE	AAQLEETLSS	LRFAARMKLV	TTEPAINEKY	DAERMVKNLE	360
	KBLALLKQEL	AIHDSLTNRT	FVTYDPMDEI	QIAEINSQVR	RYLEGLDEI	DIISLRQIKE	420
55	VFNQFRVLS	QQEQEVSTL	RRKYTLIDRN	DFAAISAIQK	AGLVDDVDGHL	VGEPEQGNFG	480
	LGVAPFSTKP	GKKAKSKKTP	KEPLRPDTPP	SKPVAEEFCK	NEQGSSEINRI	FKENKSILNE	540
	RRKRASETQ	HINAIKREID	VTKEALNFQK	SLREKQGYE	NKGLMIIDEE	EPFLILKLD	600
	LKKQYRSEYQ	DLRLDLRAEQ	YCQHLVDQCR	HRLLMEFDIW	YNESFVIPED	MQMALPKPGGS	660
	IRPGMVPVNR	IVSLGEDDQD	KFSQLQQRVL	PEGPDSISFY	NAKVKIEQKH	NYLKTMMGLQ	720
60	QAHRK						

Seq ID NO: 309 DNA sequence
Nucleic Acid Accession #: CAT cluster

65	1	11	21	31	41	51	
	TTTTTTTTTT	TTTTTTTAA	TGCTGCTGT	CATGCTCTGT	CTACCAGGGT	GAATTTCCAA	60
	AAATTTCTGC	ATAGCAATTT	TAGCCAAAAC	TATATATGTT	CTGGGGAGGA	TAGGCATAGG	120
	CACATTGAAG	ACCAAGAGAA	AGAGTGAAGA	AGTGTAGTTG	GGTCATTGTG	AATGGATGTT	180
70	TAGATTGTCA	AGAAAAGTGG	GCCAGAGGCC	CCACCTCACA	CTAGGACGGC	AATGCTCTCT	240
	CATTAGTATC	TCAGGCACCA	TGGGTCTTAT	TTGGTGTGAT	AAGAAACACC	CTCAACAAAG	300
	TAATGAACCC	TCAGCCTCCA	GCTTCTCTTC	TTCGGGATTC	TTCTTAGGGC	CTCCTTTTTC	360
	CTTTTATGTT	TCCAGTACCC	TGAATTTCTT	ATTCCCATCC	CCCATTAATA	TCTGCTTCAA	420
	AGAAAAAACA	AGAAGGACAC	ATTCACTTTA	AGATCCAAAT	GAATGATAAG	AGCTTAAAC	480
75	ATTATACTTA	TCAGTATTAT	TTGCATTTTT	ATAGAAACCA	AAACCATATT	TCAACAAAC	

Seq ID NO: 310 DNA sequence
Nucleic Acid Accession #: NM_018622.2
Coding sequence: 1-1140

80	1	11	21	31	41	51	
	ATGGCGTGGC	GAGGCTGGGC	GCAGAGAGGC	TGGGCTGGCG	GCCAGGCGTG	GGGTGCGTGG	60
	GTGGGCGGGC	GCAGCTGCGA	GGAGCTCACT	GCGGTCCTAA	CCCCGCGCGA	GCTCCTCGGA	120
85	CGCAGGTTTA	ACTTCTTTAT	TCAACAAAAA	TGCGGATTCA	GAAGAAGCACC	CAGGAAGGTT	180
	GAACCTCGAA	GATCAGACCC	AGGGACAAGT	GGTGAAGCAT	ACAAGAGAAG	TGCTTTGATT	240
	CCTCCTGTGG	AAGAAACAGT	CTTTTATCCT	TCTCCCTATC	CTATAAGGAG	TCTCATAAAA	300
	CCTTTATTTT	TTACTGTGTG	GTTTACAGGC	TGTGCATTGG	GATCAGCTGC	TATTTGGCAA	360

TATGAATCAC TGAATCCAG GGTCCAGAGT TATTTTGATG GTATAAAAGC TGATTGGTTG 420
 GATAGCATAA GACCACAAAA AGAAGGAGAC TTCAGAAAGG AGATTAACAA GTGGTGGAAAT 480
 AACCTTAAGTG ATGGCCAGCG GACTGTGACA GGTATTATAG CTGCAAAATGT CCTTGTATTTC 540
 5 TGTTTATGGA GAGTACCTTC TCTGCAGCGG ACAATGATCA GATATTTTCA ATCGAATCCA 600
 GGCTCAAAGG TCCTTTGTTC TCCAATGTTG CTGTCAACAT TCAGTCACTT CTCTTATTTC 660
 CACATGGCAG CAAATATGTA TGTTTTGTGG AGCTTCTCTT CCAGCATAGT GAACATTCTG 720
 GGTCAAGAGC AGTTTCATGGC AGTGTACCTA TCTGCAGGTG TTATTTCCAA TTTTGTTCAGT 780
 TACCTGGGTA AAGTTGCCAC AGGAAGATAT GGACCATCAC TTGGTGCATC TGGTGGCCATC 840
 10 ATGACAGTCC TCGCAGCTGT CTGCACTAAG ATCCCAAGAG GGAGGCTTGC CATTTATTTTC 900
 CTTCGAGTGT TCACGTTTCA AGCAGGGAAT GCCCTGAAAG CCATATCTGC CATGGATACA 960
 GCAGGAATGA TCCTGGGATG GAAATTTTTT GATCATGCGG CACATCTTGG GGGAGCTCTT 1020
 TTTGGAATAT GGTATGTTAC TTACGGTCAT GAACTGATTT GGAAGAACAG GGAGCCGCTA 1080
 GTGAAATCT GGCATGAAAT AAGGACTAAT GGCCCCAAAA AAGGAGGTGG CTCTAAGTAA

Seq ID NO: 311 Protein sequence:
 Protein Accession #: NP_061092.2

1 11 21 31 41 51
 20 MANRWGAQRG WGCQQAAGAS VGGRSCEELT AVLTPPOLLG RRFNFFIQOK CGFRKAPRKV 60
 EPRRSDPQTS GEAYKRSALI PPVEETVFYP SPYPFIRSLIK PLFPTVGFQT CAFGSAAIHQ 120
 YESLKRVRQS YFDGIKADWL DSRPQKEGD FRKEINKWNN NLSDDGQRTVT GIIAANVLVF 180
 25 CWRVPSLQR TMIRYFTSNP ASKVLCSPLM LSTFHSFLF HMAANMYVLW SFSSSIVNII 240
 GGEQFMAYVL SAGVISNFVS YLGKVAATRY GPSLGAAGAI MVLVAAVCTK IPEGLRAIIF 300
 LPMFTFTAGN ALKAIANDT AGMILGWKFP DHAHLGGAL FGIWYVTVGH ELIWKNNREPL 360
 VKIWHIEIRTN GPKKGGGSK

Seq ID NO: 312 DNA sequence
 Nucleic Acid Accession #: NM_000625
 Coding sequence: 195..3656

1 11 21 31 41 51
 35 CTCTCGGCCA CCTTTGATGA GGGGACTGGG CAGTTCTAGA CAGTCCCGAA GTTCTCAAGG 60
 CACAGGTCTC TTCCTGGTTT GACTGTCTCT ACCCGGGGGA GGCAGTGCAG CCAGCTGCAA 120
 GCCCCACAGT GAAGAACATC TGAGCTCAAA TCCAGATAAG TGACATAAGT GACCTGCTTT 180
 40 GTAAAGCCAT AGAGATGGCC TGTCTTGGGA AATTTCTGTT CAAGACCAAA TTCCACCAGT 240
 ATGCAATGAA TGGGGAAAAA GGCATCAACA ACAATGTGGA GAAAGCCCCC TGTGCCACCT 300
 CAGTCCAGT GACACAGGAT GACCTTCAGT ATCACAACCT CAGCAAGCAG CAGAATGAGT 360
 CCCCCGAGCC CCTCGTGGAG ACGGGAAGA AGTCTCCAGA ATCTCTGGTC AAGCTGGATG 420
 CAACCCCATT GTCCTCCCA CCGCATGTGA GGATCAAAA CTGGGGCAGC GGGATGACTT 480
 45 TCCAAGACAC ACTTCACCAT AAGGCCAAA GGATTTTAAC TTGCAGGTCC AAATCTTGCC 540
 TGGGGTCCAT TATGACTCCC AAAAGTTTGA CCAGAGGACC CAGGGACAAG CCTACCCCTC 600
 CAGATGAGCT TCTACCTCAA GTATCGAAT TTGTCAACCA ATATTACGGC TCCCTCAAAG 660
 AGGCAAAAT AGAGGAACAT CTGGCCAGGG TGGAAAGCGT AACAAAGGAG ATAGAAACAA 720
 CAGTAACCTA CCAACTGACG GGAGATGAGC TCATCTTCGC CACCAAGCAG GCCTGGCGCA 780
 50 ATGCCCCACG CTGCATTGGG AGGATCCAGT GGTCCAACCT GCAGGTCTTC GATGCCCGCA 840
 GCTGTTCCAC TGCCCGGGAA ATGTTTGAAC ACATCTGCAG ACACGTGCGT TACTCCACCA 900
 ACAATGGCAA TCGGAAGTCT GGCATCACCG TGTCCCCCA GCGGAGTGAT GGCAAGCAGC 960
 ACTTCGGGT GTGGAATGCT CAGCTCATCC GCTATGCTGG CTACCAAGATG CCAGATGGCA 1020
 GCATCAGAGG GGACCTGCCC AACGTGGAAT TCACTCAGCT GTGCATCGAC CTGGGCTGGA 1080
 55 AGCCCAAGTA CGGCCGCTTC CATGTGGTCC CCCTGGTCTC GCAGGCCAAT GGCCGTGACC 1140
 CTGAGCTCTT CGAATCCCA CCTGACCTTG TGCTTGAGGT GGCCATGGAA CATCCCAAT 1200
 ACGAGTGGTT TCGGAAGTCT GAGCTAAAGT GGTACGCCCT GCCTGCAGTG GCCAATATG 1260
 TGCTTGAGGT GGGCGGCTG GAGTTCCTCAG GGTGCCCTT CAATGGCTGG TACATGGGCA 1320
 CAGAGATCGG AGTCGGGAC TCTGTGATG TCCAGCGCTA CAACATCTG GAGGAAGTGG 1380
 60 GCAGGAGAAT GGGCCTGGAA ACGCACAAGC TGGCCTCGCT CTGGAAGAC CAGGCTGTG 1440
 TTGAGATCAA CATGTGCTGT CTCATAGTT TCCAGAAGCA GAATGTGACC ATCATGGACC 1500
 ACCACTCGGC TGCAGAACTC TTCTGAAAT ACATGCAGAA TGAATACCGG TCCCGTGGGG 1560
 GCTGCCCGGC AGACTGGAAT TGGCTGGTCC CTCCTATGTC TGGGAGCATC ACCCCGCTGT 1620
 65 TTCACCAGGA GATGCTGAAC TACGTCCTGT CCCCCTTCTA CTACTATCAG GTAGAGGCCT 1680
 GGAAACCCA TGTCTGGCAG GACGAGAAGC GGAGACCCAA GAGAAGAGAG ATTCCATTGA 1740
 AAGTCTTGTT CAAAGCTGTG CTCTTTGCCT GTATGCTGAT GCGCAAGACA ATGGCGTCCC 1800
 GAGTCAGAGT CACCATCTC TTTGCGACAG AGACAGGAAA ATCAGAGGCG CTGGCCTGGG 1860
 ACCTGGGGGC CTTATTGAGC TGTGCTTCA ACCCAAGGT TGTCTGCATG GATAAGTACA 1920
 70 GGCTGAGCTG CTGGAGGAG GAACGGCTGC TGTGGTGGT GACCAAGTAC TTTGGCAATG 1980
 GAGACTGCCC TGGCAATGGA GAGAACTGA AGAAATCGCT CTTATGCTG AAAGAGCTCA 2040
 ACAACAAATT CAGGTACGCT GTGTTTGGCC TGGGCTCCAG CATGTACCTT CGGTTCTGCG 2100
 CCTTTGCTCA TGACATTGAT CAGAAGCTGT CCCACCTGGG GGCTCTCAG CTCACCCGA 2160
 TGGGAGAAGG GGATGAGCTC AGTGGGCAAG AGGACGCTT CCGCAGCTGG GCCGTGCAAA 2220
 75 CCTTCAAGGC AGCTGTGAG ACGTTTGATG TCCGAGGCAA ACAGCACATT CAGATCCCA 2280
 AGCTCTACAC CTCCAATGTG ACCTGGGACC CGCACCACTA CAGGCTCGTG CAGGACTCAC 2340
 AGCCTTTGGA CCTCAGCAAA GCCTCAGCA GCATGCATGC CAAGAAGCTG TTCACCATGA 2400
 GGCTCAATC TCGCAGAGAT CTACAAAGTC CGATGCCACC CCGTGCCACC ATCTGGTGG 2460
 AACTCTCTG TGAGGATGGC CAAGGCTGTA ACTACCTGCC GGGGAGGAC CTGGGGTTT 2520
 80 GCCCAGGCAA CACGCCGCC CTGGTCCAAG GCATCTGGA GCGAGTGGTG GATGGGCCAT 2580
 CACCCACCA GGCAGTGGC CTGGAGGCC TGGATGAGAG TGGCAGTAC TGGGTGAGT 2640
 ACAAGAGGCT GCCCCCTGTC TCACTCAGCC AGGCCCTCAC CTACTTCTG GACATCACA 2700
 CACCCCAAC CACGCTGTCTG CTCCAAAGC TGGCCAGGT GGCCACAGAG GAGCTTGAGA 2760
 GACACAGGCT GAGGCGCTG TGCCAGCCCT CAGAGTACAG CAAGTGGAG TTCAACCA 2820
 85 GCCCACAATT CTGGAGGTG CTAGAGGAGT TCCCGTCCCT GCGGTGTCT GCTGGCTTCC 2880
 TGCTTCCCA GCTCCCATC CTGAAGCCCA GGTCTACTC CATCAGTCC CCCCAGGATC 2940
 ACACGCCCC GAGATCCAC GTGACTGTGG CCGTGTGTC CTACCAACC CGAGATGGCC 3000
 AGGTCCCTC GCACCAAGG GTCTGCAGCA CATGGCTCAA CAGCCTGAAG CCCCAAGACC 3060
 CAGTGCCTG CTTTGTGCGG AATGCCAGCG GCTTCCACT CCCCAGGAT CCTTCCATC 3120

CTTGATCCT CATCGGGCT GGCACAGGCA TCGCGCCCT CCGCAGTTTC TGGCAGCAAC 3180
GGCTCCATGA CTCCAGCAC AAGGAGTGC GGGAGGCCG CATGACCTTG GTGTTGGGT 3240
GCCGCGCCC AGATGAGGAC CACATCTACC AGGAGGAGAT GCTGGAGATG GCCCAGAAGG 3300
GGGTGCTGCA TCGGGTGCC ACAGCCTATT CCGCCTGCG TGGCAAGCCC AAGGTCTATG 3360
5 TTCAGGACAT CCTCGGCGAG CAGCTGGCCA GCGAGGTGCT CCGTGTGCTC CACAAGGAGC 3420
CAGGCCACCT CTATGTTTGC GGGGATGTGC GCATGGCCCG GGACGTGGCC CACACCCTGA 3480
AGCAGCTGGT GGCTGCCAAG CTGAAATTGA ATGAGGAGCA GGTGAGGAC TATTTCTTTC 3540
AGCTCAAGAG CCAGAAGCGC TATCAGCAAG ATATCTTTGG TGCTGTATT CTTCAGAGG 3600
10 CGAAGAAGGA CAGGGTGGCG GTGCAGCCCA GCAGCCTGGA GATGTGAGG CTCTGAGGGC 3660
CTACAGGAGG GGTAAAGCT GCCGCGCAG AACTTAAGGA TGGAGCCAGC TCTGCATTAT 3720
CTGAGGTAC AGGCCTGGG GAGATGGAGG AAAGTGATAT CCCCAGCCT CAAGTCTTAT 3780
TTCCTCAAG TTGCTCCCA TCAAGCCCTT TACTTGACCT CCTAACAACT AGCACCTGG 3840
ATTGATCGGA GCCTC

Seq ID NO: 313 Protein sequence:
Protein Accession #: NP_000616

1 11 21 31 41 51
MACPWKFLPK TKFHQYAMNG EKGINNVEK APCATSSPVT QDDLQYHNLS KQONESPOPL 60
VETGKKSPES LVKLDATPLS SPRHVRKNW GSGMTFQDTL HHKAKGILTC RSKSCLGSIM 120
TPKSLTRGRP DKPTPPDELL PQAIEFVNQY YGSLKEAKIE EHLARVEAVT KEIETTVTYQ 180
25 LTGDELIPAT KQAWRNAERC IGRIQWSNLQ VFDARSCSTA REMPEHICRH VRYSTNNNGI 240
RSAITVFPQR SDGKHDPRVW NAQLIRYAGY QMPDGSIRGD PANVEFTQLC IDLGWPKPYG 300
RFDVVLVLQ ANGRDPELEFE IPPDLVLEVA MEHPKYEWFR EELKWKYALP AVANMLLEVG 360
GLEFPGPCFPN GWYMGTEIGV RDPFDVQRYN ILEEVGRRMG LETHKLASLW KDQAVVEINI 420
AVLHSFQKQN VTIMDHSAA BSMFKYMQNE YRSRGCCPAD WILVPPMSG SITPVFHEQM 480
30 LNYVLSPPFY YQEAWKTHV WQDEKRRPKR REIPLKVLVK AVLPAFMLMR KTMASRVVVT 540
ILFATETGKS EALAWDLGAL FSCAPNPKVV CMDKYRLSCL EEBERLLVVT STFGNGDCPG 600
NGEKLKKSIF MLKELNNKFR YAVFGLGSSM YPRFCAFAHD IDQKLSHLGA SOLTPMGECD 660
ELSGQEDAFR SWAVQTFKAA CETFDVRGKQ HIQIPKLYTS NVTNDPHYR LVQDSQPLDL 720
SKALSSMHAK NVFTMRKLSR QNLQSPSSR ATILVELSCE DGQGLNLYPG EHLGVCPGNQ 780
35 PALVQGILER VVDGTPHQA VRLEALDESG SYWVSDKRLP PCSLSQALTY FLDITTPPTQ 840
LLQLKLAQVA TEPPERQRL EALCQPSSEYK WKFTNSPTFL EVLEEFPSLR VSAGFLLSQL 900
PILKPRFYI SSPRDHTPE IHLTVAVVY HTRDGGQPLH HGVCSTWLS LKQDPVPCF 960
VRNASGFHLP EDPSPHCILI GPGTGIAPFR SFWQQRHDS QHKGVRGGRM TLVFGCRRPD 1020
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40 VCGDVRMARD VAHLKQLVA AKLKLNEEQV EDYFFQLKSG KRYHEDIFGA VFPYEAKDR 1140
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Seq ID NO: 314 DNA sequence
Nucleic Acid Accession #: XM_087254
Coding sequence: 47..2332

1 11 21 31 41 51
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55 CAATGTTCAA ACTGACTGCA CTGGTGATGG TCCCTGGCAA TCCAACCTGG CACCATCGCA 360
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65 AGTATGGGTA CTACTGGGG ATAAACATGA AACAGCTGTT AGTGTGAGTT TATCATGTGG 960
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85 CTGTTTCCCG GAAGGAGAAG CAGCTGTGTC ATCTGTGGA AGAATGCTGG AACGAGTTAT 2220
AGGAAGATGT AGTCCAACCC ACATCAGCAG ATCATGGAGT GCATCGGATC CTTTCTATAC 2280
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Seq ID NO: 315 Protein sequence:
Protein Accession #: XP_087254

Seq ID NO: 316 DNA sequence
Nucleic Acid Accession #: NM_004473
Coding sequence: 661..1791

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	AGTACTAACT	GCCCTCGCTC	TGGCCTTCGA	GCCCGAAGCC	TCTTCTGCGC	GCACAACCTA	240
5	GGCAGTAATC	CTAAACTAGC	GGGCACCACA	GACCAAGCTG	AGCCACCCCA	ACCCAGGGAT	300
	CACCTCCGGA	CCCCTCGACC	GCCCGGCACC	AGCGCGCAAG	GGACCCCTCA	GCCGAGAGCC	360
	AGAGTCCAGT	CCCCTGCGCG	AGGCCACCGC	CGCTGCCCGC	CTCGAGAAGC	ACAACGCGGG	420
	CTGAGCCGTC	GGCTAGCGGG	TCACTCCCGA	GCCTCTGTCT	GCACCGCGCC	AGCCCCAGAC	480
	CACGACGCT	GAGCTCCAG	CGCGCGCCAG	CCTGGGCGCG	TGGGCTCTCC	GGGCCAGCCC	540
10	GCGACGATCC	CCTGAGCTCT	CGCAGAAAGG	GCCGAGCGTC	CGTTCCGCGG	ACGCCAGGCC	600
	CGCCCCCGCC	CCCCGACAGC	CGCGGGGATC	CAGAGCCCGG	GGGTGCGGGA	CGCCCGCGCC	660
	ATGACTGCCG	AGAGCGGGCC	GCCCGCGCCG	CAGCCGAGAG	TGCTGGCTAC	CGTGAAGGAA	720
	GAGCGCGGGG	AGAGCGGCAG	AGGGGCGGGG	GTCCGAGGGG	AGGCCACGGG	CGCGGGGCGG	780
	GGCGGGCGGC	GCCCAAGCGG	CCCCCTGCAG	CGCGGGAAGC	CGCCCTACAG	CTACATCGCG	840
	CTCATCGCCA	TGGCGCTGCG	GACGCGCGCC	GAGCGCGCGC	TCACGCTGGG	CGGCATCTAC	900
15	AAGTTTATCA	CCGAGCGCTT	CCCTTCTTAC	CGCGACAACC	CCAAAAAGTG	GCAGAACAGC	960
	ATCCGCCACA	ACCTCACACT	CAACGACTGC	TTCTCTAAGA	TCCGCGCGCA	GGCGGCGCGC	1020
	CCGGGTAAGG	GCAACTACTG	GGCGCTCGAC	CCCAACGCGG	AGGACATGTT	CGAGAGCGGC	1080
	AGCTTCTCTG	GCCGCGCGCA	GCGCTTCAAG	CGCTCGGACC	TCTCCACCTA	CCCGGCTTAC	1140
20	ATGACGAGC	CGGCGGCTGC	CGCAGCCCGC	GCTGCCGCGC	CCGCGCGCGC	CGCGCGCGCC	1200
	GCGCGCATCT	TCCAGGCGCG	GGTGCCCGCC	GCGCGCGCCC	CCTACCCGGG	CGCGGCTCTAT	1260
	GCAGGCTACG	CGCGCGCGCG	CGCGCTCCAG	TCTACTACCC	CGCGGCGTCG		1320
	CCGCGCCCTT	GCCGCGCTCT	CGGCTGTGTT	CCTGAGCGCG	CGCTCAGCCC	AGAGCTGGGG	1380
	CCCGCACCGT	CGGCGCGCGG	CGGCTCTTGC	GCCTTTGCGT	CCGCGCGCGC	CCCCGCTACC	1440
25	ACCAAGCGCT	AGCGCGCGCG	AGGCTGCACC	GGGGCGCGCG	CGGCCAACCC	CTCTGCCTAT	1500
	GCGGCTGCCT	ACGCGGGCGC	CGAGCGCGCG	TACCGCGAGG	GCGCGCGCAG	TGCGATCTTT	1560
	GCCGCTGCTG	GCCGCGCTGG	GGGACCGCGT	TCCGCGCGCG	CGGGCGCGCAG	CAGTGGCGGC	1620
	GTGGAGACCA	CGGTGGACTT	CTACGGGCGC	ACGTGCGCGG	GCCAGTTCCG	AGCGCTGGGA	1680
	GCCTGTCTACA	ACCTTGGCGG	GCAGCTCGGA	GGGGCGCGTG	CAGGCGCCTA	CCATGCTCGC	1740
30	CATGCTGCGG	CTTATCCCGG	TGGGATAGAT	CGGTTCTGTG	CCGCCATGTG	AGCCAGCGTA	1800
	GGGACGAAAA	CTCATAGACA	CATCGGCTGT	TCAACGTTTC	CCCGCAACCT	GAGAACGAAAC	1860
	AGGAATGGAG	AGAGGACTCA	ACTGGGACCC	ACGTGGAAAA	GACCGAGCAG	GCCACAGAGG	1920
	CTCGGTCTCC	CCGCGCACAG	CGTAGGCACC	CTGTGTACTC	TGTAAACCGG	AGGAGGTGGG	1980
	GCGAGGCAGC	CAGAGCCCTT	GGACTGGCAC	AGGGACCCCT	GATGGAGCGA	AGCCCTCAAA	2040
35	CGGGATGCTT	TCTGGCATTC	TATCGGGGAG	GGTCTTGGC	GGTAACGAGA	GGGACGCGTA	2100
	GTGTCAACAC	CAGAGACGAG	GATCCAAATT	GTGGGGAATC	AGTTTACGCC	TTCCATGTGC	2160
	TGCCGGAAC	CGGGCCTTTT	TACGCGGTTT	GTCTCTAGT	GCCTTTAACT	CGGTTACTAC	2220
	AATAAAGGCG	TGCGGCAGCG	CCTTCTTTCT	TAAAGTGAGG	AGGACAAATT	TGCAAAAGAA	2280
	ATAGGCTTTT	CTTCTTTTCT	AAATTGGAGA	AATCTCTGCT	CTGGTTGACC	TGGGCTGGTT	2340
40	TTCCCTGTCT	CTGAGAACTT	GAGACCTAGC	TCCGAGTTGA	ACTGTGCGTC	AGCACTCCAG	2400
	TCCCATCACC	TGAACCTTCA	GTCTCCCCCA	TCTGTTACAC	TAGAGGGCTG	CAGGACTCTA	2460
	TCCACCGCCC	CCGGGTATAC	ATTCAAGGCC	CCATCATCTT	GGATGCTGCC	CTGCGTATTT	2520
	GGCAGCAATG	GTGGGCCACC	CAGGGCCTCT	GAGTAGCCAC	CCAAAGCCTA	GCCGCTGTTC	2580
	TAGGGAACGG	AAAAGAGTTC	ATGGCCAGGC	GTCTAACCTA	AAGTCCCAGG	ATTGGCTCCA	2640
45	GGCAGCAATT	ATATCATAA	TTATGAACT	TTTGAGCAGG	ACGTGCTGGT	AATTTTCATG	2700
	CTGTACTGCG	CCAGTCATAA	ATCTGCTTTT	CCATTATAAG	GCAGAGAGAA	GTACATTCGT	2760
	TCATTTGTGC	ACTGTTTCTT	GTCTACAGC	AGCCCTGGAC	CCAAAGGGTG	AACTAAAGTT	2820
	TAAGGAGATG	AGAGGATTCA	AGGAGCCCGT	TGGTGACGCC	TTTCAGTAGC	TGGGAGGGGC	2880
	TCTTCCATCC	CCAGCACCCC	CTGCTACACC	TCAGCAGCCT	CCCCCATGCA	AAAAGGAAAG	2940
50	AGAAAAATTA	AGTTAGGGCA	GTCACTAAAG	TGAGCTTTAG	AAAGAAACTG	GAATTTTAAAC	3000
	TTCAATTTGT	ATCTTGCTTA	AGTAGCAGGC	TCACTAAAAA	TAGAGAAAGT	CCAATAACTC	3060
	TCCCGCTTTC	CCTTGAGAAA	TCTTTAAGTT	TGGAATCTGG	AGCAAAAACT	TTTCTGTATA	3120
	AATATTTTCG	AGGCTCCATT	CACAGCTTTC	AGATAAACTG	GAGTGTTCAG	ATGGACTGTT	3180
	TTAATAAAAA	TCTTTGAGCA	AGTGAGTTAT	GGCAAGAGAA	ACTCAGCCTC	TTTCTGTATA	3240
55	AACTTAACAG	GGAGGGGCTG	GGGTGTGAAA	AAGAAGATTG	TATGAAAAAC	ATTGGTAATT	3300
	TTTATTTTTT	ATTTTGGGGA	CTGCACATAT	CTGTTTACGA	AGACATGTGA	ACTTGGTTCA	3360
	GTCCAAATGG	GAGTTTGTAT	AAACCAAGTG	TCTCCATTAG	AAATATGGTG	CAAGCCACAT	3420
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	AA						

Seq ID NO: 317 Protein sequence:
Protein Accession #: NP_004464

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65	FKHLTHYROI	DTRANSCRIP	TIONFACTOR	TFMTAESGP	PPPQPEVLAT	VKEERGETAA	60
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	PFYRDNPKKW	QNSIRHNLTL	NDCFLKIPRE	AGRPGKGNVW	ALDPNAEDMF	ESGSFLRRRK	180
	RFKRSDLSTY	PAYMHDAAAA	AAAAAATAAA	AAAAAIFPGA	VPAARPPYPG	AVYAGYAPPS	240
70	LAAPPVVIYP	AASPGPCRVF	GLVPERPLSP	ELGPAPSGPG	GSCAFASAGA	PATTTGYQPA	300
	GCTGARPNP	SAYAAAYAGP	DGAYPQGAGS	ALFAAAGRLA	GPASPPAGGS	SGGVETTVD	360
	YGRTPGQFG	ALGACYNPFG	QLGGASAGAY	HARHAAAYPG	GIDRFVSAM		

Seq ID NO: 318 DNA sequence
Nucleic Acid Accession #: NM_005688
Coding sequence: 126..4439

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	AGAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCTC	GGGTATAGAA	180
	GTGTAGGGGA	GAGAACCCAG	ACTTCTGGGA	CGCACAGAGA	CCGTGAAGAT	TCCAAGTTCA	240
	GGAGAACTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
85	TCTCTCTTGA	TGCCCTCCATG	CATTCTCAGC	TCAGAATCCT	GGATGAGGAG	CATCCCAAGG	360
	GAAAGTACCA	TGATGGCTTG	AGTGTCTGTA	AGCCCATCCG	GACTACTTCC	AAACACCAGC	420
	ACCCAGTGGA	CAATGCTGGG	CTTTTCTTCT	GTATGACTTT	TTCGTGGGCT	TCTTCTCTGG	480

	CCCGTGTGGC	CCACAAGAG	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
	AAGTTGGGCC	AGACGCTGCT	TCCCTGCGAA	GGGTTGTGTG	GATCTTCTGC	CGCACCAGGC	660
5	TCATCTGTGC	CTATGCTGTG	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAAGCT	720
	TCATGTTGAA	ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CAGTACAGCT	780
	TGTTGTTAGT	GCTGGGCTCT	CTCCTGACGG	AAATCGTGGC	GTCTTGGTCT	CTTGCACTGA	840
	CTTGGGCATT	GAATTACCGA	ACCGGTGTCC	GCTTGGCGGG	GGCCATCTCTA	ACCATGGCAT	900
	TTAAGAAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
10	TTTGCTCCAA	CGATGGGCAG	AGAATGTTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGCTG	1020
	GAGGACCCGT	TGTTGCCATC	TTAGGCATGA	TTTATAATGT	AATTATTCTG	GGACCAACAG	1080
	GCTTCTGGG	ATCAGCTGTT	TTTATCTCT	TTTACCCAGC	AATGATGTTT	GCATCACGGC	1140
	TCACAGCATA	TTTCAGGAGA	AAATGCGTGG	CCGCCACCGA	TGAACGTGTC	CAGAAGATGA	1200
	ATGAAGTTCT	TACTTACATT	AAATTTATCA	AAATGTATGC	CTGGGTCAAA	GCATTTTCTC	1260
15	AGAGTGTCCA	AAAAATCCGC	GAGGAGGAGC	GTGCGATATT	GGAAAAAGCC	GGGTACTTCC	1320
	AGGGTATCAC	TGTGGGTGTG	GCTCCCATTT	TGGTGGTGAT	TGCCAGCGTG	GTGACCTTCT	1380
	CTGTTTCATAT	GACCTCTGGG	TTGATCTGA	CAGCAGCACA	GGCTTTCACA	GTGGTGACAG	1440
	TCCTTCAATTC	CATGACTTTT	GCTTTGAAAG	TAACACCGTT	TTCAGTAAAG	TCCCTCTCAG	1500
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20	TAAAGAACAA	AAAGTCCAGT	CCTCACATCA	AGATAGAGAT	GAAAAATGCC	ACCTTGGCAT	1620
	GGGACTCCTC	CCACTCCAGT	ATCCAGAACT	CGCCCAAGCT	GACCCCAAAA	ATGAAAAAAG	1680
	ACAAGAGGGC	TCCAGGGGCG	AGAAAGAGA	AGGTGAGGCA	GCTGCAGCGC	ACTGAGCATC	1740
	AGGCGGTGCT	GGCAGAGCAG	AAAGGCCACC	TCTCTCTGGA	CAGTGACGAG	CGGCCAGTCT	1800
	CCGAAGAGGA	AGAAGGCAGG	CACATCCACC	TGGGCCACCT	GCGCTTACAG	AGGACACTGC	1860
25	ACAGCATCGA	TCTGGAGATC	CAAGAGGGTA	AACCTGTTGG	AATCTGCGCG	AGTGTGGGAA	1920
	TGTGAAAAAC	CTCTCTCAT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGCAACTCTT	GCTTATGTGG	CCCAGCAGGC	CTGGATCTCT	AATGCTACTC	2040
	TGAGAGACAA	CATCTGTGTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAAC	TCTGTGCTGA	2100
	ACAGCTGCTG	CCTGAGGCCT	GACCTGGCCA	TTCTTCCAG	CAGCGACCTG	ACGGAGATTG	2160
30	GAGAGCGAGG	AGCCAACCTG	AGCGGTGGGC	AGCGCCAGAG	GATCAGCTTT	GCCCGGCCCT	2220
	TGTATAGTGA	CAGGAGCATC	TACATCTCTG	ACGACCCCTT	CAGTGCCTTA	GATGCCCATG	2280
	TGGGCAACCA	CATCTTCAAT	AGTGTATCTC	GGAAACATCT	CAAGTCCAAG	ACAGTTCTGT	2340
	TTGTTACCCA	CCAGTTACAG	TACCTGGTTG	ACTGTGATGA	AGTGTCTTCT	ATGAAAGAGG	2400
	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AACTGATGAA	TTTAAATGGT	GACTATGCTA	2460
35	CCATTTTAA	TAACTGTGTT	CTGGAGAGGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
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	GTTCAAGTGC	CTGGTCAGTA	TATGGTGTCT	ACATCCAGGC	TGCTGGGGGC	CCCTTGGCAT	2700
	TCTCTGTTAT	TATGGCCCTT	TTTATGCTGA	ATGTAGGCAG	CACCGCCTTC	AGCACCTGGT	2760
40	GGTTGAGTTA	CTGATATCAAG	CAAGGAAGCG	GGAAACACAC	TGTGACTCGA	GGGAACGAGA	2820
	CCTCGGTGAG	TGACAGCATG	AAGGACAATC	CTCATATGCA	GTAATATGCC	AGCATCTACG	2880
	CCCTCTCCAT	GGCAGTCTAT	CTGATCTGTA	AAGCCATTCT	AGGAGTTGTC	TTTGTCAAGG	2940
	GCACGCTGCG	AGCTTCTCTC	CGGCTGCTAT	ACGAGCTTTT	CCGAAGGATC	CTTCGAAGCC	3000
	CTATGAAGTT	TTTTGACACG	ACCCCCACAG	GGAGGATTTT	CAACAGGTTT	TCCAAAGACA	3060
45	TGGATGAAGT	TGACGTGCGG	CTGCCGTCTC	AGGCCGAGAT	GTTTATCCAG	AACGTTATCC	3120
	TGGTGTCTCT	CTGTGTGGGA	ATGATGCGAG	GAGTCTTCCC	GTGGTTCCCT	GTGGCAGTGG	3180
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	TGAAGCGTCT	GGACAATATC	ACCGAGTCAC	CTTCTCTCTC	CCACATCACG	TCCAGCATAC	3300
	AGGGCCTTGC	CACCATCCAC	GCCTACAATA	AAGGGCAGGA	GTTTCTGCAC	AGATACCAGG	3360
50	AGCTGTGGA	TGACAACCAA	GTCTCTTTT	TTTTGTTTAC	GTGTGCGATG	CGGTGGCTGG	3420
	CTGTGCGGCT	GGACCTCATC	AGCATCGCCC	TCATCACCAC	CACGGGCTG	ATGATCGTTC	3480
	TTATGCAAGG	AACACTTCCC	CCAGCCTATG	CGGGTCTGCG	CATCTCTTAT	GCTGTCCAGT	3540
	TAAAGGGGCT	GTTCCAGTTT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTCCACT	3600
	CGGTGGAGAG	GATCAATCAC	TACATTAAGA	CTCTGTCTCT	GGAAAGCACCT	GCCAGAATTA	3660
55	AGAACAAGGC	TCCCTCCCTT	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	GAGAACGCGAG	3720
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	CTAAAGAGAA	GATTGGCATT	GTGGGGCGGA	CAGGATCAGG	GAAGTCTCTG	CTGGGGATGG	3840
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	GTGATATTGG	CCTTGGCCGAC	CTCCGAAGCA	AACTCTCTAT	CATTCTCTCA	GAGCCGGTGC	3960
60	TGTTCACTGG	CACCTGTGAG	TCAAATTGAG	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
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	TGAAATCTGA	AGTGTGAGG	AATGGGGATA	ACTTCTCAGT	GGGGGAACGG	CAGCTCTTGT	4140
	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTAGATGAA	GCCACAGCTG	4200
	CCATGGACAC	AGAGACAGAG	TTATTGATT	AAGAGACCAT	CCGAGAAGCA	TTTGACAGCT	4260
65	GTACCATGCT	GACCATGTCC	CATCGCTGCG	ACACGCTTCT	AGGCTCCGAT	AGGATTATGG	4320
	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GGTCTCTCTG	TCCAACGACA	4380
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	CCCTCATGCG	GGCTCTCTTA	CCGAAACCTT	GCCTTTCTCG	ATTTTATCTT	TGCGACAGCA	4560
70	GTTCGCGATT	GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGAT	TATTGTATTT	4620
	ATTCCATATT	CATGTAACA	AAATTTAGTT	TTTGTCTCTA	ATTGCACTCT	AAAAGGTTCA	4680
	GGGAACCGTT	ATTATAATTG	TATCAGAGGC	CTATAATGAA	GCTTTATACG	TGTAGCTATA	4740
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	CTCTAGCTGG	TGGTTTCACG	GTGCCAGGTT	TTCTGGGTGT	CCAAAGGAAG	ACGTGTGGCA	4980
	ATAGTGGGCG	CTCCGACAGC	CCCTCTGCCC	GCCTCCCATC	AGCGCTCCCA	GGGGTGGCTG	5040
	GAGACGGGTG	GGCGGCTGGA	GACCATGCGA	AGCGCCGTGA	GTTCTCAGGG	CTCCTGCCTT	5100
	CTGTCTGTGT	GCTACTTACT	GTCTCTGTCA	GGGAGCAGC	GGGGCGAAGC	CCAGGCCCTT	5160
80	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
	TTTCTGCTCT	TCTTCTTTT	GCTGTGTGTT	CTAAACAAGA	ATCAGTCTAT	CCACAGAGAG	5280
	TCCCATGCCC	TGAGGTTTCT	ATGGCTGGCC	ACTGCACAGA	GCTCTCCAGC	TCCAAGACCT	5340
	GTTGGTTCCA	AGCCCTGGAG	CCAACCTGCT	CTTTTGTAGG	TGGCACTTTT	TCAATTTCCCT	5400
	ATTCACACAC	TGCTCCGAGG	GCTGCGCAGG	GCTCAGGATT	TGCTGGGTCT	GTTTCTCTTT	5460
	CTACCCGCG	TGCTCGCACA	GTCTCTCTCT	CTCTCTCCCC	TCAAAGTCTG	CAACTTTAAG	5520
85	CAGCTCTTGC	TAATCAGTGT	CTCACACTGG	CGTAGAAGTT	TTTGTACTGT	AAAGAGACCT	5580
	ACCTCAGGTT	GCTGGTTGCT	GTGTGGTTTG	GTGTGTTCCC	GCAAACCCCC	TTTGTGCTGT	5640
	GGGGCTGGTA	GCTCAGGTGG	GCGTGGTCAC	TGCTGTCTAT	AGTTGAATGG	TCAGCGTTGC	5700

ATGTCGTGAC CAACTAGACA TTCTGTCGCC TTAGCATGTT TGCTGAACAC CTTGTGGAAG 5760
CAAAAAATCTG AAAATGTGAA TAAATATT TTGGATTTG TAAAAA AAAA 5820
AAAAA AAAA

5

Seq ID NO: 319 Protein sequence:
Protein Accession #: NP_005679

10 1 11 21 31 41 51
MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFRP TRPLECQDAL ETAARAEGLS 60
LDASMHSQLR ILDEEHKPKG YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSSLAR 120
VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEELNEV GPDAASLRV VWIFCRTLRI 180
LSIVCLMITQ LAGFSGPAFM VKHLEYTQA TSNLQYSL LVLGLLLTEI VRSWSLALTW 240
15 ALNVRTGVRL RGAILTMAPK KILKLKNIKE KSLGELINIC SNDGORMFEA AAVGSLLAGG 300
PVVAILGMIY NVIILGPTGF LGSAPFILPY PAMMFASRLT AYFRKRCVAA TDERVQKME 360
VLTYIKFKIM YAWVKAFSOS VQKIREEBERR ILEKAGYFQG ITVGVAPIV VIASVVTFSV 420
HMTLGFDLTA AQAFVTVTVF NSMTFALKVT PFSVKSLESA SVAVDRFKSL FLMEEVHMIK 480
NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPOMKKDK RASRGKKEKV RQLQRTEHQA 540
20 VLAQKQHL LDDSDERSPE EEEGKHIHLG HRLRQRTLHS IDLEIQEGL VGCISVSGS 600
KTSLSAILG QMTLLEGSIA ISGTAYVAQ QAWILNATLR DNILFQKEYD EERYNSVLNS 660
CCLRPDLAIL PSSDLTEIGE RGNLSGGQR QRISLARALY SDRSIYILD PLSALDAHVG 720
NHIFNSAIRK HLKSKTVLFV THQLQVLDV DEVIFMKEGC ITERGTHEEL MNLNGDYATI 780
25 FNNLLGETP FVEINSKET GSGQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKGGQS 840
VPWSVYGVYI QAAGGPAFL VIMALEMLNV GSTAFSTWVL SYWIKQSGN TTVTRGNETS 900
VSDSMKDNPH MQYASIAL SMAMVLLKA IRGVVFKGT LRASSRLHDE LFRRLRSFM 960
KFFDTTPTGR ILNRFSDMD EVDVRLPFA EMFIQNVIL FFCVGMIAV FFWFLVAVGP 1020
LVILPSVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLHRYQEL 1080
30 LDDNQAPFLL FTCAMRLAV RLDLISIALI TTTGLMIVLM HGIIPPAYAG LAISYAVQLT 1140
QLFQFTVRLA SETEARTSV ERINHVIKTL SLEAPARIKN KAPSPDPQOE GEVTFENAEM 1200
RYRENLPVLV KKVSTFIKPK EKIGIVGRTO SCKSSLMAL FRLVELSGGC IKIDGVRI SD 1260
IGLADLRSLK SIIPQEPVLF SGTVRNLDP FNQYTEDQIW DALERTHME CIAQLPLKLE 1320
SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLIQE TIREAFADCT 1380
35 MLTIAHRLHT VLGSDRIMVL AQQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVKG

Seq ID NO: 320 DNA sequence
Nucleic Acid Accession #: AK022089.1
Coding sequence: 181-1488

40 1 11 21 31 41 51
AGCAGTTGCA CAACTTCCAG CAACTTCTC AGCCGGCTAC TAATGAGCTG AAAGCCAGGA 60
ACATCCGAGG AGAAGAGAAA GCTTCCAGCC CTCCTCCCTT CACCTCGAA ATCCAGACAC 120
45 CCCCACCCCC ACCCTCAGAT CACTTTAAGA TAATTTCTTT ATTCTGTTGC CCGACAGACC 180
ATGGCTCCCT TTGAAGAGAA CTGCTAAAG ACTCGGCATA AAAACAGATC TCCAACTAAA 240
GACATGGAAT CAGAAGAGAA GGAATTTGTG GTTTGGGTTT GCCAAGAAGA GAAGCTTGTC 300
TGTGGGCTGA CTAAACGCAC CACCTCTGCT GATGTCATCC AGGCTTTGCT TGAGGAACAT 360
50 GAGGCTACGT TTGAGAGAAA ACGATTTCTT CTGGGGAAGC CCAAGTATTA CTGCATCATA 420
GAGAAGTGGG GAGGCTCCGA AAGGGTTCTT CCTCCACTAA CTAGAATCCT GAAGCTTTGG 480
AAAGCGTGGG GAGATGAGAC GCCAATATG CAATTTGT TTGGTTAAAGC AGATGCTTTT 540
CTTCCAGTTC CTTTGTGGCG GACAGCTGAA GCCAAATTAG TGCAAAACAC AGAAAAATTG 600
TGGGAGCTCA GCCCAGCAAA CTACATGAAG ACTTTACCAC CAGATAAACA AAAAAGAAAT 660
55 GTCAGGAAAA CTTTCCGGAA ACTGGCTAAA ATTAAGCAGG ACACAGTTTC TCATGATCGA 720
GATAATATGG AGACATTAGT TCATCTGATC ATTTCCAGG ACCATACAT TCATCAGCAA 780
GTCAGAGAAA TTGAAGAGCT GGATCTGGA ATTGAAGAGT GTGAAGCTAA GTTCATCTT 840
GATCGAGTAG AAAATGATGG AGAAAACTAT GTTCAGGATG CATATTTAAT GCCCAGTTTC 900
60 AGTGAAGTTG AGCAAAATCT AGACTTGCG TATGAGGAAA ACCAGACTCT GGAGGACCTG 960
AGCGAAAGTG ATGGAATTGA ACAGCTGGAA GAACAGCTGA AATATTACCG AATACTCATT 1020
GATAAGCTCT CTGCTGAAAT AGAAAAAGAG GTAAAAAGTG TTTGCATTGA TATAAATGAA 1080
GATGCGAAG GGAAGCTGCG AAGTGAAGT GAAAGCTCTA ATTTAGAGAG TGTTAAGTGT 1140
GATTTGGAGA AAAGCATGAA AGCTGGTTTG AAAATCTACT CTCATTTGAG TGGCATCCAG 1200
AAAGAGATTA AATACAGTGA CTCATTGCTT CAGATGAAAG CAAAAGAAAT TGAATCCTG 1260
65 GCCAAGGAAT TCAATTCAT TCACATTAGC AACAAAGATG GGTGCCAGT AAAGGAAAC 1320
AGAGCGAAGG AATCTGAGGT TCCAGTAGC AATGGGAGA TTCCTCCCTT TACTCAAAGA 1380
GTATTTAGCA ATTACACAAA TGACACAGAC TCGACACTG GTATCAGTTC TAACCACAGT 1440
CAGGACTCCG AAACAACAGT AGGAGATGTG GTGCTGTTGT CAACATAGTT CCAATGGCTC 1500
CTTTCTGACC TGCTTTTCATG TTTTAATGTT TGTTTAATTT AATAGGAAAC CTCATTTTAA 1560
70 ATATAACACT CAAAAAATG TAAATCATAT TGTTAGTATC AATAGTTAAT AAAAATCTGA 1620
GAAATGTGTT GTTTCTG

Seq ID NO: 321 Protein sequence:
Protein Accession #: NP_005438.1

75 1 11 21 31 41 51
MAPFGRNLLK TRHKNSRPTK DMDSEEKIV VWVCQEEKLV CGLTKRTTSA DVIQALLEEH 60
EATFGKRLP LGKPSDYCI I EKWGGSERV PPLTRILKLW KAWGDEQPNM QFVLVKADAF 120
80 LPVPLWRTAE AKLVQNTTEK WELSPANMYK TLEPPDKQRI VRKTFRLAK IKQDVTSHDR 180
DNMETLVHLI ISQDHTIHQQ VKRMKELDL IEKCBKPHL DRVENDGENY VQDAYLMPSF 240
SEVEQNLDIQ YEENQTLLED SEDGIEQL ERLKYRILI DKLSAEIEKE VKSVCIDINE 300
DAEGEASSEL ESSNLESVKC DLEKSMKAGL KIHSHLSGIQ KEIKYSDSL QMKAKYELL 360
AKEFNSLHIS NKDGQCLKEN RAKESEVPSS NGEIPFFTOR VFSNYTNDTD SDTGISSNHS 420
85 QDSEITVGDV VLLST

Seq ID NO: 322 DNA sequence
Nucleic Acid Accession #: NM_030920.1

Coding sequence: 317-1123

	1	11	21	31	41	51	
5	AGCATTTGAAG	GGGAAGGAAC	TGCGGGTGTG	GTGTGTGTAT	GTGTGTGTGT	ATGTGTGTGC	60
	GGCGCGTGGC	TGCGTGTGTG	TGCGCGCGCT	AGTGTGTGGA	CAAGGAGGTG	GGGGCAGCTG	120
	AGTTAGAGTC	CCAACTCTTG	GACTCCATTT	GCTATTCTCT	TCTTTCTCCC	CCACACCTAT	180
	CTGGTGGTGG	TAGTGGGCGT	TTATATTGTC	GTTCCTTTTC	ATTCATTTCT	AAATCTCTTA	240
10	AAAATTTTGG	GTTGGGGGTA	TTGGGGAAGG	CAGGAAAGGG	AAAAGGAGAG	TAGTAGCTGA	300
	AGAGCAAGAG	GAGGACATGG	AGATGAAGAA	GAAGATTAC	CTGGAGTTAA	GGAACAGATC	360
	CCCGGAGGAG	GTGACAGAGT	TAGTCCCTGA	TAATTGCCCTG	TGTGTCAATG	GGGAAATTGA	420
	AGGCCTGAAT	GATACTTTCA	AAGAACTAGA	ATTTCTGAGT	ATGGCTAATG	TGGAATAAG	480
	TTCCGTGGCC	CGGCTTCCCA	GCTTAAATAA	ACTTCGAAAA	TTGGAGCTTA	GTGATAATAT	540
	AATTTCTGGA	GGCTTGGGAG	TCCTGGCAGA	GAAATGTCCA	AATCTTACCT	ACCTCAATCT	600
15	GAGTGGAAAC	AAAATAAAG	ATCTCAGTAC	AGTAGAAGCT	CTGCAAAATC	TTAAAAATTT	660
	GAAAACTCTT	GACCTGTTTA	ACTGTGAGAT	CACAAACCTG	GAAGATTATA	GAGAAAGTAT	720
	TTTTGAACCTA	CTGCAGCAAA	TCACATACTT	AGATGGATT	GATCAGGAGG	ATAATGAAGC	780
	GGCGGACTCT	GAAGAGGAGG	ATGATGAGGA	TGGAGATGAA	GATGATGAAG	AGGAAGAGGA	840
20	AAATGAAGCT	GGTCCACCGG	AAGGATATGA	GGAAGAGGAG	GAGGAAGAGG	AAGAGGAGGA	900
	TGAGGATGAG	GATGAAGATG	AAGATGAAGC	AGGTTCAAGG	TGGGAGAGG	GAGAAGAGGA	960
	AGTGGGCTCT	TCATACTTAA	TGAAGAAGA	AATTCAAGAT	GAAGAAGATG	ATGATGACTA	1020
	TGTTGAAGAA	GGGGAAGAGG	AGGAAGAAGA	GGAAGAAGGA	GGTCTTCGAG	GGGAGAAGAG	1080
	GAAACGAGAT	GCTGAAGACG	ATGGAGAGGA	AGAAGATGAC	TAGATCATTC	TAAAGACCAGA	1140
	TTCTCTAATG	GGCTTGGGTG	TGCAATAGAG	TGATCACATC	TTTGTTCCTT	CATGTACGAT	1200
25	AGCTATCCCT	ACAGAAGATA	ATGTGTAAC	TTTTATAGGA	AAAGTGTGGT	TTTACTATTT	1260
	TTGCCCTATC	ATTCCAAATA	AGAACTAGTC	TGTTAATGAT	CATATTGTAT	GTAGAGAAAA	1320
	ATTTTCATTG	ACTCCCATTG	TGGAATTCCC	TAGCAATTTA	TTTAGACTTA	ATTTTATAAA	1380
	TTCAAGCTTA	CTGTATTATG	CATTTTATAG	CCATAATTAA	AACATGATCA	CTTTTAAACA	1440
	GGTGTAGTAT	GGTGCACTTC	ATTCCTTATT	TATAGATTAA	CTGAAATTAC	AGTTTGTCTAT	1500
30	AATATAAAT	GACATAGTCT	TCTTGAGTGG	TAAGTTGGTT	ATTTTCTTAG	AGGTGATCCA	1560
	GGAACTCTTA	GTTTGAAGGC	AGTTACCTTT	TTTTTTTTTT	TTTTTTTTTG	ACTAAGAGTG	1620
	TTTGGTTGCT	TTTTTGTGCT	AAGTAACCTG	GAAAAATAGAA	GCAGAAATAGT	AAAGGTCTCTA	1680
	TTCAAGCAAC	TAGTTCATGG	ATTTTGTGGA	GGTCTTATTC	AGTAATATGG	TTCATGGATT	1740
35	TAGTGTGAC	TGATTAAGAT	TTATTTTGA	AGGAAAAATT	GCTTATACTA	AGTCCAGAGA	1800
	CATGAGGTG	AGCCCTTTTG	TCAGGCTGCA	AATCATGACA	TGCCGATGGT	TGTTTATTTT	1860
	GTTTTTAGGT	GTGCATTCCT	TTTCTTCTTA	GCAATTCCTT	TATGATCACC	TTCCCTTCTT	1920
	GTTTCACTCC	CTCCGCTCT	CTCAAAAGGA	ACTTGGGAAA	CTTGTGAAC	CCAGGAAAAC	1980
	CTTTAGCTCT	ATACCTCAAC	TACGTTTCAG	TCCTGTCTGG	GTTTAAATA	AGTGAAGTAG	2040
40	AAGAAATCTA	TGATTTCTTG	ACATAAGAA	ATATTATCAA	TACAGTTTAA	TGCAGTAAAC	2100
	TCCTCTTACC	ATAAATGTTT	CTTGGTTGAC	AACATCTAAG	ACAATATTAG	TGGGATGAAG	2160
	AAAGAAAGAG	AGGGGTGCTT	TTGGAAGCAG	TGTTAGTGTT	CCTCAAAAGT	CGGAACAATT	2220
	GCTGTGTGAT	ATATTAAATA	GACATTAAAG	TCAAAATTTA	ATGTTGGCCT	CTCAATGAT	2280
	TTGGATACCA	CTCTGCAAG	TATTTCTAAC	CTTTAATTC	CAGTTTAA	ACAGATATAA	2340
45	TAATAGCATT	TAATTGGAAT	ATACTAGGCA	GCTGGAAAG	TATTTGAAC	TAAATTGACA	2400
	TTAAATTAAT	GATTTGTTTT	CAAGTGGATG	TCCATTAAAA	GTAGAAAAAT	ATTGGGATA	2460
	AGTGAGTGTG	TGTTTCTCTA	CATGGCTACT	AAATAAATA	TAATGAGTAT	ACAAGTATAT	2520
	CTCCTCTTTT	GCTATGGAGG	CTCCATGTTT	AAGGCAATGG	CTTTTAAAT	CTTGGCTATC	2580
	TAAAATTTTT	TCCCTTTGTT	TTGAATATTT	GTAAGTTTTT	AAGAAGTTAG	TGTCAGCAAA	2640
50	TTAATGAAG	TTATGCTCT	ATACGGGAC	ATATTTAAAT	ACTGAGTATA	GTACTGCTGC	2700
	TACTGCTTCT	ACAATGTAAA	ATGTATGACT	TGGTGTTTTA	AAGTAAAAAT	TATGATGTTA	2760
	CTTGTGGAGA	GCTTAAAAAT	GTGTACAAC	TGACCGAAAG	AAAACCCCTG	GGGATAAGTT	2820
	TAGTGAGGGG	ATTGGAATCC	CCAAAAAGAT	AACATTTTTC	TTCTGCTTTT	AAAAACTGAA	2880
	ATTCCTGTTT	CTAGTTCTCA	ACAATTCTCA	TTACATACTA	TGCCAGATTA	CAAAATACTT	2940
55	ATTTTAAAA	TGAATCTAT	ATATTGACTT	TCTTATCAAT	CATCTTACTG	TGCAATCAAA	3000
	ATTAGAGTAC	TTTGGTTTGA	AAACAACACT	TAGAGCCTCC	AGATAACTTT	TAAAGACTTAT	3060
	TTAGCTTTGT	GCGGTGCTAT	TTCATGCAAA	TAAAGTAAAGG	TGGGTTTTAT	ATTTTGTAGA	3120
	AGTTTTCGGT	CCTATTTTAA	TGCTCTTGT	ATGGCAGTAT	GTATATATTG	TGTTAAGTTC	3180
60	CTCAAGAATC	TCCTTAAAAA	CTTTGAAGTT	AATACTTTTG	TGCAACTGTG	TTTTGAATAA	3240
	AGCCATGACA	GTGTTAAAAA	CAAAC				

Seq ID NO: 323 Protein sequence:
Protein Accession #: NP_112182.1

	1	11	21	31	41	51	
65	MEMKKKINLE	LRNRPSEVET	ELVLDNCLCV	NGEIEGLNDT	FKELEFLSMA	NVELSSLARL	60
	PSLNKLRKLE	LSDNIISGGL	EVLAEKCPNL	TYLNLSGNKI	KDLSTVEALQ	NLKNLKSLLD	120
	FNCEITNLED	YRESIFELLQ	QITYLDGFDQ	EDNEAPDSEE	EDDEDGDEDD	EEEEENEAGP	180
70	PEGYEEEEEE	EEEEDEDEDE	DEDEAGSELG	EGEEEVGLSY	LMKEEIQDEE	DDDDYVEEGE	240
	EEEEEBEGGL	RGEKKRDAE	DDGEEEDD				

Seq ID NO: 324 DNA sequence
Nucleic Acid Accession #: NM_003812
Coding sequence: 224..2722

	1	11	21	31	41	51	
75	TCCTCTGCGT	CCCGCCCGCG	GAGTGGCTGC	GAGGCTAGGC	GAGCCGGGAA	AGGGGGCGCC	60
	GCCAGCCCCC	GAGCCCCCGG	CCCGGTGCCC	CGAGCCCGGA	GCCCCCTGCC	CGCGGGCGCA	120
80	CCATGCGCGC	CGAGCCGCGC	TGACCGGCTC	CGCCCGCGGC	CGCCCGCGAG	CTAGCCCGGC	180
	GCTCTCGCGC	GCCACACGGA	GCGGCGCCCG	GGAGCTATGA	GCCATGAAGC	CGCCCGGCAG	240
	CAGCTCGCGC	CAGCCGCCCC	TGGCGGGCTG	CAGCCTTGCC	GCGCTTCTCT	CGCGCCCCCA	300
	ACGCGGCCCG	GCGGCTGCTG	TGCTGCGCAG	CGCCCGCGCC	CGCAGCGCGC	CCTGCGCGCT	360
	GCTTCTCGTC	CTTCTCTGTC	TGCCTCGGCT	CGCCGCTCG	TCCCGGCCCG	CGCGCTGGGG	420
85	GGCTGCTGCG	CCCAGCGCTC	CGCATTGGAA	TGAAACTGCA	GAAAAAATT	TGGGAGTCTT	480
	GGCAGATGAA	GACAATACAT	TGCAACAGAA	TAGCAGCAGT	AATATCAGTT	ACAGCAATGC	540
	AATGCAGAAA	GAAATCACAC	TGCCTTCAAG	ACTCATATAT	TACATCAACC	AAGACTCGGA	600

	AAGCCCTTAT	CACGTTCTTG	ACACAAAGGC	AAGACACCAG	CAAAAACATA	ATAAGGCTGT	660
	CCATCTGGCC	CAGGCAAGCT	TCCAGATTGA	AGCCTTCGGC	TCCAAATTCA	TTCTTGACCT	720
	CATACTGAAC	AATGGTTTGT	TGCTTCTGA	TTATGTGGAG	ATTCACTACG	AAAATGGGAA	780
5	ACCACAGTAC	TCTAAGGGTG	GAGAGCACTG	TTACTACCAT	GGAGCATCA	GAGGCGTCAA	840
	AGACTCCAAG	GTGGCTCTGT	CAACCTGCAA	TGGACTTCAT	GGCATGTTTG	AAGATGATAC	900
	CTTCGTGTAT	ATGATAGAGC	CAC TAGAGCT	GGTTTCATGAT	GAGAAAGCA	CAGGTCGACC	960
	ACATATAATC	CAGAAAACCT	TGGCAGGACA	GTATTCTAAG	CAATGAAGA	ATCTCACTAT	1020
	GGAAAGAGGT	GACCAGTGGC	CCTTCTCTC	TGAATTACAG	TGGTTGAAAA	GAAGGAAGAG	1080
10	AGCAGTGAAT	CCATCACGTG	GTATATTGTA	AGAAATGAAA	TATTTGGAAC	TTATGATTGT	1140
	TAATGATCAC	AAAACGTATA	AGAAGCATCG	CTCTTCTCAT	GCACATACCA	ACAACCTTTC	1200
	AAAGTCCGTG	GTCAACCTTG	TGGATTCTAT	TTACAAGGAG	CAGCTCAACA	CCAGGTTTGT	1260
	CCTGGTGGCT	GTAGAGACCT	GGACTGAGAA	GGATCAGATT	GACATACCA	CCAACCCCTG	1320
	GCAGATGCTC	ACTGAATTCT	CAAAATACCG	GCAGCGCATT	AAGCAGCATG	CTGATGCTGT	1380
15	GCACCTCATC	TGCGGGGTGA	CATTTCACTA	TAAAGAGAAGC	AGTCTGASTT	ACTTTGGAGG	1440
	TGCTGTGTCT	CGCACAAAG	GAGTTGGTGT	GAATGAGTAT	GGTCTTCCAA	TGGCAGTGGC	1500
	ACAAGTATTA	TGCGAGAGCC	TGGCTCAAAA	CCTTGGAAATC	CAATGGGAAC	CTTCTAGCAG	1560
	AAAGCCAAAA	TGTGACTGCA	CAGAATCCTG	GGGTGGCTGC	ATCATGGAGG	AAACAGGGGT	1620
	GTCCCATCTC	CGAAATTTT	CAAAGTGCAG	CATTTTGGAG	TATAGAGACT	TTTACAGAG	1680
20	AGGAGGTGGA	GCCTGCCTTT	TCAACAGGCC	AACAAAGCTA	TTTGAGCCCA	CGGAATGTGG	1740
	AAATGGATAC	GTGGAAGCTG	GGGAGGAGTG	TGATTGTGGT	TTTCATGTGG	AATGCTATGG	1800
	ATTATGCTGT	AAGAAATGTT	CCCTCTCCAA	CGGGGCTCAC	TGCAGCGACG	GGCCCTGCTG	1860
	TAAATATACC	TCATGTCTTT	TTGAGCCACG	AGGGTATGAA	TGCCGGGATG	CTGTGAACGA	1920
	GTGTGATATT	ACTGAATTCT	GTACTGGAGA	CTCTGGTCAG	TGCCCAACAA	ATCTTCATAA	1980
25	GCAAGACGGA	TATGCATGCA	ATCAAAATCA	GGGCCGCTGC	TACAATGGCG	AGTGAAGAC	2040
	CAGAGACAAC	CAGTGTCACT	ACATCTGGGG	AACAAAGGCT	GCAGGGTCTG	ACAAGTTCTG	2100
	CTATGAAAAG	CTGAATACAG	AAGGCACTGA	GAAGGGAAGC	TGCGGGAAGG	ATGGAGACCG	2160
	GTGGATTGAT	TGCAGCAAC	ATGATGTGTT	CTGTGGATTC	TTACTCTGTA	CCAATCTTAC	2220
	TCGAGCTCCA	CGTATTGGTC	AACCTCAGGG	TGAGATCATT	CCAACCTCCT	TCTACCATCA	2280
30	AGGCCGGGTG	ATTGACTGCA	GTGGTGCCCA	TGTAGTTTTA	GATGATGATA	CGGATGTGGG	2340
	CTATGTAGAA	GGTGAACGCG	CATGTGGCCC	GTCTATGATG	TGTTTAGATC	GGAAGTGCCT	2400
	ACAAATTCAA	GCCCTAAATA	TGAGCAGCTG	TCCACTCGAT	TCCAAGGGTA	AAGTCTGTTC	2460
	GGGCCATGGG	GTGTGTAGTA	ATGAAGCCAC	CTGCATTTGT	GATTTCACCT	GGGCAGGGAC	2520
	AGATTGCACT	ATCCGGGATC	CAGTTAGGAA	CCTTCAACCC	CCCAAGGATG	AAGGACCCAA	2580
35	GGGTCTAGT	GCCACCAATC	TCATAATAGG	CTCCATCGCT	GGTGCCATCC	TGGTAGCAGC	2640
	TATTGTCTCT	GGGGGCACAG	GCTGGGGATT	TAAAAATGTC	AAGAAGAGAA	GGTTCGATCC	2700
	TACTCAGCAA	GGCCCCATCT	GAATCAGCTG	CGCTGGATGG	ACACCGCCTT	GCACGTGTGG	2760
	ATTCTGGGTA	TGACATCTC	GCAGCAGTGT	TACTGGAATC	ATTAAGTTTG	TAAACAAAAC	2820
	CTTTGGGTGG	TAATGACTAC	GGAGCTAAAG	TTGGGGTGAC	AAGGATGGGG	TAAAGAAAAA	2880
40	CTGTCTCTTT	TGGAATAAT	GTCAAAGAAC	ACCTTTCACC	ACCTGTGAGT	AAACGGGGGA	2940
	GGGGGCAGAA	GACCATTGTA	TAAAAAGAAC	TGTTCCAGAA	TCTTTTITTT	TCCCTAATGG	3000
	ACGAAGGAAC	AACACACACA	CAAAAATTAA	ATGCAATAAA	GGAATCATTA	AAAA	

Seq ID NO: 325 Protein sequence:
Protein Accession #: NP_003803

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	MKPPGSSSRQ	PPLAGCSLAG	ASCGPQRGPA	GSVPASAPAR	TPPCRLLLV	LLLPLLAASS	60
50	RPRAMGAAAP	SAPHWNETAE	KNLGVLADED	NTLQONSSSN	ISYSNAMQKE	ITLPSRLIYY	120
	INQDSESPYH	VLDTKARHQ	KHNKAVHLAQ	ASFQIEAFGS	KFILDILINN	GLLSSDYVEI	180
	HYENGKPYYS	KGSEHCYHYG	SIRGVKDSKV	ALSTCNGLHG	MFEDDTFVYM	IEPLELVHDE	240
	KSTGRPHIIQ	KTLAQVYSKQ	MKNLTMERGD	QWPFLESLQW	LKRRKRAVNP	SRGIFEEEMKY	300
	LELMIVNDHK	TYKHRSSHA	MTNPFKSVV	NLVDLSIYKEQ	LNTRVVLVAV	ETWTEKDQID	360
55	ITTNVQMLH	EFISKYRORIK	QHADAHLIS	RVTFFHYKRSS	LSYFPGVCSS	TRGVGVNEYG	420
	LPMVAQVLS	QSLAQNLGIQ	WEPSSSRKPKC	DCTESWGGCI	MEETGVSHSR	KFSKCSILEY	480
	RDFLQRGGGA	CLFNRPRTKLF	EPTCEGNGYV	EAGEECDCGF	HVECYGLCKC	KCSLSNGAHC	540
	SDGPPCMMYS	CLFQPRGYEC	RDVNECDIT	EYCTGDSGQC	PPNLHKQDGY	ACNQNGRCY	600
	NGECKTRNTS	QYTWGTKAA	GSDKFCYEKL	NTEGTEKGNC	GKGDWRNIQC	SKHDVPCGFL	660
60	LCTNLTRAER	IGQLQGEIIP	TSFYHQGRVI	DCSGAHVVL	DDTDVGVYED	GTFCGFSMMC	720
	LDRKCLQIQ	LNMSSCPIDS	KGVKCSGHGV	CSNEATCICD	FTWAGTDCSI	RDPVRNLHPP	780
	KDEGPKGPSA	TNLIIGSIAG	AILVAAIVLG	GTGWGPKNVK	KRRFDPTQQG	PI	

Seq ID NO: 326 DNA sequence
Nucleic Acid Accession #: AK074418.1
Coding sequence: 244-1515

65	1	11	21	31	41	51	
	CTTCTCCAA	GACGCGCGGC	CATGCTCTCC	TCCTCTGCCA	GTCTCCTCCA	CCACTCTCTA	60
70	ACCTGAGAGC	CTGTGGAACC	TGCCCGTCTC	CCCTCCTCCA	TCAGACACAC	CTGCCTAGGA	120
	AACAGATGGA	AAAAGTGAGG	GACCGGTGAG	TGACTTGCTG	CTAAAGTTTA	TACCAGATGC	180
	AAATGACAGA	GCTGGAGTTC	TGCTGTGCCCT	GGAAAGGACC	TCGGAAGTCT	TCTAAGGAGA	240
	GTCTGGCGGT	ATTACACAGG	GCCTTCAGTG	GAGACCTCCA	TCATCAAGTT	CAAAGACCAG	300
	GACTTTACCA	CCTTGCGGGA	TCACTGCCTG	AGCATGGGCC	GGACGTTTAA	GGATGAGACA	360
75	TTCCCGCAG	CAGATTCTTC	CATAGGCCAG	AAGCTGCTCC	AGGAAAAACG	CCTCTCCAAT	420
	GTGATATGGA	AGCGGCCACA	GGATCTACCA	GGGGGTCTCT	CTCACTTCAT	CCTGGATGAT	480
	ATAAGCAGAT	TTGACATCCA	ACAAGGAGGC	GCAGCTGACT	GCTGGTTCTC	GGCAGCACTG	540
	GGATCCTTGA	CTCAGAACCC	ACAGTACAGG	CAGAAGATCC	TGATGGTCCA	AAGCTTTTCA	600
	CACCAATATG	CTGGCATTTT	CCGTTTCCGG	TTCTGGCAAT	GTGGCCAGTG	GGTGGAAATG	660
80	GTGATTGATG	ACCGCCTTAC	TGTCCAGGGA	GATAAATGCC	TCTTTGTGCG	TCCTCGCCAC	720
	CAAAACCAAG	AGTTCTGCGC	CTGCCTGCTG	GAGAAGGCCT	ATGCCAAGCT	GCTCGGATCC	780
	TATTCGATC	TGCATATGG	CTTCCTCGAG	GATGCCCTGG	TGGACCTCAC	AGGAGGCGTG	840
	ATCACCAACA	TCCATCTGCA	CTCTTCCCCT	GTGGACCTGG	TGAAGGCAGT	GAAGACAGCG	900
	ACCAAGGCAG	GCTCCCTGAT	AACCTGTGCC	ACTCCAAGTG	GGCCCAACAGA	TACAGCACAG	960
85	GCATATGGA	ATGGCTGTGT	GAGTCTCCAT	GCCTACACTG	TGACTGGGGG	TGAGCAGATT	1020
	CAATACCGAA	GGGGCTGGGA	AGAAATTATC	TCCTGTGGGA	ACCCCTGGGG	CTGGGGCGAG	1080
	ACCAATGGA	GAGGGCGCTG	GAGTGATGGG	TCTCAGGAGT	GGGAGGAAAC	CTGTGATCCG	1140

	CGGAAAAGCC	AGCTACATAA	GAAACGGGAA	GATGGCGAGT	TTTGGATGTC	GTGTCAAGAT	1200
	TTCCACACAGA	AATTCATCGC	CATGTTTATA	TGTAGCGAAA	TTCCAAATTAC	CCTGGACCAT	1260
	GGAAACACAC	TCCACGAAGG	ATGGTCCCAA	ATAATGTTTA	GGAAGCAAGT	GATTCTAGGA	1320
5	AACACTGCAG	GAGGACCTCG	GAATGATGCT	CAATTCAACT	TCTCTGTGCA	AGAGCCAATG	1380
	GAAGGCACCA	AATGTTGTCG	GTGCGTCACA	GTGCTGTGCA	CACCATCAAA	TTTGAAGCA	1440
	GAAGATGCAA	AATTTCCACT	CGATTTCCAA	GTGATTCTGG	CTGGCTCACA	GAAACACTGT	1500
	CCAAAGCTCA	AATAATAAAT	TCCGCGCGAA	CTTCACCATG	ACTTACCATC	TGAGCCCTGG	1560
	GAACATATGT	GTGGTTGCAC	AGACACGGAG	AAAATCAGCG	GAGTTCCTGC	TCCGAATCTT	1620
10	CCTGAAAATG	CCAGACAGTG	ACAGGCACCT	GAGCAGCCAT	TTCAACCTCA	GAATGAAGGG	1680
	AAGCCCTTCA	GAACATGGCT	CCCAACAAAG	CATTTTCAAC	AGATATGCTC	AGCAGGTATG	1740
	GTACCTAGCA	CCCAGGGGCC	TTACGTGGGA	TTGGAGAAAG	GGGACCTGAG	GGAGGGACAG	1800
	CCCTCACAGG	CCCTTACTGG	GATGCAGAGA	GGAGAAGTGA	CTTGATGGAC	TATTTTACCT	1860
	GCCTCTCTTC	CTGGATCGTC	TCCAGAACTG	CTGTGGCTGC	CAAGCTCGGT	AGAGACGTGG	1920
	CGCCCCACCC	AGTCTCATCC	GGGGGACTTC	AAGCTGGAAT	GCAGAGCTTA	GAAAGGGAGG	1980
15	GGATAATTAT	GGGGTGTGAG	GTGCATTGCC	CTCTAAATCT	TTAAACAAGC	AATTGGCAGT	2040
	ACCCCGTGAA	AACTTTCAGT	CTCTACTCG	GCCACCTCCC	ACCAACCTGG	CATCGTTCTT	2100
	CCCGGGAGCT	AGCCAGCTTC	AGAAAGCACA	TACAGCATCC	TTGCTGCCAA	ACCACCTATG	2160
	TGCACACAGG	ATTTCCTTAA	TGGCTTAATA	AACTGTTATA	AAGAACTCCT	TGACTTGTCA	2220
20	GAATAAAATA	GCTGCCAGGG	GCTCTGCACA	ATGAGCCTCT	TACCGTTAAA	AAAAAAAAAA	2280
	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA				

Seq ID NO: 327 Protein sequence:
Protein Accession #: BAB85075.1

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	IWKRPQDLBG	GPPHFILDDI	SRFDIQQGG	ADCFWLAALG	SLTNPQYRQ	KILMVQSFHS	120
30	QYAGIFRFRF	WQCGQWVEV	IDRLFPVQGD	KCLFVRPRHQ	NQEFWPCLE	KAYAKLLGSY	180
	BDLHYGFLED	ALVDLTGVI	TNIHLHSSPV	DLVKAVKTAT	KAGSLITCAT	PSGPTDTAQA	240
	MENGLVSLHA	YTVTGAEIQI	YRRGWEEIIS	LWNPWGNET	ENRGRWSDGS	QWEETCDPR	300
	KSQHLHKRED	GEFWMSCQDF	QQKFIAMFIC	SEIPITLDHG	NTLHEGWSQI	MFRKQVILGN	360
	TAGGPRNDAQ	FNFSVQEPME	GTNVVVCVTV	AVTPSNLKA	DAKFLDFQV	ILAGSQKHCP	420
35	KLK						

Seq ID NO: 328 DNA sequence
Nucleic Acid Accession #: BC017490.1
Coding sequence: 74-2788

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45	GCGTGGCGGA	GGCAATGATC	CTCTCACCTC	CAGCCCTGGC	CGAAGCTCCC	GGCGTACTGA	180
	TGCCCTCAC	TCCAGCCCTG	GCCGTGACCT	TCCACCATTT	GAGGATGAGT	CCGAGGGGCT	240
	CCTAGGCACA	GAGGGGCCCC	TGGAGGAAGA	AGAGGATGGA	GAGGAGCTCA	TTGGAGATGG	300
	CATGGAAGG	GACTACCGCG	CCATCCGAGA	GCTGGACGCC	TATGAGGCCG	AGGGACTGGC	360
	TCTGGATGAT	GAGGACGTAG	AGGAGCTGAC	GGCCAGTCAG	AGGGAGGCAG	CAGAGCGGGC	420
50	CATGCGGCAG	CGTGACCGGG	AGGCTGGCCG	GGGCTGGGCG	CGCATGCGCC	GTGGGCTCCT	480
	GTATGACAGC	GATGAGGAGG	ACGAGGAGCG	CCTTGCCGCG	AAGCGCCGCC	AGGTGGAGCG	540
	GGCCACGGAG	GACGGCGAGG	AGGACGAGGA	GATGATCGAG	AGCATCGAGA	ACCTGGAGGA	600
	TCTCAAAGG	CACCTCTGTC	GCGAGTGGGT	GAGCATGGCG	GGCCCCGGCG	TGGAGATCCA	660
	CCACCGCTTC	AAGAACTTCC	TGCGCACTCA	CGTCGACAGC	CACGCCACCA	ACGTCTTCAA	720
55	GGAGCGCATC	AGCGACATGT	GCAAAGAGAA	CCGTGAGAGC	CTGGTGGTGA	ACTATGAGGA	780
	CTTGGCAGCC	AGGGAGCACG	TGCTGGCCTA	CTTCTGCCT	GAGGCACCGG	CGGAGCTGCT	840
	GCAGATCTTT	GATGAGGCTG	CCCTGGAGGT	GGTACTGGCC	ATGTACCCCA	AGTACGACCG	900
	CATCACCAAC	CACATCCATG	TCCGCACTTC	CCACCTGCCT	CTGGTGGAGG	AGCTGCGCTG	960
	GCTGAGGCG	CTGCATCTGA	ACCACTGAT	CCGCACCACT	GGGGTGGTGA	CCAGCTGCAC	1020
60	TGGCGTCTTG	CCCCAGCTCA	GCATGGTCAA	GTACAACTGC	AACAAGTGCA	ATTTCGTCTT	1080
	GGGTCCCTTC	TGCCAGTCCC	AGAAACGAGG	GGTGAACCA	GGCTCCTGTC	CTGAGTGCCA	1140
	GTGCGCGCGC	CCCTTTGAGG	TCAACATGGA	GGAGACCATC	TATCAGAACT	ACCAGCGTAT	1200
	CCGAATCCAG	GAGATCCAG	GCAAAGTGGC	GGCTGGCCGG	CTGCCCGCTG	CCAAGGACGC	1260
	CATTCTCTCT	GCAGATCTGG	TGGACAGCTG	CAAGCCAGGA	GACGAGATAG	AGCTGACTGG	1320
65	CATCTATCAC	AACAATCTAT	ATGGCTCCCT	CAACACTGCC	AATGGCTTCC	CTGTCTTTGC	1380
	CACCTGTCATC	CTAGCCAACC	ACGTGGCCAA	GAAGGACAAC	AAGGTTGCTG	TAGGGGAAC	1440
	GACCGATGAA	GATGTGAAGA	TGATCACTAG	CCTCTCCAAG	GATCAGCAGA	TCCGAGAGAA	1500
	GATCTTTGCC	AGCATTTGCTC	CTTCCATCTA	TGGTCATGAA	GACATCAAGA	GAGGCCTGGC	1560
	TCTGGCCCTG	TTCCGAGGGG	AGCCCAAAAA	CCCAAGTGGC	AAGCACAAGG	TACGTGGTGA	1620
70	TATCAACGTG	CTCTGTGTGG	GAGACCTGGG	CACAGCGAAG	TCCAGATTTC	TCAAGTATAT	1680
	TGAGAAAGTG	TCCAGCCGAG	CCATCTTCAC	CACCTGGCCAG	GGGGCGTCCG	CTGTGGGCTT	1740
	CACGGCGTAT	GTCCAGCGGC	ACCCTGTTCAG	CAGGGAGTGG	ACCTTGGAGG	CTGGGGCCCT	1800
	GGTTCTGGCT	GACCGAGGAG	TGTGTCTCAT	TGATGAATTT	GACAAGATGA	ATGACCAGGA	1860
	CAGAACCAAG	ATCCATGAGG	CCATGGAGCA	ACAGAGCATC	TCCATCTCGA	AGGCTGGCAT	1920
75	CGTCACTCC	CTGCAGGCTC	GCTGCACGGT	CATTGCTGCC	GCCCAACCCA	TAGGAGGGCG	1980
	CTACGACCCC	TGCTGACTTT	TCTCTGAGAA	CGTGGACCTC	ACAGAGCCCA	TCACTCTCAG	2040
	CTTTGACATC	CTGTGTGTGG	TGAGGGACAC	CGTGGACCCA	GTCCAGGACG	AGATGCTGGC	2100
	CGCTTTCGTG	GTGGGACGCC	ACGTCAAGCA	CCACCCAGC	AACAAGGAGG	AGGAGGGGCT	2160
	GGCCAAATGC	AGCGCTGCTG	AGCCCGCCAT	GCCTAACACG	TATGGCGTGG	AGCCCTTGCC	2220
80	CAGGAGGTC	CTGAAGAAAT	ACATCATCTA	CGCCAAAGGAG	AGGGTCCACG	CGAAGCTCAA	2280
	CCAGATGGAC	CAGGACAAGG	TGGCCAAGAT	GTACAGTGAC	CTGAGGAAAG	AATCTATGGC	2340
	GACAGGCAGC	ATCCCCATTA	CGGTGCGGCA	CATCGAGTCC	ATGATCCGCA	TGGCGGAGGC	2400
	CCAAGCGCGC	ATCCATCTGC	GGGACTATGT	GATCGAAGAC	GACGCTCAAC	TGGCCATCCG	2460
	CGTGATGCTG	GAGAGCTTCA	TAGACACACA	GAAGTTCAGC	GTCATGCGCA	GCAATGCGCA	2520
85	GACTTTTGCC	CGCTACCTTT	CATTCCGGCG	TGACAACAAT	GAGCTGTGTC	TCTTCATACT	2580
	GAAGCAGTTA	GTGGCAGAGC	AGGTGACATA	TCAGCGCAAC	CGCTTTGGGG	CCGACGAGGA	2640
	CACATATTGAG	GTCCCTGAGA	AGGACTTGGT	GGATAAGGCT	CGTCAGATCA	ACATCCACAA	2700

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 TTCTGGTTTG GGGTGGTCAG TGCCCTCTGT GCTTTATGGA CACAAAACCA GAGCACTTGA 2880
 TGAACCTGGG GTACTAGGGT CAGGGCTTAT AGCAGGATGT CTGGCTGCAC CTGGCATGAC 2940
 TGTCTTACTT TCCAGCCTG CTTTGTGCTT CTCACCTTTG GGTGGGATGC CTGGCAGTGT 3000
 TGTCTTACTT GGTGTCTGAA CATCTTGCCA CCTCCGAGTG CTTTGTCTCC ACTCAGTACC 3060
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 TGCCCTTTGGC CAGAGAGCTG GTTGAAGATG TTTGTAATCG TTTTCAGTCT CTGTCAGGTT 3240
 TCTGTGCCCC TGTGGTGGAA GAGGGCAGCA CAGTGCACGC GCAGCGTTCT GGGCTCCTCA 3300
 GTGCGAGGGG TGGGATGTGA GTCATGCGGA TTATCCACTC GCCACAGTTA TCAGCTGCCA 3360
 TTGCTCCCTG TCTGTTTCCC CACTCTCTTA TTTGTGCATT CGGTTTGGTT TCTGTAGTTT 3420
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Seq ID NO: 329 Protein sequence:
Protein Accession #: AAH17490.1

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 DREAGRLGR MRRGLLYDSD EDEEREPARK RRQVERATED GEDEEEMIES IENLEDLKGH 180
 SVREWVSMAG PRLEIHHRFK NFLRTHVDSH GHNVFKERIS DMCKENRESL VVNYEDLAAR 240
 EHVLAFLPE APAELLQIFD EAALEVVLAM YPKYDRITNH IHVRISHLPL VBEELSLRQL 300
 HLNQLIRTSQ VVTSCTGVLP QLSMVKYNCN KCFVLGPFC QSQNQEVKPG SCPECQSAGP 360
 FEVNMERTTY QNYQIRIQE SPGKVAAGR L PRSKDAILLA DLVDSCKPGD EIELTGIYHN 420
 NYDGSJLNTAN GFPVPATVIL ANHVAKDKNK VAVGELTDED VKMTISLSKD QQIGEKIFAS 480
 IAPSIYGHED IKRGLALALF GEPKPNPGGK HKVRGDINVL LCGDPGTAKS QFLKYIEKVS 540
 SRAIFTTGGQ ASAVGLTAYV QRHPVSREWT LEAGALVLAD RGVCLIDEFD KMNDQDRTSI 600
 HEAMEQSSIS ISKAGIVTSL QARCTVIAAA NPIGGRYDPS LTFSENVDLT EPIISRFDIL 660
 CVVRDITVDPV QDEMLARFV GSHVRHHPN KEEGLANGS AAEPAMPNTY GVEPLPQEV L 720
 KKYIYAKER VHPKLNQMDQ DKVAKMYS DL RKESMATGSI PITVRHIESM IRMAEAHARI 780
 HLRDVIYEDD VNMALRVMLB SFIDTQKPSV MRSMRKTPAR YLSFRDRDNE LLLFILKQLV 840
 AEQVTYQRNR PGAQQDTIEV PEKDLVDKAR QINIHNLSAF YDSELPFRMNK FSHDLKRKMI 900
 LQQF

Seq ID NO: 330 DNA sequence
Nucleic Acid Accession #: M17254
Coding sequence: 257-1645

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 Protein Accession #: AAA52398

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 DDFQLRTPSY NADILLSHLH YLRETFPLPHL TSDDVDKALQ NSPRLMHARN TDLPEYPPRR 240
 SAWTGHGHT PQSKAAQPSF STVPKTEDQR PQLDPYQILG PTSRLANPG SQQQLWQFL 300
 LELLSDSNS SCITWEGTNG EFKMTDPDEV ARRWGERKSK FNNYDKLSR ALRYYYDKNI 360
 MTKVHGKRYA YKDFDFGIAQ ALQPHPESS LYKYPDLFY MGSYHAHPQK MNFVAPHEPA 420
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 GCTTCCAAAG CTCAAAGAA ATTTGGCTCC ATCCAAGAA GCTCCAGCTC CCTACTGGG 3360
 CCCTGGCTTC AGGCCACAC CCTGGGCCA GGSCCAGAGA GTGTGTCTCA GGAGAAITCA 3420
 ATGGGCTCTA GAGAGACACA CAGAAAGTTT GGGCATTGGG GAAATTTTCA AGGRTGTATG 3480

TATGGYTCAC GTATGGWCCA GGTGTCTCTG GTCCYKGGGT GCAGGGAAGT GGGCTGCAGG 3540
 GAAGTGGATT GGAGGGGAGC TTGAGGAATA TAAGGAGCGG GGGTGGAGAC TCAGGCTATG 3600
 GACAAAGACA GCCCCAGAGT TGGGAAGACC TGGCCTTAGT CGTCCTCAGC CTAGGGCAGG 3660
 GCAGTGAAGA AAGCTCTCCC CGCTCCTGCT GTAATGACCC AGAGTAGCCT CCCCAAGCCG 3720
 GCATCTTATG TGTGTCTTCC ACCATCCTCA TGGTGGCACT TTTCTAGGCC TGTCTCCAG 3780
 CATTGTGCAA GGCTCGGAAG AGAACCAGGA AGTGAACTG GGTGAAAACA GAAAGCTCAA 3840
 TGGATGGGCT AGGTTCCAGC ATCATTAGGG CAGAGTTTGC ACCTCCTCTG GTTCACTGGG 3900
 AATCCACCCA GCCCAGCAAT CATCTCCCTC TTTGAAGGAT TTTWATTCT ACTGGGTTTT 3960
 GGAACAACT CCTGCTGAGA CCCACAGCC AGAACTGAA AGCAGCAGCT CCCCAAGGCC 4020
 TGGAAATCC CTAAGAGAAG GCCTGGGGGA MAGGAATGG AGTGACAGGG GACAGGTAGA 4080
 GAGAAGGGGG CCCAATGGCC AGGAGTGAA GGAGGTGGCG TTGCTGAGAG CAGTCTGCAC 4140
 ATGCTTCTGT CTGAGTGACG GAAGGTGTTT CAGGGTCGAA ATTACACTTC TCGTACCTGG 4200
 AGACGCTGTT TGTGGGAGCA CTGGGCTCAT GCCTGGCACA CAATAGGTCT GCAATAAACC 4260
 ATGGTTAAAT CCTGAAAAAA AAAAAA

Seq ID NO: 333 Protein sequence
 Protein Accession #: NP_000011

1 11 21 31 41 51
 MTLGSPRKGL LMLLMALVTQ GDPVKPSRGP LVTCTCESPH CKGPTCRGAW CTVVLVREEG 60
 RHPQEHRCGG NLHRELRCGR PTEFVNHYCC DSHLCNHVNS LVLEATQPPS EQPGTDGQLA 120
 LILGPVLALL ALVALGVGLL WHVRRRQEKQ RGLHSELGES SLILKASEQG DTMLGDLLDS 180
 DCTTSGSGSL PFLVQRTVAR QVALVECVGK GRYGEVWRGL WHGESVAVKI FSSRDEQSWF 240
 RETEIYNTVL LRHDNILGFI ASDMTSRNSS TQLWLITHYH EHGSLYDFLQ RQTLPEPLAL 300
 RLAVSAACGL AHLHVEIFGT QGKPAIAHRD FKSRNVLVKS NLQCCIDILG LAVMHSQGS D 360
 YLDIGNNPRV GTRKRYMAPEV LDEQIRTDCE ESYKWTDIWA FGLVLWEIAR RTIVNGIVED 420
 YRPPFYDVVP NDPSPFDMKK VVCVDQQTPT IPNRLAADPV LSLGAQMMRE CWPYPNPSARL 480
 TALRIKKTILQ KISNSPEKPK VIQ

Seq ID NO: 334 DNA sequence
 Nucleic Acid Accession #: NM_004126.1
 Coding sequence: 108-329

1 11 21 31 41 51
 GGCACGAGCT CGTGCCGGCC TTCAGTTGTT TCGGGACGCG CCGAGCTTCG CCGCTCTTCC 60
 AGCGGCTCCG CTGCCAGAGC TAGCCCGAGC CCGGTTCTGG GCGGAAAATG CTGCGCTTTC 120
 ACATCGAAGA TTTGCCAGAG AAGGAAAAAC TGAAAAATGA AGTTGAGCAG CTTCGCAAG 180
 AAGTGAAGTT GCAGAGACAA CAAGTGTCTA AATGTTCTGA AGAAATAAAG AACTATATTG 240
 AAGAACGTTT TGGAGAGGAT CCTCTAGTAA AGGGAATTCC AGAAGACAAG AACCCCTTTA 300
 AAGAAAAAGG CAGCTGTGTT ATTTTCATAA TAACTTGGGA GAAACTGCAT CCTAAGTGGA 360
 AGAACTAGTT TGTTTATGTT TTCCAGATA AAACCAACAT GCTTTTAAAG GAAGGAAGAA 420
 TGAATATAAA AGGAGACTTT CTTAAGCACC ATATAGATAG GGTATGTAT AAAAGCATAT 480
 GTGCTACTCA TCTTTGCTCA CTATGCAGTC TTTTAAAGA GAGCAGAGAG TATCAGATGT 540
 ACAATTATGG AAATAAGAAC ATTACTTGAG CATGACACTT CTTTCAGTAT ATTGCTTGAT 600
 GCTTCAAATA AAGTTTGTGC TT

Seq ID NO: 335 Protein sequence
 Protein Accession #: NP_004117.1

1 11 21 31 41 51
 MPALHIEDLP EKEKLMKEVE QLRKEVKLQR QVSKCSEBI KNYIEERSGE DPLVKGIPED 60
 KNPFKEKGGC VIS

Seq ID NO: 336 DNA sequence
 Nucleic Acid Accession #: NM_005795
 Coding sequence: 555-1940

1 11 21 31 41 51
 GCACGAGGGA ACAACCTCTC TCTCTSCAGC AGAGAGTGTG ACCTCCTGCT TTAGGACCAT 60
 CAAGCTCTGC TAACTGAATC TCATCCTAAT TGCAGGATCA CATTGCAAGG CTTTCACTCT 120
 TTCCACCTTT GCTTGTGGGT AAATCTCTTC TGCGGAATCT CAGAAAGTAA AGTTCCATCC 180
 TGAGAAATATT TCACAAGAA TTTCTTAAAG AGCTGGACTG GGTCTTGACC CCTGGAATTT 240
 AAGAAATTTT TAAAGACAAT GTCAAATATG ATCCAAGAGA AAATGTGATT TGAGTCTGGA 300
 GACAATTTGT CATATCGTCT AATAATAAAA ACCCATACTA GCCTATAGAA AACAATATTT 360
 GAATAATAAA AACCCATACT AGCCTATAGA AAACAAATAT TGAAAGATTG CTACCACTAA 420
 AAAGAAAACCT ACTACAACCT GACAAGACTG CTGCAAACTT CAATTGGTCA CCACAACCTG 480
 ACAGAGTTGC TATAAAACAA GATTGCTACA ACTTCTAGTT TATGTTATAC AGCATATTTT 540
 ATTTGGGCTT AATGATGGAG AAAAAGTGTA CCCTGTATTT TCTGGTTCTC TTGCCTTTTT 600
 TTATGATTCT TGTTACAGCA GAATTAGAAG AGAGTCTGTA GGACTCAATT CAGTTGGGAG 660
 TTACTAGAAA TAAATCATG ACAGCTCAAT ATGAATGTTA CCAAAGATTG ATGCAAGACC 720
 CCATTCAACA AGCAGAAAGG GTTTACTGCA ACAGAACCTG GGATGGATGG CTTCTGCTGGA 780
 AGGATGTTGC AGCAGGAACG GAATCAATGC AGCTCTGCCC TGATTACTTT CAGGACTTTG 840
 ATCCATCAGA AAAAGTTACA AAGATCTGTG ACCAAGATGG AAATGTTTTT AGACATCCAG 900
 CAAGCAACAG AACATGGACA AATTATACCC AGTGTAATGT TAACACCCAC GAGAAAGTGA 960
 AGACTGCACCT AAATTGTTT TACCTGACCA TAATTGGACA CGGATTGTCT ATTGCATCAC 1020
 TGCTTATCTC GCTTGGCATA TTCTTTTATT TCAAGAGCCT AAGTTGCCAA AGGATTACCT 1080
 TACACAAAAA TCTGTTCTTC TCATTGTTT GTAACTCTGT TGTAACAACT ATTCACCTCA 1140
 CTGCAGTGGC CAACAACCGC GCCTTAGTAG CCACAATCC TGTTAGTTGC AAAGTGTCCC 1200
 AGTTCAATCA TCTTTACCTG ATGGGCTGTA ATTACTTTT GATGCTCTGT GAAGGCATTT 1260
 ACCTACACAC ACTCATTGTG GTGGCCGTGT TTGCAGAGAA GCAACATTTA ATGTGTATT 1320
 ATTTCTTGG CTGGGAGATT CCACTGATTC CTGCTGTAT ACATGCCATT GCTAGAAGCT 1380

TATATTACAA TGACAAATGCG TGGATCAGTT CTGATACCCA TCTCCTCTAC ATTATCCATG 1440
 GCCCAATTG TGCTGCTTTA CTGGTGAATC TTTTTCCTT GTTAAATATT GTACGCGTTC 1500
 TCATCACCAA GTTAAAGATT ACACACCAAG CGGAATCCAA TCTGTACATG AAAGCTGTGA 1560
 GAGCTACTCT TATCTTGGTG CCATTGCTTG GCATTGAATT TGTGCTGATT CCATGGCGAC 1620
 CTGAAGGAAA GATTGCAGAG GAGGTATATG ACTACATCAT GCACATCCTT ATGCACTTCC 1680
 AGGGTCTTTT GGTCTCTACC ATTTTCTGCT TCTTTAATGG AGAGGTTCAA GCAATTCTGA 1740
 GAAGAAACTG GAATCAATAC AAAATCCAAT TTGGAACAG CTTTTCACAC TCAGAAGCTC 1800
 TTCGTAGTGC GTCTTACACA GTGTCAACAA TCAGTGATGG TCCAGGTTAT AGTCATGACT 1860
 GTCCTAGTGA ACACCTAAAT GGAAAAAGCA TCCATGATAT TGAAAATGTT CTCTTAAAC 1920
 CAGAAAAATT ATATAATTGA AAATAGAAGG ATGGTTGTCT CACTGTTTGG TGCTTCTCCT 1980
 AACTCAAGGA CTTGGACCCA TGACTCTGTA GCCAGAAGAC TTCATATATA AATGACTTTG 2040
 GGAATAGTCA TAAAGAAGAG CCTTCACATG AAATTAGTAG TGTGTTGATA AGAGTGTAAC 2100
 ATCCAGCTCT ATGTGGGAAA AAAGAAATCC TGGTTTGTAA TGTTTGTGAG TAAATACTCC 2160
 CACTATGCGT GATCTGAGCG TACTAACCTG ACATCACCAA GTGTGGAATT GGAGAAAAGC 2220
 ACAATCAACT TTTCTGAGCT GGTGAAGCC AGTTCAGCA CACCATTGAT GAATTCAAAC 2280
 AAATGGCTGT AAAACTAAAC ATCATGTTG GGCATGATT TACCCTTATT CSCCCCAAGA 2340
 GACCTAGCTA AGGTCTATAA ACATGAAGGG AAAATTAGCT TTTAGTTTAA AAACCTCTTA 2400
 TCCCATCTTG ATTTGGGCGAG TTGACTTTTT TTTTTCCTCA GAGTGCCGTA GTCTCTTTTG 2460
 TAACTACCTC CTCAAATGGA CAATACCAGA AGTGAATTAT CCCTGCTGGC TTTCTTTTCT 2520
 CTATGAAAAG CAACCTGAGTA CAATTGTTAT GATCTACTCA TTTGCTGACA CATCAGTTAT 2580
 ATCTTGTGGC ATATCCATTG TGGAACTGG ATGAACAGGA TGTATAATAT GCAATCTTAC 2640
 TTCTATATCA TTAGGAAAAC ATCTTAGTTG ATGCTACAAA ACACCTTGTC AACCTCTTCC 2700
 TGTCTTACCA AACAGTGGGA GGAATTCCT AGCTGTAAAT ATAAATTTTG CCCTTCCATT 2760
 TCTACTGTAT AAACAAATTA GCAATCATT TATATAAAGA AAATCAATGA AGGATTTCTT 2820
 ATTTTCTTGG AATTTGTAA AAAGAAATG TGAATAATGA GCTTGTAAAT ACTCCATTAT 2880
 TTTATTTTAT AGTCTCAAAAT CAAATACATA CAACCTATGT AATTTTAA GCAATATAT 2940
 AATGCAACAA TGTGTGTATG TTAATATCTG ATACTGTATC TGGGCTGATT TTTTAAATAA 3000
 AATAGAGTCT GGAATGCT

Seq ID NO: 337 protein sequence
 Protein Accession #: NP_005786.1

1 11 21 31 41 51
 MEKKCTLYFL VLLPFFMILV TAELEESPED SIQLGVTRNK IMTAQYECYQ KIMQDPIQQA 60
 EGVYCNRTWD GNLWNVDVAA GTESMQLCPD YFQDFDPSEK VTKICDQDGN WFRHPASNRT 120
 WNTYTCNVN THEKVKTALN LFYLTIIHGH LSIASLLISL GIFFYFKSL S QORITLHKNL 180
 FPFVFCNSV TIIHLTAVAN NQALVATNPV SCKVSOPIHL YLMGCNRYFWM LCEGIYHLTL 240
 IVVAVPAEKQ HLMWYFLLGW GFPLIPACIH AIARSLYND NCWISSDTHL LYIHHGPICA 300
 ALLVNLFELL NVRVLITKL KVTHQAESNL YMKAVRATLI LVPLLGIEFV LIPWRPEGKI 360
 AEEVYDIYMH LLMHFQGLLV STIFCFPNEG VQAILRRNWN QYKIQFGNSF SNSEALRSAS 420
 YTVSTISDGP GYSHDCPSEH LNGKSIHDIE NVLLKPNLY N

Seq ID NO: 338 DNA sequence
 Nucleic Acid Accession #: NM_001795
 Coding sequence: 25-2379

1 11 21 31 41 51
 GCACGATCTG TTCCTCCTGG GAAGATGCAG AGGCTCATGA TGCTCCTCGC CACATCGGGC 60
 GCCTGCTCGG CCCTGCTGGC AGTGGCAGCA GTGGCAGCAG CAGGTGCTAA CCCTGCCCAA 120
 CGGGACACCC ACAGCCTGCT GCCCACCCAC CGGCGCCAAA AGAGAGATTG GATTTGGAAC 180
 CAGATGCACA TTGATGAAGA GAAAAACACC TCACTTCCCC ATCATGTAGG CAAGATCAAG 240
 TCAAGCGTGA GTCGCAAGAA TGCCAAGTAC CTGCTCAAAG GAGAATATGT GGGCAAGGTC 300
 TTCGGGTCG ATGCGAGAGC AGGAGAGCTG TTCGCCATTG AGAGGCTGGA CCGGAGAAAT 360
 ATCTCAGAGT ACCACCTCAC TGCTGTCAAT GTGGACAAGG ACACCTGGTG AAACCTGGAG 420
 ACTCTTCCCA GCTTCAACAT CAAAGTTCAT GACGTGAACG ACAACTGGCC TGTGTTCAAG 480
 CATCGGTTGT TCAATGCGTC CGTGCTGAG TCGTGGCTG TGGGGACCTC AGTCATCTCT 540
 GTGACAGCAG TGGATGCAGA CGACCCCACT GTGGGAGACC ACGCCTCTGT CATGTACCAA 600
 ATCTCTAAGG GGAAGAGATA TTTTGCCATC GATAAATCTG GACGTATTAT CACAATAACG 660
 AAAAGCTTGG ACCGAGAGAA GCAGGCCAGG TATGAGATCG TGGTGAAGC GCGAGATGCC 720
 CAGGGCCTCC GGGGGGACTC GGGCACGGCC ACCGTGCTGG TCACTCTGCA AGACATCAAT 780
 GACCACTTCC CTTCTCTCAC CCAGACCAAG TACACATTTG TCGTGCTGTA AGACACCCGT 840
 GTGGGCACCT CTGTGGGCTC TCTGTTTGTG GAGGACCCAG ATGAGCCCCA GAACCGGATG 900
 ACCAAGTACA GCATCTTGCG GGGCGACTAC CAGGACGCTT TCACCATTTA GACAAACCCC 960
 GCCCACAAAC AGGGCATCAT CAAGCCCATG AAGCCTCTGG ATTATGAATA CATCCAGCAA 1020
 TACAGCTTCA TCGTCAAGGC CACAGACCCC ACCATCGACC TCCGATACAT GAGCCCTCCC 1080
 GCGGGAACCA GAGCCAGGT CATTATCAAC ATCAGAGATG TGGACGAGCC CCCCATTTTC 1140
 CAGCAGCCTT TCTACCATTT CCAGCTGAAG GAAAACCCAGA AGAAGCCTCT GATTGGCACA 1200
 GTGCTGGCCA TGGACCTGTA TCGGCTAGG CATAGCATTG GATACTCCAT CCGCAGGACC 1260
 AGTGACAAGG GCCAGTTCTT CCGAGTCACA AAAAAGGGGG ACATTTACAA TGAGAAAGAA 1320
 CTGGACAGAG AAGTCTACCC CTGGTATAAC CTGACTGTGG AGGCCAAAGA ACTGGATTCC 1380
 ACTGGAACCC CCACAGGAAA AGAATCCATT GTGCAAGTCC ACATTGAAGT TTTGGATGAG 1440
 AATGACAATG CCCCAGGATT TGCCAAGCCC TACCAGCCCA AAGTGTGTGA GAACGCTGTC 1500
 CATGGCCAGC TGGTCTCGCA GATCTCGCA ATAGACAAGG ACATAACACC ACGAAACGTG 1560
 AAGTTCAAAT TCACCTTGAA TACTGAGAAC AACTTTACCC TCACGGATAA TCACGATAAC 1620
 ACGGCCAACA TCACAGTCAA GTATGGGCGG TTTGACCGGG AGCATACCAA GGTCCACTTC 1680
 CTACCCGTGG TACCTCTAGA CAATGGGATG CCAAGTCGCA CGGGCACCCG CACGCTGACC 1740
 GTGGCCGTGT GCAAGTGCAA CGAGCAGGGC GAGTTCACCT TCTGCGAGGA TATGGCCGCC 1800
 CAGGTGGGCG TGAGCATCCA GGCAGTGGTA GCCATCTTAC TCTGCATCCT CACCATCACA 1860
 GTGATCACCC TGCTCATCTT CCTGCGGCGG CGGCTCCGGA AGCAGGCCCG CGCGCACGGC 1920
 AAGAGCGTGC CGAGATCCA CGAGCAGCTG GTCACCTACG ACGAGGAGGG CGGCGGCGAG 1980
 ATGGACACCA CAGCTACGTA TGTGTCGGTG CTCACCTCGG TGGCCGCGGG CGGGGCCAAG 2040
 CCCCCTGGCG CGCGCTGGA CGCCCGGCCCT TCCCTCTATG CGCAGGTGCA GAAGCCACCG 2100
 AGGCACGCGC CTGGGGCACA CGGAGGGGCC GGGGAGATGG CAGCCATGAT CGAGGTGAAG 2160
 AAGGACGAGG CGGACACGGA CGGCGACGGC CCCCCTACG ACACGCTGCA CATCTACGGC 2220
 TACGAGGGCT CCGAGTCCAT AGCCGAGTCC CTCAGCTCCC TGGGCACCGA CTCATCCGAC 2280

5	TCTGACGTGG	ATTACGACTT	CCTTAAACGAC	TGGGGACCCA	GGTTTAAAGT	GCTGGCTGAG	2340
	CTGTACGGCT	CGGACCCCGG	GGAGGAGCTG	CTGTATTAGG	CGGCCGAGGT	CACTCTGGGC	2400
	CTGGGGACCC	AAACCCCTCG	CAGCCACAGG	CAGTCAGACT	CCAGGCACCA	CAGCCTCCAA	2460
	AAATGGCAGT	GAGTCCCCAG	CCAGCACCCG	CTTCCTCGTG	GGTCCCAGAG	ACCTCATCAG	2520
	CCTTGGGATA	GCAAACTCCA	GGTTCTTGAA	ATATCCAGGA	ATATATGTCA	GTGATGACTA	2580
	TTCTCAAAATG	CTGGCAAAATC	CAGGCTGGTG	TTCTGTCTGG	GCTCAGACAT	CCACATAACC	2640
	CTGTACCCCA	CAGACCGCCG	TCTAACTCAA	AGACTTCCTC	TGGCTCCCCA	AGGCTGCAA	2700
	GCAAAACAGA	CTGTGTTTAA	CTGCTGCAGG	GTCTTTTCTT	AGGGTCCCTG	AACGCCCTGG	2760
10	TAAGGCTGGT	GAGGTCTCTG	TGCCTATCTG	CCTGGAGGCA	AAGGCCTGGA	CAGCTTGACT	2820
	TGTGGGGCAG	GATTCTCTGC	AGCCCATTCG	CAAGGGAGAC	TGACCATCAT	GCCCTCTCTC	2880
	GGGAGCCCTA	GCCCTGCTCC	AACCTCCATC	TCCACTCCAA	GTGCCCCACC	ACTCCCCAAC	2940
	CCCTCTCCAG	GCCTGTCAAG	AGGGAGGAAG	GGGCCCCATG	GCAGCTCCTG	ACCTTGGGTC	3000
	CTGAAGTGAC	CTCACTGGCC	TGCCATGCCA	GTAACGTGTC	TGTACTGAGC	ACTGAACCAC	3060
15	ATTCAGGGAA	ATGCTTATTA	AACCTTGAAG	CAACTGTGAA	TTCATTCTGG	AGGGGCAGTG	3120
	GAGATCAGGA	GTGACAGATC	ACAGGGTGAG	GGCCACCTCC	ACACCCACCC	CCTCTGGAGA	3180
	AGGCTCTGAA	GAGCTGAGAC	CTTGCTTTGA	GACTCCTCAG	CACCCCTCCA	GTTTTCCTTG	3240
	AGAAGGGGCA	GATGTTCCCG	GAGATCAGAA	GACGTCCTCC	CTTCTCTGCC	TCACCTGGTC	3300
	GCCAAATCCAT	GCTCTCTTTC	TTTTCTCTGT	CTACTCCTTA	TCCCTTGGTT	TAGAGGAACC	3360
20	CAAGATGTGG	GCTTGTAGCA	AACCTGACAA	GTCCAAACCC	ACTCATGACT	GCATGACGGA	3420
	GCCGAGCATG	TGTCTTTACA	CCTCGCTGTT	GTCCATCTCT	AGGGAACATG	CCCTCAGGCA	3480
	CACCTTGAGG	AGGAAGGCCG	CTGCCCTGCC	CAACCTCTGT	GGTCACCCAT	GCATCATTCC	3540
	ACTGGAACGT	TTCAGTCAA	ACACACCTTG	GAGAAGTGGC	ATCAGTCAAC	AGAGAGGGGC	3600
	AGGGAAGGAG	ACACCAAGCT	CACCCCTCGT	CATGACCGGA	GGTTCCTCACT	CTGGCAAAGC	3660
25	CCCTCACACT	GCAAGGGATT	GTAGATAACA	CTGACTTGTT	TGTTTTAAC	AATAACTAGC	3720
	TTCTTATAAT	GATTTTTTTC	CTAATGATAC	TTACAAGTTT	CTAGCTCTCA	CAGACATATA	3780
	GAATAAGGTT	TTTTGCTATA	TAAGCAGGTT	GTTATTAGG	TTAACAATAT	TAATTTCAGGT	3840
	TTTTTAGTTG	GAAAAACAAT	TCCTGTAACC	TTCTATTTTC	TATAATTGTA	GTAATTGCTC	3900
	TACAGATAAT	GTCTATATAT	TGGCCAAACT	GGTGCAATGAC	AAGTACTGTA	TTTTTTTATA	3960
30	CCTAAATAAA	GAAAAATCTT	TAGCCTGGGC	AACAAAAAAA			

Seq ID NO: 339 Protein sequence
Protein Accession #: NP_001786

35	1	11	21	31	41	51	
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	NTSLPHRVGK	IKSSVSRKQA	KYLLKGEYVG	KVFRVDAETG	DVFAIERLDR	ENISEYHLTA	120
	VIVDKDTGEM	LETSSFTIK	VHDVNDNWPV	FTHRLFNASV	PESSAVGTSV	ISVTAVDADD	180
40	PTVGDHASVM	YQILKGKEYF	AIDNSGRIIT	ITKSLDREKQ	ARYEIVVEAR	DAQGLRGDSG	240
	TATVLVLTQD	INDNFPPFTQ	TKYTFVVPED	TRVGTSVGSL	FVEDPDEFQV	RTMKYSILRG	300
	DYQDAFTIET	NPAHNEGIIK	PMKPLDYEYI	QYQSFIYEAT	DPTIDLRYS	PPAGNRAQVI	360
	INITVDDEPP	IFQQPFYHFQ	LKENQKKPLI	GTVLAMPDA	ARHSIGYSIR	RTSDKGQFPR	420
	VTKKGDIIYE	KELDREVPW	YNLTVEAKBL	DSTGTPTGKE	SIVQVHIEVL	DENDNAPEFA	480
45	KPYQPKVCEN	AVHGQLVLQI	SAIDKDIPTP	NVKFKFTLNT	ENNFLTLDNH	DNTANITVKY	540
	GQFDRHRTIV	HFLPVVISDN	GMPSRTGTST	LTVAVCCKNE	QGEPTFCEDM	AAQVGVSIQA	600
	VVAILLCLIT	ITVITLLIFL	RRRLRKQARA	HGKSVPEIHE	QLVTYDEBGG	GEMDTTSYDV	660
	SVLNSVRRGG	AKPFRPALDA	RPSLYAQVQK	PPRHAPGAHG	GPGEAMAMIE	VKKDEADHDG	720
50	DGPPYDTLHI	YGYEGSESIA	ESLSGLGTDG	SDSDVDYDFL	NDWGRPRFML	AELYGSDPRE	780
	ELLY						

Seq ID NO: 340 DNA sequence
Nucleic Acid Accession #: NM_003088
Coding sequence: 112-1593

55	1	11	21	31	41	51	
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60	CCCGCACCC	ACCTCCCGGG	GCCGCGCAGC	GGCCTCTCGT	CTACTGCCAC	CATGACCGCC	120
	AACGGCACAG	CCGAGGCGGT	GCAGATCCAG	TTCCGCTCTA	TCAACTGCGG	CAACAAGTAC	180
	CTGACGGCCG	AGGCGTTCCG	GTTCAAGGTG	AACGCGTCCG	CCAGCAGCCT	GAAGAAGAAG	240
	CAGATCTGGA	CGCTGGAGCA	GCCCCCTGAC	GAGGCGGGCA	GCGCGGCGGT	GTGCTCGCGC	300
	AGCCACCTGG	GCCGCTACCT	GCGCGCGGAC	AAGGACGGCA	ACGTGACCTG	CGAGCGCGAG	360
65	GTGCCCGGTC	CCGACTGCGG	TTTCTTCATC	GTGGCGCACG	ACGACGCTCG	CTGGTCGCTG	420
	CAGTCCGAGG	CGCACC GGCG	CTACTTCGGC	GGCACCGAGG	ACCGCCTGTC	CTGCTTCGGG	480
	CAGACGGTGT	CCCCCGCCGA	GAAGTGGAGC	GTGCACATCG	CCATGACACC	TCAGGTCAAC	540
	ATCTACAGTG	TCACCCGTAA	GCGCTACGCG	CACCTGAGCG	CGCGGCGGGC	CGACGAGATC	600
	GCCGTGGACC	GCGACGTGCC	CTGGGGCGTC	GACTCGCTCA	TCACCCTCGC	CTTCCAGGAC	660
70	CAGCGCTACA	GCGTGCAGAC	CGCCGACCAC	CGCTTCCTGC	GCCACGACGG	GCGCCTGGTG	720
	GCGCGCCCGG	AGCCGGCCAC	TGGCTACACG	CTGGAGTTCC	GCTCCGCGAA	GGTGGCCTTC	780
	CGCGACTGCG	AGGGCCGTTA	CCTGGCGCGG	TCGGGGCCCA	GCGGCACGCT	CAAGGCGGGC	840
	AAGGCCACCA	AGGTGGGCAA	GGACGAGCTC	TTTGCTCTGG	AGCAGAGCTG	CGCCACAGTC	900
	GTGCTGCAGG	CGGCCAACGA	GAGGAACGTG	TCCACGCGCC	AGGGTATGGA	CCTGTCGTCC	960
75	AATCAGGACG	AGGAGACCGA	CCAGGAGACC	TTCCAGCTGG	AGATCGACCG	CGACACCAAA	1020
	AAGTGTGCCT	TCCGTACCCA	CACGGGCAAG	TACTGGACGC	TGACGGCCAC	CGGGGCGGTG	1080
	CAGTCCACCG	CTCCAGCAAA	GAATGCCAGC	TGCTACTTTG	ACATCGAGTG	CGGTGACCCG	1140
	CGCATCACAC	TGAGGGCGTC	CAATGGCAAG	TTTGTGACCT	CCAAGAAGAA	TGGGCGAGTC	1200
	GCCGCTCGGG	TGGAGACAGC	AGGGGACTCA	GAGCTCTTCC	TCATGAAGCT	CATCAACCCG	1260
80	CCCATCATCG	TGTTCCGGGG	GGAGCATGGC	TTCCATCGGT	GCCGCAAGGT	CACGGGCACC	1320
	CTGGACGCCA	ACCGCTCCAG	CTATGACGTC	TTCCAGCTGG	AGTTCACCGA	TGGCGCTTAC	1380
	AACATCAAG	ACTCCACAGG	CAAACTACTG	ACGGTGGGCA	GTGACTCCGC	GGTCAACGAC	1440
	AGCGGCGACA	CTCCTGTGGA	CTTCTTCTTC	GAGTTCTGCG	ACTATAACAA	GGTGGCCATC	1500
	AAGGTGGGCG	CGGCTTACCT	GAGGGGCGAC	CACGACGGCG	TCCTGAAGCG	CTCGGCGGAA	1560
	ACCGTGGACC	CGGCTCGGCT	CTGGGAGTAC	TAGGGCCGGC	CGGTCTCTCC	CGGCCCTCTC	1620
85	CCACATGGGG	GCTCCTGCCA	ACCCTCCCTG	CTAACCCCTT	CTCCGCGCAG	TGGGCTCCAG	1680
	GGCGGGAGGC	AAGCCCCCTT	GCCTTTCAAA	CTGGAACCCC	CAGAGAAAC	GGTGCCCCCA	1740
	CCTGTGCGCC	CTATGGACTC	CCCACTCTCC	CCTCGCGCCG	GGTTCCTTAC	TCCCTCGGGG	1800

TCAGCGGCTG CGGCGCTGGCC CTGGGAGGGA TTTCAGATGC CCCTGCCTTC TTGCTCTGCCA 1860
 CGGGGCGAGT CTGGCACCTC TTTCTTCTGA CCTCAGACGG CTCTGAGCCT TATTTCTCTG 1920
 GAAGCGGCTA AGGAGCGGTT GGGGGCTGGG AGCCCTGGGC GTGTAGTGTA ACTGGAATCT 1980
 TTTGCTCTCT CCAGCCACCT CCTCCAGCC CCCCAGGAGA GCTGGGCACA TGTCCTCAAGC 2040
 CTGTCACTGG CCTCCCTGG TCACTGTCC CCGAAACCCC TGCTTGGGAA GGAAGCTGT 2100
 CGGGAGGGCT AGGACTGACC CTGTGTGTGT TTTTGTGGGT GGTGGCTGGA AACAGCCCCT 2160
 CTCCACGCTG GGAGAGGCTC AGCCTGGCTC CCTTCCCTGG AGCGGCAGGG CGTGACGGCC 2220
 ACAGGGTCTG CCGCTGCAC GTTCTGCCAA GGTGGTGGTG GCGGGCGGGT AGGGGTGTGG 2280
 GGGCGCTCTT CTCTCTGTCT CTTTCTTTT ACCCTAGCCT GACTGGAAGC AGAAAATGAC 2340
 CAAATCAGTA TTTTCTTAA TGAATATTA TTGCTGGAGG CGTCCCAGGC AAGCCTGGCT 2400
 GTAGTAGCGA GTGATCTGGC GGGGGGCGTC TCAGCACCTC CCCCAGGGGG TGCATCTCAG 2460
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 CGCAGAGCCC CTGCTGTGAT TGGTGTCTCC TGGGCTCTCC GGGTGGATGA AGCCAGGCGT 2580
 CGCCCCCTCC GGGAGCCGAT GGGTGAGCCG CCGGGGCCCC CCGTCTGCCA GCCTCCCCCG 2640
 TCCCCAACAT GCATCTCACT CTGGGTGTCT TGGTCTTTA TTTTGTGTA GTGTCAATTG 2700
 TATAACTCTA AACGCCCATG ATAGTAGCTT CAAACTGGAA ATAGCGAAAT AAAATAAATC 2760
 AGTCTGC

Seq ID NO: 341 Protein sequence
 Protein Accession #: NP_003079

1 11 21 31 41 51
 MTANGTAEAV QIQFGLINCG NKYLTAFAFG FKNVASASSL KKKQIWTLEQ PPDEAGSAAV 60
 CLRSHLGRYL AADKGNVTC EREVPGPDCR FLIVAHDDGR WSLQSEAHRR YPGGTEDRLS 120
 CFAQTVSPAE KWSVHIAHHP QVNIYSVTRK RYAHLSARPA DEIAVDRDVP WGVDSLITLA 180
 FQDQRYSVQT ADHRFLRHDG RLVARPEPAT GYTFLEFRSGK VAFRDCEGRY LAPSPSGTL 240
 KAGKATKVGK DELFALEQSC AQVVLQAANE RNVSTRQGM DLSANQDEETD QETFQLEIDR 300
 DTKKCAPRTH TGKYWTLTAT GGVQSTASSK NASCYFDIEW RDRRITLRAS NGKFVTSKN 360
 GQLAASVETA GSELEFLMKL INRP11VFRG EHGFIGCRKV TGTLDANRSS YDVFQLEFND 420
 GAYNIKDSTG KYWTVGSDSA VTSSGDTFVD FPFEPDYNK VAIKVGGRYL KGDHAGVLKA 480
 SAETVDPASL WEY

Seq ID NO: 342 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 660..1705

1 11 21 31 41 51
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 CTCGAGCGGG ACAGATCCAA GTTGGGAGCA GCTCTGCGTG CCGGGCCCTCA GAGAATGAGG 240
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 CACCCCACTG CCGAGCGTGC TGGCTGCTCG GCCTCGGGGG CCTGCTACAG CCGTGCACCC 360
 GCTACCATGA AGCGCGAGG GGCAGAGGAG GCCTGCATCC TGGCAGGTGG GCGGCTCAGC 420
 ACCGTGCGTG CCGAGCGCGA GTGCGCGCT GTGCTCGCGC TCGTGGGGC AGGCCAGGG 480
 CCGGAGGGGG GCTCCAAAGA CCTGCTGTTC TGGGTGCGAC TGGAGCGCAG CGGTCCCCAC 540
 TGCACCTCTG AGAAGCAGCC TTTGCGGGGT TTCTCTCTGC TGTCCTCCGA CCGCGGCGGT 600
 CTCGAAAGCG ACACGCTGCA GTGGGTGGAG GAGCCCCAAC GCTCCTGCAC CCGCGGAGAG 660
 TGGCGGTGAC TCCAGGCCAC CGGTGGGGTC GAGCCCCGAG CTGGAAGGAG ATGCGATGCC 720
 ACCTGCGCGC CAAAGCGTAC CTGTGCAAGT ACCAGTTTGA GGTCTTGTGT CCGCGCGCGC 780
 GCGCCGGGGC CGCTCTAAC TTGAGCTATC GCGCGCCCTT CCAAGCTGAC AGCGCGGCTC 840
 TGGACTTCAG TCCACTCTGG ACCGAGGTGA GTGCGCTCTG CCGGGGACAG CTCCCGATCT 900
 CAGTTACTTG CATCGCGGAC GAAATCGGCG CTCGCTGGGA CAAACTCTCG GCGATGTGT 960
 TGTGTCCCTG CCGCGGAGG TACCTCCGTG CTGGCAAAAT CGCAGAGCTC CCTAATCTGC 1020
 TAGACGACTT GGGAGGCTTT GCCTGCGAAT GTGCTACGGG CTTCGAGCTG GGAAGGAGG 1080
 GCGGCTCTTG TGTGACCACT GGGGAAGGAC AGCCGACCCCT TGGGGGAGCC GGGGTGCCCA 1140
 CCAGGCGCCC GCGGCGCACT GCAACCAGCC CCGTGCCGCA GAGAACATGG CCAATCAGGG 1200
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 TGAGCACAGC AGTAGTAGTG TTGGTGATCT TGACCATGAC AGTACTGGGG CTTGTCAAGC 1500
 TCTGCTTTCA CGAAAGCCCC TCTTCCAGC CAAGGAAGGA GTCTATGGGC CCGCGGGGCC 1560
 TGGAGAGTGA TCTGAGCCCC GCTGCTTTGG GCTCCAGTTC TGCACATTGC ACAAACAATG 1620
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 CCCCCTCTGG CTCTAGTAGT GCATAG

Seq ID NO: 343 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
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 IARIYKELEQ IYKKKKPTKT LRTHFLSRPK GNCWPLGPRG DSWQLGGPSG ARAEGKGGGT 120
 GLGKPAVEGG DRAPDTALRP RAGQIQVGSS SACGASENEA GVRPVPLAG ALARAGRRT 180
 PHCRPCNLLG LGGLLQAPAP YHEAAGRG G LHPARWGAQH RACGRRAARC ARAPAGRPR 240
 RRGQLRPAVL GRTGAQAPPL HPGERAFAGF LLAVLRFRS RKRHAAVGGG APTLLHRAEM 300
 RGTGPHRWGR ARSWKEMRCH LRANGYLCKY QFEVLCAPAP PGAASNLVSR APFQLHSAAL 360
 DFSPPGTEVS ALCRGQLPIS VTCIADEIGA RWDKLSGDVL CPCPGRYLRA GKCAELPNCL 420
 DDLGGFACCE ATGFELGKDG RSCVTSGBGQ PTLGGTGVP RTTPATATSP VPQRTWPIRV 480
 DEKLGETPLV PEDDNSVTSI PEIPRWGSQS TMSTLQMSLQ AESKATITPS GSVISKFNST 540
 TSSATPAQFD SSSAVVFIFV STAVVVLVIL TMTVLGLVKL CFHESPSSQP RKESMGPFGL 600
 ESDPEPAALG SSSAHCTNNG VKVGDCDLRD RAEGALLAES PLGSSDA

Seq ID NO: 344 DNA sequence
Nucleic Acid Accession #: NM_012072
Coding sequence: 149-2107

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	AAAGCCCTCA	GCCTTTGTGT	CCTTCTCTGC	GCCGAGTGG	CTGCAGCTCA	CCCCTCAGCT	60
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	GCTGCTGCTC	CTGACCCAGC	CCGGGGCGGG	GACGGGAGCT	GACACGGAGG	CGGTGGTCTG	240
	CGTGGGGACC	GCCTGCTACA	CGGCCCACTC	GGGCAAGCTG	AGCGCTGCCG	AGGCCCAGAA	300
	CCACTGCAAC	CAGAACGGGG	GCAACCTGGC	CACTGTGAAG	AGCAAGGAGG	AGGCCCAGCA	360
5	CGTCCAGCGA	GTACTGGCCC	AGCTCCTGAG	GCGGGAGGCA	GCCCTGACGG	CGAGGATGAG	420
	CAAGTTCTGG	ATTGGGCTCC	AGCGAGAGAA	GGGCAAGTGC	CTGGACCCCTA	GTCTGCGCGT	480
	GAAAGGCTTC	AGCTGGGTGG	GCGGGGGGGA	GGACACGCCT	TACTCTAACT	GGCACAAGGA	540
	GCTCCGGAAC	TCGTGCATCT	CAAAGCGCTG	TGTGTCTCTG	CTGCTGGACC	TGTCCCAGCC	600
	GCTCCTTCCC	AACCGCTGCG	CCAAGTGGTC	TGAGGGCCCC	TGTGGGAGCC	CAGGCTCCCC	660
10	CGGAAGTAAC	ATTGAGGGCT	TCGTGTGCAA	GTTCAGCTTC	AAAGGCATGT	GCCGGCCTCT	720
	GGCCCTGGGG	GGCCCGAGTC	AGGTGACCTA	CACCAACCCC	TTCCAGACCA	CCAGTTCTCT	780
	CTTGGAGGCT	GTGCCCTTTG	CCTCTGCGGC	CAATGTAGCC	TGTGGGGAAG	GTGACAAGGA	840
	CGAGACTCAG	AGTCATTATT	TCCTGTGCAA	GGAGAAGGCC	CCCAGTGTGT	TCGACTGGGG	900
	CAGCTCGGGC	CCCCCTCTGT	TCAGCCCCAA	GTATGGCTGC	AACCTTCAACA	ATGGGGGCTG	960
15	CCACCAAGAC	TGCTTTGAAG	GGGGGGATGG	CTCCTTCTCT	TGCGGCTGCC	GACCAGGATT	1020
	CCGGCTGCTG	GATGACCTGG	TGACCTGTGC	CTCTCGAAAC	CCTTGCAGCT	CCAGCCCATG	1080
	TCGTGGGGGG	AGCTGGGTGG	TCCTGGGACC	CCATGGGAAA	AACCTACAGT	GCCGCTGCCC	1140
	CCAAGGGTAC	CAGCTGGACT	CGAGTCAGCT	GGAAGTGTGT	GACGTGGATG	AATGCCAGGA	1200
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20	TGGCTATGAG	CGGGCGGCTC	CTGGAGAGGG	GGCCTGTGAG	GATGTGGATG	AGTGTGCTCT	1320
	GGGTGCGCTG	CCTTGGCGCC	AGGGCTGCAC	CAACACAGAT	GGCTCATTTT	ACTGCTCCTG	1380
25	TGAGGAGGGG	TACGTCTCTG	CCGGGGAGGA	CGGGACTCAG	TGCCAGGACG	TGGATGAGTG	1440
	TGTGGGCCCC	GGGGGCCCCC	TCTGCGACAG	CTTGTGCTTC	AACACACAAG	GGTCTCTCCA	1500
	CTGTGGCTGC	CTGCCAGGCT	GGGTGCTGGC	CCCAATGGG	GTCTCTTGCA	CCATGGGGCC	1560
	TGTGTCTCTG	GGACCAACAT	CTGGGCCCCC	CGATGAGGAG	GACAAAGGAG	AGAAGAAGG	1620
30	GAGCAGCGTG	CCCCCGCTGT	CAACAGCCAG	TCCCAACAAG	GGCCCCGAGG	GCACCCCAAA	1680
	GGCTACACCC	ACCCTGAGTA	GACCTTCTGT	GTCTCTGAC	GCCCCCATCA	CATCTGCCCC	1740
	ACTCAAGATG	CTGGCCCCCA	GTGGGTCTCT	AGGCGTCTGG	AGGGAGCCCA	GCATCCATCA	1800
	CGCCACAGCT	GGCTCTGGCC	CCCAGGAGCC	TGCAGGTGGG	GACTCTCCCG	TGGCCACACA	1860
35	AAACAAAGAT	GGCACTGACG	GGCAAAAGCT	GCTTTTATTC	TACATCTTAG	GCACCGTGGT	1920
	GGCCATCCTA	CTCCTGCTGG	CCCTGGCTCT	GGGGCTACTG	GTCTATCGCA	AGCGGAGAGC	1980
40	GAAAGAGGGG	TAGCTGAAGT	AGAAGAAGCC	CCAGAATGCG	GCAGACAGTT	ACTCTGGGT	2040
	TCCAGAGCGA	GCTGAGAGCA	GGGCCATGGA	GAACCAATAC	AGTCCGACAC	CTGGGACAGA	2100
	CTGCTGAAGG	TGAGGTGGCC	CTAGAGACAC	TAGAGTCACC	AGCCACCATC	CTCAGAGCTT	2160
45	TGAACTCCCC	ATTCCAAAGG	GGCACCCACA	TTTTTTTGAA	AGACTGGACT	GGAATCTTAG	2220
	CAAACTATTT	TAACTCTCTT	CCTTAAAGGC	CCCTTGGAAC	ATGCAAGTAT	TTTCTACGGG	2280
	TGTTTGATGT	CCCTGAGTGG	GAACTGTGTT	GTTGGCGTGC	CACGGTGGGG	ATTTCTGTAC	2340
	TCTATAATGA	TTGTTACTCC	CCCTCCCTTT	TCAAATTTCA	ATGTGACCAA	TTCCGGATCA	2400
	GGGTGTGAGG	AGGCTGGGGC	TAAGGGGCTC	CCCTGAAATAT	CTTCTCTGCT	CACCTTCCACC	2460
50	ATCTAAGAGG	AAAAGGTGAG	TGTCTCATGC	TGATTAGGAT	TGAAATGATT	TGTTTCTCTT	2520
	CCTAGGATGA	AAACTAAATC	AATTAATAT	TCAATTAGGT	AAGAAGATCT	GGTTTTTTTG	2580
	TCAAAGGGAA	CATGTTGCGA	CTGGAAACAT	TTCTTTACAT	TTGCATTCCT	CCATTTCGCC	2640
	AGCACAAGTC	TTGCTAAATG	TGATACTGTT	GACATCTCTC	AGAATGGCCA	GAAGTGAAT	2700
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55	CTTGGGTTTA	TTTGCAAAAG	AAGCTTGAAA	AATATGAGAA	AAGTTGCTTG	AAGTGCATTA	2820
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	CACAGATACT	TGAATTAATT	CATCCAAATG	TACTGAGGTT	ACCACACACT	TGACTACGGA	2940
	TGTGATCAAC	ACTAACCAAG	AAACAAATTC	AAGGACAACC	TGTCTTTGAG	CCAGGGCAGG	3000
	CCTCAGACAC	CCTGCTGTGT	GGCCCGCCTC	CACCTTCTCC	TGCCCGGAAT	GCCAGTGCTC	3060
60	CGAGCTCAGA	CAGAGGAAGC	CCTGCAGAAA	GTTCCATCAG	GCTGTTCTCT	AAAGGATGTG	3120
	TGAACGGGAG	ATGATGCACT	GTGTTTGAAG	AGTTGTCTAT	TTAAAGCAAT	TTAGCACAGT	3180
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	CACACCAAGT	AGGGAGCTAG	TGAGGCAGTT	TGCTTAAGGA	ACTTTTGTTC	TCTGTCTCTT	3300
	TTCCCTTAAA	TTGGGGGTAA	GGAGGGAAGG	AAGAGGGAAG	GAGATGACTA	ACTAAATACA	3360
65	TTTTTACAGC	AAAACTGCTT	CAAAGCCATT	TAAATTATAT	CCTCATTTTA	AAAGTTACAT	3420
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	TCTCTCTCAC	ACACACACAC	ACACACACAC	ACACACACAC	AGAGACACCG	CACCATTCCTG	3540
	CCTGGGGCAC	TGGAACACAT	TCTTGGGGGT	CACCGATGGT	CAGAGTCACCT	AGAAGTTACC	3600
	TGAGTATCTC	TGGGAGGCCCT	CATGTCTCCT	GTGGGCTTTT	TACCACCACT	GTGCAGGAGA	3660
70	ACAGACAGAG	GAAATGTGTC	TCCCTCCAAG	GCCCCAAAGC	CTCAGAGAAA	GGGTGTTTCT	3720
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	CAAGGTGCAG	GGTTAATACT	CTTGCCAGTT	TTGAAATATA	GATGCTATGG	TTGAGATTGT	3840
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	TGATGTGGGC	ATTGGAACCT	TCCTTTTAAA	GTCTCTCTAT	GGTCTCCAGT	TTTCAGTTGG	3960
75	AACTCTGCTG	TTTAACTATT	AAGGGAGACA	AAGGCTGTGT	CCATTTGGCA	AAACTTCCTT	4020
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	CTGTCTGGCC	ATTGAGAGGA	TTCTAAAGAC	ATGGCTGGAT	GCCTGTCTGA	CCAACATCAG	4140
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	TCATTTGGGG	TGAAGGAGAC	ATTTCTGTCC	TGGGCTTCCC	ACAGCCCCAA	CGCAGTCTGT	4260
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80	GCCCCAGGCC	ATCGTCTGTT	CTCTGAATGC	AGCCCTGTTC	TCAACAACAG	GGAGGTCATG	4380
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	AACCACTGGG	CTCAACACAG	TGCTTTATTC	TCCTGTTTAT	TTTTGCTGTT	ACTTTGAAGC	4620
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	GCCAAGAGGC	CATTAACAAA	TCGTCTCTGT	CCTGAGGGGC	CCCAGCTTGC	TCGGGCGTGG	4740
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Seq ID NO: 345 Protein sequence
Protein Accession #: NP_036204

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1 11 21 31 41 51
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EDTPYSNWHK ELRNSCISKR CVALLDLSQ PLLPNRLPKW SEQPCGSPGS PGSNIEGFVC 180
KFSFKGMCPR LALGGPGQVT YTPFQTSS SLEAVPFASA ANVACGEGDK DETQSHYPLC 240
KEKAPDFVFD GSSGPLCVSP KYGCNFNNGG CHQDCPEGGD GSFLCGCRPG FRLLDDLVT 300
ASRNPSSSP CRGGATCVLG PHGKNYTCRC PQGYQLDSSQ LDCVDVDEQD DSPCAQECVN 360
TPGGFRBCBW VGYEPGGPGE GACQDVDECA LGRSFCAGQC TMTDGSFHCS CEEGYVLAGE 420
DGTQCQDVDE CVGPGGPLCD SLCFNTQGSF HCGCLPGWVL APNGVSCIMG PVSGLPPSGP 480
DEEDKGEKE GSTVPRPAA SPTRGPEGTP KATPTTSRPS LSSDAPITSA PLKMLAPSGS 540
SGVWREPSVI HATAASGPQE PAGDSSSVAT QNNDGTDGQK LLLFYILGTV VAILLLALA 600
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Seq ID NO: 346 DNA sequence
Nucleic Acid Accession #: Z31560
Coding sequence: <1-966

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1 11 21 31 41 51
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AGCCCGGACC GCCTCAAGCG GCCCATGAAT GCCTTCATGG TGTGGTCCCG CGGGCAGCGG 180
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Seq ID NO: 347 Protein sequence
Protein Accession #: CAA83435

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1 11 21 31 41 51
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KTLMKDKYCT LPGGLLAPGG NSMASGVGVG AGLGAGVNQR MDSYAHMNGW SNGYSMMQD 180
QLGYPQHFGI NAHGAAQMQP MHRYDVSALQ YNSMTSSQTV MNGSPTYSMS YSQQTPGMA 240
LGSMGVS VKS EASSSPFVVT SSSHSRAPCQ AGDLRDMISM YLPGAIEVPEP AAPSRLLHMSQ 300
HYQSGPVPGT AINGTLPLSH M

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Seq ID NO: 348 DNA sequence
Nucleotide Accession #: NM_002638
Coding sequence: 120-473

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10     GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
      TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG 180
      AGGCAGCTGT CACGGGAGTT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
      TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCACTTAA AGGTCAAGAT AAAGTCAAAG 300
      CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360
15     TCCGGTGGCG CATGTTGAAT CCCCTAACC GCTGCTTGAA AGATACTGAC TGCCAGGAA 420
      TCAAGAAAGT GTGTGAAGGC TCTTGGCGGA TGGCCTGTTT CGTTCGCCAG TGAAGGGAGC 480
      CGGTCTCTGC TGACCTGTGT CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540
      TGCTGCCCTT CCCCTTCCCA CACTGTCCAT TCTTCTCCC ATTCAGGATG CCCACGGCTG 600
      GAGCTGCCTC TCTCATCCAC TTTCGAATAA A
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Seq ID NO: 349 Protein sequence:
Protein Accession #: NP_002629

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      AQEPVKGPVS TKPGSCPIL IRCAMLNPPN RCLKDTCFPG IKKCEGSCG MACFVPQ
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Seq ID NO: 350 DNA sequence
Nucleic Acid Accession #: NM_007183
Coding sequence: 75-2468

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      |      |      |      |      |      |
      GAATTCGGGA CAGGACGTGA AGATAGTTGG GTTTGGAGGC GGCCCGCCAG CCCAGGCCCG 60
      GTGGACCTGC CGCCATGCAG GACGGTAAC TCTGTCTGTC GGCCCTGCAG CCTGAGGCCG 120
      GCGTGTGCTC CCTGGCGCTG CCTCTGACC TGCAGCTGGA CCGCCGGGGC GCCGAGGGGC 180
      CGGAGGCCGA GCGGCTGCGG GCAGCCCGCG TCCAGGAGCA GGTCGCGCGC CGCCTCTTGC 240
40     AGCTGGGACA GACGCGCGCG CACAACGGGG CCGCTGAGCC CGAGCCTGAG GCCGAGACTG 300
      CCAGAGGCAC ATTCAAGGGG CAGTACCACA CCCTGCAGGC TGGCTTCAGC TCTCGCTCTC 360
      AGGGCTGAGT TGGGGAAGA ACCTCGGGCT TCCGGCCCAT GCCTACAGCC GCCTACAGCC 420
      CAGCCTCTCTG TCCCTCCCGC TCCGCGGTGG ATCTGAGCTG CAGTCGGAGG CTGAGTTTCA 480
      CCCACAATGG GGGCAGCGCC TTTGGGGCCG CTGGGTACGG GGGTGCCCGC CCCACCCCTC 540
      CCATGCCCAC CAGGCCCGTG TCCTTCCATG AGCGCGGTGG GGTGAGGAGC CGGGCGGACT 600
45     ATGACACACT CTCCTCGCGC TCGCTGCGGC TGGGGCCCGG GGGCCTGGAC GACCGCTACA 660
      GCGTGGTGTG TGAGCAACTG GAGCCCGCGG CCACCTCCAC CTACAGGGGC TTTGCTAGC 720
      AGCGCCAGGC CAGCTCCAGC TCCAGCCGGG CAGGGGGGCT GGACTGGCCC GAGGCCACTG 780
      AGGTTTCCCC GAGCCGAGAC ATCCGTGCCC CTGCGGTGCG GACCCTGCAG CGATTCCAGA 840
      GCAGCCACCG GAGCCCGGGG GTAGGCGGGG CAGTGCCGGG GCGCGTCTCT GAGCCAGTGG 900
50     CTCGAGCGCC ATCTGTGCGC AGCCTCAGCC TCAGCCTGGC TGACTCGGGC CACCTGCCC 960
      ACGTGATGG GTTCAAGAGC TACGGTAGCC ACCGAACCTT GCAGAGACTC AGCAGCGGTT 1020
      TTGATGACAT TGACCTGCCC TCAGCAGTCA AGTACCTCAT GGCTTCAGAC CCCAACCTGC 1080
      AGGTGCTGGG AGCGGCTTAC ATCCAGCACA AGTGCTACAG CGATGCAGCC GCCAAGAAGC 1140
      AGGCCCGCAG CCTTCAGGCC GTGCTTAGGC TGGTGAAGCT CTTCAACCAC GCCAACCAGG 1200
55     AAGTGACAGC CCATGCCACA GGTGCCATGC GCAACCTCAT CTACGACAAC GCTGACAAC 1260
      AGCTGGCCCT GGTGAGGAGG AACGGGATCT TCGAGCTGCT CGGGAACATG CGGGAGCAGG 1320
      ATGATGAGCT TCGCAAAATG GTCAAGGGA TCTGTGGAA CCTTTCATCC AGCGACCACC 1380
      TGAAGGACCG CCGGAGAGAT GACACGCTGG AGCAGCTCAC GGAACCTGGT TTGAGCCCCC 1440
      TGTCGGGGGC TGGGGGTCCC CCCCTCATCC AGCAGAAGCG CTCGGAGGCG GAGATCTTCT 1500
60     ACAAGCCGAC CGGCTTCTCT AGGAACCTCA GCTCAGCCTC TCAGGCCACT CGCCAGAAGA 1560
      TGCGGGAGTG CCAAGGGCTG GTGGACGCC TGGTCACTTC TATCAACCAC GCCCTGGACG 1620
      CGGGCAATG CGAGGACAAG AGCGTGGAAG ACGCGGTGTG CGTCTGCGG AACCTGTCTCT 1680
      ACCGCTCTA CGAGAGATG CCGCGTCCG CGCTGCAGCG GCTGGAGGGT CGCGGCCGCA 1740
      GGGACCTGGC GGGGGCGCGC CCGGGAGAGG TCGTGGGCTG CTTCAAGCCG CAGAGCCGCG 1800
65     GGCTGCGCGA GCTGCCCTCT GCGGCCGATG CGCTCACCTT CGCGGAGGTG TCCAAGGACC 1860
      CCAAGGGCCT CGATGGCTG TGGAGCCCC AGATCGTGGG GCTGTACAAC CGGCTGCTCG 1920
      AGCGCTGCGA GCTCAACCGG CACACGACCG AGCGGGCGCG CGGGCGCGCT CAGAACATCA 1980
      CGGCAGGCGA CCGCAGGTGG GCGGGGGTGC TGAGCCGCTT GGCCCTGGAG CAGGAGCGTA 2040
      TTCTGAACCC CCGTCTAGAC CGTGTCAAG CCGCCGACCA CCACAGCTG CGCTCACTGA 2100
70     CTGGCCTCAT CCGAAACCTG TCTCGGAACG CTAGGAACAA GGACGAGATG TCCACGAAGG 2160
      TGGTGAGCCA CCGTATCGAG AAGCTGCCAG GCAGCGTGGG TGAGAAGTCG CCCCAGCCG 2220
      AGGTGCTGGT CAACATCATA GCTGTGCTCA ACAACCTGGT GGTGGCCAGC CCGATCGCTG 2280
      CCGGAGACTT GCTTATTTT GACGAGCTCC GAAAGCTCAT CTTTCATCAAG AAGAAGCGGG 2340
75     ACAGCCCGA CAGTGAGAAG TCCTCCCGGG CAGCATCCAG CCTCTGGCC AACCTGTGGC 2400
      AGTACAACAA GCTCCACCGT GACTTTCGGG CGAAGGGCTA TCGGAAGGAG GACTTCTGG 2460
      GCCCATAGGT GAAGCTTCTT GGAGGAGAAG GTGACGTGGC CCAGGTCCA AGGGACAGAC 2520
      TCAGTCCAG GCTGCTTGGC AGCCAGCCTT GGAGGAGAAG GCTAATGACG GAGGGGCCCC 2580
      TCGTGGGGC CCGTGTGTGC ATCTTTGAGG GTCTGGGGCC ACCAGGAGGG GCAGGGTCTT 2640
80     ATAGCTGGGG ACTTGGCTTC CGCAGGGCAG GGGGTGGGGC AGGGCTCAAG GCTGCTCTGG 2700
      TGTATGGGGT GGTGACCCAG TCACATTGGC AGAGGTGGGG GTTGGCTGTG GCCTGGCAGT 2760
      ATCTTGGGAT AGCCAGCACT GGGAAATAAG ATGGCCATGA ACAGTCAACA AAAAAAAAAA 2820
      AAAAGGAATT C
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Seq ID NO: 351 Protein sequence
Protein Accession #: NP_009114.1

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85     1      11      21      31      41      51
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	1	11	21	31	41	51	
	MQDGNFLLSA	LQPEAGVCSL	ALPSDLQLDR	RGAEGPEAER	LRAARVQEQV	RARLLQLGQQ	60
	PRHNGAAEPE	PEAETARGTS	RGQYHTLQAG	FSRSRQGLSG	DKTSQGRFIA	KPAYSPASWS	120
5	SRSAVDLSGS	RRLSSAHNGG	SAFGAAGYGG	AQPTPPMPTR	PVSFHERGGV	GSRADYDTLS	180
	LRLSLRLPGG	LDRLSYLVSE	OLEPAATSTY	RAFAYERQAS	SSSSRAGGLD	WPEATEVSPS	240
	RTIRAPAVRT	LQRFQSSHRS	RGVGGAVPGA	VLEPVARAPS	VRLSLSLAD	SGHLDPVHGF	300
	NSYGSHTRLQ	RLSSGFDDID	LPSAVKYLMA	SDPNLQVLGA	AYIQHKCYSD	AAAKKQARSL	360
	QAVPRLVKLF	NHANQEVQRH	ATGAMRNLIY	DNADNKLALV	EENGIFELLR	TLREQDDELRL	420
10	KNVTGILWNL	SSSDHLKDRL	ARDTLEQLTD	LVLSPLSGAG	GPPLIQONAS	EAEIFYNATG	480
	FLRNLSSASQ	ATRQKMRECH	GLVDALVTSI	NHALDAGKCE	DKSVENAVCV	LRNLSYRLYD	540
	EMPPSALQRL	EGRGRRLDLAG	APPGEVVGCF	TPQSRRLREL	PLAADALTFA	EVSKDPKGLE	600
	WLNSPQIVGL	YNRLQLQRCCL	NRHTTEAAAG	ALQNTAGADR	RWAGVLSRLA	LEQERILNPL	660
	LDRVRTADHH	QLRSLTGLIR	NLSRNARNKD	EMSTKVVSHL	IEKLPGSVGE	KSPPAEVLVN	720
15	IIAIVLNNLVV	ASPIAARDLL	YFDGLRLKLF	IKKKRDSFDS	EKSSRAASSL	LANLWQYNKL	780
	HRDFRAXGYR	KEDFLGP					

Seq ID NO: 352 DNA sequence
Nucleic Acid Accession #: M31469
Coding sequence: 1-651

	1	11	21	31	41	51	
	ATGGCTGCGC	AGGGAGAGCC	CCAGGTCCAG	TTCAAACCTG	TATTGGTTGG	TGATGGTGGT	60
	ACTGGAAGAA	CGACCTTCGT	GAAACGTCAT	TTGACTGGTG	AATTTGAGAA	GAAGTATGTA	120
25	GCCACCTTGG	GTGTTGAGGT	TATCCCCCTA	GTGTTCCACA	CCAACAGAGG	ACCTATTAA	180
	TTCAATGTAT	GGGACACAGC	CGGCCAGGAG	AAATTCGGTG	GACTGAGAGA	TGGCTATTAT	240
	ATCCAAGCCC	AGTGTGCCAT	CATAATGTTT	GATGTAACAT	CGAGAGTTAC	TTACAAGAAT	300
	GTGCCTAACT	GGCATAGAGA	TCTGGTACGA	GTGTGTGAAA	ACATCCCCAT	TGTGTTGTGT	360
30	GGCAACAAAG	TGGATTATTA	GGACAGGAAA	GTGAAGGCGA	AATCCATTGT	CTTCCACCGA	420
	AAGAAGAATC	TTTCAGTACTA	CGACATTTCT	GCCAAAAGTA	ACTACAACCT	TGAAAAGCCC	480
	TTCTCTGGC	TTGCTAGGAA	GCTCATTTGA	GACCCTAACT	TGGAATTTGT	TGCCATGCCT	540
	GCTCTCGCCC	CACAGGAAGT	TGTCATGGAC	CCAGCTTTGG	CAGCACAGTA	TGAGCACGAC	600
35	TTAGAGGTG	CTCAGACAA	TGCTCTCCG	GATGAGGATG	ATGACCTGTG	A	

Seq ID NO: 353 Protein sequence
Protein Accession #: AAA36546

	1	11	21	31	41	51	
	MAAQGEPOVQ	FKLVLVGDGG	TGKTTFVKRH	LTGEFEKKYV	ATLGVEVHPL	VFHTNRGPIK	60
	PNVNDTAGQE	KFGGLRDGY	IQACAIIMF	DVTSRVTYKN	VPNWHRLVR	VCENIPIVLC	120
	GNKVIDIKDR	VKAKSIVFHR	KKNLQYYDIS	AKSNYNPEKP	FLWLARKLIG	DPNLEFVAMP	180
45	ALAPPEVMD	PALAAQYEH	LEVAQTALP	DEDDDL			

Seq ID NO: 354 DNA sequence
Nucleic Acid Accession #: NM_002820
Coding sequence: 304-831

	1	11	21	31	41	51	
	CCGGTTCCGA	AAGAAGCTGA	CTTCAGAGGG	GGAAACTTTC	TTCTTTTAGG	AGGCGGTTAG	60
	CCCTGTTCCA	CGAACCCAGG	AGAACTGCTG	GCCAGATTAA	TTAGACATTG	CTATGGGAGA	120
55	CGTGTAACAA	CACACTTAT	CATTGATGCA	TATATAAAAC	CATTTTATTT	TCGCTATTAT	180
	TTCAGAGGAA	GGCCCTCTGA	TTTGTTTCTT	TTTTCCCTTT	TTGCTCTTTC	TGGCTGTGTG	240
	GTTTGGAGAA	AGCACAGTTG	GAGTAGCCGG	TTGCTAAATA	AGTCCCGAGC	GCGAGCCGAG	300
	ACGATGCAGC	GGAGACTGGT	TCAGCAGTGG	AGCGTCGCGG	TGTTCTTGCT	GAGCTACGCG	360
	GTGCCCTCCT	GCGGGCGCTC	GGTGGAGGGT	CTCAGCCGCC	GCCTCAAAG	AGCTGTGTCT	420
60	GAACATCAGC	TCTCTCATGA	CAAGGGGAA	TCCATCCAAG	ATTACCGCG	ACGATTCTTC	480
	CTTCACCATC	TGATCGCAGA	AATCCACACA	GCTGAAATCA	GAGCTACCTC	GGAGGTGTCC	540
	CCTAACTCCA	AGCCCTCTCC	CAACACAAAG	AACCACCCCG	TCCGATTGG	GTCTGATGAT	600
	GAGGGCAGAT	ACCTAACTCA	GGAAACTAAC	AAGGTGGAGA	CGTACAAAGA	GCAGCCGCTC	660
65	AAGACACCTG	GGAAGAAAAA	GAAAGGCAAG	CCCGGGAAAC	GCAAGGAGCA	GGAAAAGAAA	720
	AAACGGCGAA	CTCGCTCTGC	CTGGTTAGAC	TCTGGAGTGA	CTGGGAGTGG	GCTAGAAGGG	780
	GACCACTGT	CTGACACCTC	CACAACGTCG	CTGGAGCTCG	ATTCACGGTA	ACAGGCTTCT	840
	CTGGCCCGTA	GCCTCAGCGG	GGTGCTCTCA	GCTGGGTTTT	GGAGCCTCCC	TTCTGCCTTG	900
	GCTTGGACAA	ACCTAGAATT	TTCTCCCTTT	ATGTATCTCT	ATCGATTGTG	TAGCAATTGA	960
70	CAGAGAATAA	CTCAGAATAT	TGCTCGCCTT	AAAGCAGTAC	CCCCCTACCA	CACACACCCC	1020
	TGTCCTCCAG	CACCATAGAG	AGGCGCTAGA	GCCCATTCCT	CTTTCTCCAC	CGTCACCCAA	1080
	CATCAATCCT	TTACCACTCT	ACCAAATAAT	TTCATATTCA	AGCTTCAGAA	GCTAGTGACC	1140
	ATCTTCATAA	TTTGCTGGAG	AAGTGATTTT	CTTCCCCTTA	CTCTCACACC	TGGGCAAACT	1200
	TTCTTCAGTG	TTTTTCATTT	CTTACGTTCT	TTCACTTCAA	GGGAGAATAT	AGAAGCATTT	1260
75	GATATTATCT	ACAAACACTG	CAGAACAGCA	TCATGTCTATA	AACGATTCTG	AGCCATTAC	1320
	ACTTTTTATT	TAATTAATAT	TATTTAATTA	AATCTCAAAT	TTATTTTAAT	GTAAGAAGCT	1380
	TAAATTATGT	TTTAAACACA	TGCCTTAAAT	TTGTTTAATT	AAATTTAACT	CTGGTTTCTA	1440
	CCAGCTCATA	CAAAATAAAT	GGTTTCTGAA	AATGTTTAA	TATTAACCTA	CAAGGATATA	1500
80	GGTTTTTCTC	ATGTATCTTT	TGTTTCATTG	GCAAGATGAA	ATAATTTTTC	TAGGGTAATG	1560
	CCGTAGGAAA	AATAAACTTT	CACATTTAAA	AAAAA			

Seq ID NO: 355 Protein sequence
Protein Accession #: NM_002820

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	MQRRLVQQWS	VAVFLLSYAV	PSCGRSVEGL	SRRLKRAVSE	HQLLHDKGKS	IQDLRRRFFL	60
85	HHLIAETHTA	EIRATSEVSE	NSKPSFNTKN	HPVRFSGSDE	GRYLQTETNK	VETYKEQPLK	120

TPGKKKKGKP GKRKEQEKKK RRTRSAWLDS GVTGSGLEGD HLSDTSTTSL ELSDR

Seq ID NO: 356 DNA sequence
Nucleic Acid Accession #: NM_017522
Coding sequence: 1-2100

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10
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35
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CTGCTGCTGC	TGCGGCTCCA	GCATCTTGCG	GCGGCAGCG	CTGATCCGCT	GCTCGGCGGC	120
CAAGGGCCGG	CCAAGGAGTG	CGAAAAGGAC	CAATTCAGT	GCCGGAACGA	GCGCTGCATC	180
CCCTCTGTGT	GGAGATGCGA	CGAGGACGAT	GACTGCTTAG	ACCACAGCGA	CGAGGACGAC	240
TGCCCCAAGA	AGACCTGTGC	AGACAGTGAC	TTACCTGTG	ACAACGGCCA	CTGCATCCAC	300
GAACGGTGG	AGTGTGACGG	CGAGGAGGAG	TGTCCTGATG	GCTCCGATGA	GTCCGAGGCC	360
ACTTGCACCA	AGCAGGTGTG	TCCTGCAGAG	AAGCTGAGCT	GTGGACCCAC	CAGCCACAAG	420
TGTTGACTCT	CCTCGTGGCG	CTGCGACGGG	GAGAAAGGACT	GCGAGGGTGG	AGCGGATGAG	480
GCCGGCTGTG	CTACCTCACT	GGGCACCTGC	CGTGGGGACG	AGTTCAGATG	TGGGGATGGG	540
ACATGTGTCC	TTGCAATCAA	GCATGCAAC	CAGGAGCAGG	ACTGTCCAG	TGGAGTGTAT	600
GAAGCTGGCT	GCCTACAGGG	GCTGAACGAG	TGTCGACACA	ACAATGGCGG	CTGCTCACAC	660
ATCTGCACTG	ACCTCAAGAT	TGGCTTTGAA	TGCACGTGCC	CAGCAGGCTT	CCAGCTCCTG	720
GACCAGAAGA	CTTGTGGCGA	CATTGATGAG	TGCAAGGACC	CAGATGCCTG	CAGCCAGATC	780
TGTGTCAATT	ACAAGGGCTA	TTTTAAGTGT	GAGTGTCTACC	CTGGCTGCGA	GATGGACCTA	840
CTGACCAAGA	ACTGCAAGGC	TGCTGTCTGG	AAGAGCCCAT	CCCTAATCTT	CACCAACCGC	900
ACGAGTGGCG	GGCTACAGGC	TGTGAAGCGG	AACCTATTAC	GCCTCATCCC	CATGCTCAAG	960
AATGTCTGGG	GCCTAGATGT	GGAAAGTGCC	ACCAATCGCA	TCTACTGGTG	TGACCTCTCC	1020
TACCGTAAGA	TCTATGCGCG	CTACATGGAC	AAGGCCAGTG	ACCCGAAAGA	GCGGGAGGTC	1080
CTCATTGACG	AGCAGTTGCA	CTCTCCAGAG	GGCCTGGCAG	TGGACTGGGT	CCACAAGCAC	1140
ATCTACTGGA	CTGACTCGGG	CAATAAGACC	ATCTCAGTGG	CCACAGTTGA	TGGTGGCCCG	1200
CGAGCGACTC	TCTTCCAGCG	TAACTCAGT	GAACCCCGGG	CCATCGCTGT	TGACCCCTCG	1260
CGAGGGTTCA	TGTATTGGTC	TGACTGGGGG	GACCAGGCCA	AGATTGAGAA	ATCTGGGCTC	1320
AACGGTGTGG	ACCGGCAAA	ACTGGTGTCA	GACAATATTG	AATGGCCCAA	CGGAATCACC	1380
CTGGATCTGC	TGAGCCAGCG	CTTGTACTGG	GTAGACTCCA	AGCTACACCA	ACTGTCCAGC	1440
ATTGACTTCA	GTGGAGGCAA	CAGAAAGACG	CTGATCTCCT	CCACTGACTT	CCTGAGCCAC	1500
CCTTTGGGA	TAGCTGTGTT	TGAGGACAAG	GTGTTCTGGA	CAGACCTGGA	GAACGAGGCC	1560
ATTTTCACTG	CAAATCGGCT	CAATGGCCTG	GAATCTCCCA	TCTTGGCTGA	GAACCTCAAG	1620
AACCCACATG	ACATTGTCTAT	CTTCCATGAG	CTGAAGCAGC	CAAGAGCTCC	AGATGCGCTG	1680
GAGCTGAGTG	TCCAGCCTAA	TGGAGGCTGT	GAATACCTGT	GCCTTCTGTC	TCCTCAGATC	1740
TCCAGCCACT	CTCCCAAGTA	CACATGTGCC	TGTCCTGACA	CAATGTGGCT	GGGTCCAGAC	1800
ATGAAGAGGT	GCTACCGAGA	TGCAAAATGAA	GACAGTAAGA	TGGGCTCAAC	AGTCACTGCC	1860
GCTGTTATCG	GGATCATCGT	GCCCATAGTG	GTGATAGCCC	TCTGTGTCAT	GAGTGGATAC	1920
CTGATCTGGA	GAAACTGGAA	CGGGAAGAAC	ACCAAAAGCA	TGAATTTTGA	CAACCCAGTC	1980
TACAGGAAAA	CAACAGAAGA	AGAAGATGAA	GATGAGCTCC	ATATAGGGAG	AACCTGCTCAG	2040
ATTGGCCATG	TCTATCTCTG	ACGAGTGGCA	TTAAGCCTTG	AAGATGATGG	ACTACCCTGA	2100
GGATGGGATC	ACCCCTCTCG	TGCCCTCATG	AATTCAGTCC	CATGCACTAC	ACTCCGGATG	2160
GTGATGACT	GGATGAATGG	GTCTCTATAT	ATGGGTCTGT	GTGAGTGTAT	GTGTGTGTGT	2220
GATTTTPTTT	TTTAAATTTT	TGTTGCGGAA	AGGTAACCAC	AAAGTTATGA	TGAACCTGCA	2280
ACATCCAAAG	GATGTGAGAG	TTTTTCTATG	TATAATGTTT	TATACACTTT	TTAACTGGTT	2340
GCACTACCCA	TGAGGCAATC	GTGGAAATGG	TACTGCTGAC	TAACATGATG	CACATAACCA	2400
AATGGGGGCC	AATGGGCACG	TACCTTACTC	ATCATTTAAA	AACTATATTT	ACAGAAGATG	2460
TTTGGTGTCT	GGGGGGCTTT	TTTAGGTTT	GGGCATTGTT	TTTTTGTAAA	TAAGATGATT	2520
ATGCTTTGTG	GCTATCCATC	AACATAAGT				

Seq ID NO: 357 Protein sequence
Protein Accession #: NP_059992

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70

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MGLPEPGLR	LLALLLLLLL	LLLRLQHLA	AAAADPLLGG	QGPKECEKD	QFQCRNERCI	60
PSVWRCEDD	DCLDHSDEDD	CPKKTCAUSD	FTCDNGHCII	ERWKCDEBEE	CPDGSDESEA	120
TCTKQVCPAE	KLSCGPTSHK	CVPASWRCDG	EKDCGGGADE	AGCATSLGTC	RGDEFQCGDG	180
TCVLAIKHCN	QEQDCPDGSD	EAGCLQGLNE	CLHNNGGCSH	ICTDLKIGFE	CTCPAGFQLL	240
DQKTCGDIDE	CKDPDACSQI	CUNYKGYFKC	ECYPGCEMDL	LTNKNCAAAG	KSPSLIFTNR	300
TSABDRPVKR	NYSRLIFMLK	NVVALDVEVA	TNRIYWCDSL	YRKIYSAYMD	KASDPKEREV	360
LIDBQLHSPE	GLAVDNVHKH	IYWTDSGNKT	ISVATVDGGR	RRTLFERNLS	EPRAIADVPL	420
RGFMVSWDNG	DQAKIEKSLG	NGVDRQTLVS	DNIEWPNGIT	LDLLSQRLYW	VDSKLHQLSS	480
IDFSGGNRKT	LISSTDFLSH	PFGLAVFEDK	VFWTDLENEA	IFSANRLNGL	EISILAENLN	540
NPHDIVIFHE	LKQPRAPDAC	ELSVQPNNGC	EYLCCLPAQI	SSHSPKYTCA	CPDTMWLGPD	600
MKRCYRDANE	DSKMGSTVTA	AVIGIIVPIV	VIALLCMSGY	LIWRNWKRNK	TKSMNFDNFP	660
YRKTEEDEDE	DELHIGRTAQ	IGHVYPARVA	LSLEDDGLP			

Seq ID NO: 358 DNA sequence
Nucleic Acid Accession #: M27826
Coding sequence: <1-503

75
80
85

1	11	21	31	41	51	
AGCCCAAGAA	ACATCTCACC	AATTTCAAAT	CTGATCTATT	CGGCTTAGCG	ACTGAAGATT	60
GACGCTGCC	GATCGCTCCG	GAAATCCCTT	GGACCATCAC	AGAAGCCGAG	CTTCGGGTAA	120
CTCTCACAGT	GGAGGGTAAG	TCCATCCCTT	GTTTAAATCGA	TACGGGGGCT	ACCCACTCCA	180
CGTTGCTTTC	TTTTCAAGGG	CCTGTTTCCC	TGCCCCCAT	AACCTGTTGT	GGTATTGACG	240
GCCAAAGCTC	AAAACCCCTG	AAAACCTCCC	CACCTCTGGT	CCAACCTTGA	CAACACTCTT	300
TTATGCACTC	TTTTTTAGTT	ATCCCCACCT	GCCCACTTCC	CTTATTAGGC	CGAAATATTT	360
TAACCAAAAT	ATCTGCTTCC	CTGACTATT	CTGGAGTACA	GCTACATCTC	ATTGCTGCCC	420
TTCTTCCCAA	TCCAAAGCCT	CCTTTGTGTC	CTCTAACATC	CCCAATATAT	CAGCCCTTAC	480
CACAAGACCT	CCCTCAGCT	TAATCTCTCC	CACCTAGGTT	TCCCACGCGG	CCCCTAATCC	540
CACCTGAAGC	AGCCCTGAGA	AACATCGCCC	ATTCTCTCTC	CATACACCCC	CCCAAAATT	600
TTCCGCGCTC	CAACACTTCA	ACACTATTTT	GTTTATTATT	TCTTATTAA	ATCAGAAGGC	660

AGGAATGTCA GGCCTCTGAG CCCAGGCCAG GCCATCGCAT CCCCTGTGAC TTGCACGTAT 720
 ACATCCAGAT GGCCTGAAGT AACTGAAGAT CCACAAAAGA AGTAAAAACA GCCTTAACTG 780
 ATGACATTCC ACCATTGTGA TTTGTTCTCG CCCACCCCTA ACTGATCAAT GTACTTTGTA 840
 ATCTCCCCCA CCTTAAAGAA GGTTCCTTTG AATTCTCCCC ACCCTTGAGA ATGTACTTTG 900
 TGAGATCCAC CCTGCCCCAC CAGAGAACAA CCCCTTTTGA TTGTAATTTT TTATTACCTT 960
 CCCAAATCCT ATAAAAACAG CCCACCCCTA TCTTCCTTCA CTGACTCTCT TTTGCGACTC 1020
 AGCCACCGGC ACCCAGGTGA AATAAACAGC TTTATTGCTC AC

Seq ID NO: 359 Protein sequence
 Protein Accession #: AAA65999

1 11 21 31 41 51
 PKKHLTNFKS DLFGLATEDW RCPIASEVPW TITEAELRVT LTVEGKSIPC LIDTGATHST 60
 LPSPQGFVSL APITVVGIDG QASKPLKTPP LWCQLGQHSF MHSFLVIPTC FLPLLGRNII 120
 TKLSASLTIP GVQLHLIAL LFNPKPPLCP LTSPQYQPLP QDLPSA

Seq ID NO: 360 DNA sequence
 Nucleic Acid Accession #: NM_001854
 Coding sequence: 162-5582

1 11 21 31 41 51
 AACCATCAAA TTTAGAAGAA AAAGCCCTTT GACTTTTTC CCTCTCCCT CCCCAATGGC 60
 TGTGTAGCAA ACATCCCTGG CGATACCTTG GAAAGGACGA AGTTGGTCTG CAGTCGCAAT 120
 TTCTGGGGTT GAGTTCACAG TGTGAGTGC GGGGCTCGGA GATGGAGCCG TGGTCCTCTA 180
 GGTGGAAGAC GAAACGGTGG CTCTGGGATT TCACCGTAAC AACCTCGCA TTGACCTTCC 240
 TCTTCCAAGC TAGAGAGGTC AGAGGAGCTG CTCCAGTTGA TGTACTAAAA GCCTAGATT 300
 TTCACAAATC TCAGAGGGA ATATCAAAAA CAACGGGATT TTGCACAAAC AGAAAGAAAT 360
 CTAAGGCTCT AGATACGTCT TACAGAGTTT CAAAGCAAGC ACAACTCAGT GCCCAACAA 420
 AACAGTTATT TCCAGTGGGA ACTTTCCCGA AAGACTTTTC AATACTATT ACAGTAAAA 480
 CAAAAAAGG AATTCACTCT TCCCTTTTAT CTATATATA TGAGCATGGT ATTCAGCAA 540
 TTGGTGTGTA GGTGGGAGA TCACCTGTTT TCTGTGTTGA AGACCACACT GGAACACCTG 600
 CCCCAGAAGA CTATCCCTTC TCAGAACTG TTAACATCGC TGACGGGAAG TGGCATCGGG 660
 TAGCAATCAG CGTGGAGAAG AAAACTGTGA CAATGATTGT TGATTGTAAG AAGAAAACCA 720
 CGAAACCACT TGATAGAAGT GAGAGAGCAA TTGTGTATAC CAATGGAAATC ACGGTTTTTG 780
 GAACAAGGAT TTTGGATGAA GAAGTTTTTG AGGGGGACAT TCAGCAGTTT TTGATCAGAG 840
 GTGATCCCAA GGCAGCATAT GACTACTGTG AGCATTATAG TCCAGACTGT GACTCTTCAG 900
 CACCAAGGCT TGCTCAAGCT CAGGAACCTC AGATAGATGA GTATGCACCA GAGGATATA 960
 TCGAATATGA CTATGAGTAT GGGGAAGCAG AGTATAAAGA GGCTGAAAGT GTAACAGAGG 1020
 GACCCACTGT AACTGAGGAG ACAATAGCAC AGACGGAGGC AAACATCGTT GATGATTTTC 1080
 AAGAAACAA CTATGGAACA ATGGAAGATT ACCAGACAGA AGCTCCTAGG CATGTTTCTG 1140
 GGACAAATGA GCAAAATCCA GTTGAAGAAA TATTTACTGA AGAATATCTA ACGGGAGAGG 1200
 ATTATGATTC CCAGAGGAAA AATTCTGAGG ATACACTATA TGAACACAA GAAATAGACG 1260
 GCAGGGATTG TGATCTTCTG GTAGATGGAG ATTTAGGCGA ATATGATTTT TATGAATATA 1320
 AAGAAATATG AGATAAACCA ACAAGCCCCC CTAATGAAGA ATTTGGTCCA GGTGTACAG 1380
 CAGAACTCTG TATTACAGAA ACAAGCATAA ATGGCCATGG TGCAATATGA GAGAAAGGAC 1440
 AGAAAGGAGA ACCAGCAGTG GTTGAGCCTG GTATGCTTGT CGAAGGACCA CCAGGACCA 1500
 CAGGACCTGC AGGTATTATG GGTCTCTCAG GTCTACAAGG CCCCACTGGA CCCCTGTGTG 1560
 ACCCTGGCGA TAGGGGCCCC CCAGGACGCT CTGGCTTACC AGGGGCTGAT GGTCTACCTG 1620
 GTCTCTCTGG TACGTGTTG ATGTTACCGT TCCGTTATGG TGGTGTATGG TCCAAAGGAC 1680
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	ACCCGGGTCC	TGTTGGTTTT	CCTGGAGATC	CTGGTCTCCT	TGGGGAACCT	GGCCCTGCAG	4140
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	AAGGGGAAAA	AGGTGACCGA	GGGCTCCCTG	GAATCTCAAG	ATCTCCAGGA	GCAAAAGGGG	4620
15	ATGGGGGAAT	TCTTGTCTCT	GCTGGTCCCT	TAGGTCCACC	TGGTCTCTCA	GGCTTACCAG	4680
	GTCCTCAAGG	CCCAAAGGGT	AACAAAGGCT	CTACTGGACC	CGCTGGCCAG	AAAGGTGACA	4740
	GTGGTCTTCC	ATGGCCTCCT	GGGCCTCCAG	GTCCACCTGG	TGAAGTCATT	CAGCCTTTAC	4800
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25	AAGGAAATTC	CATCAATATG	GTGCAATGA	CATTCTGAA	ACTTCTGACT	GCCTCTGCTC	5280
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30	ACTTTGGTGA	TCAGAACTAG	AAGTTCGGAT	TTGAAGTTGG	TCCTGTTTGT	TTTCTTGGCT	5580
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	TTTTGTGCCA	TGCAAGTGT	TTGAATAAGG	ATGTATGGAA	AACAACGCTG	CATATACAGG	5700
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35	TTCTCACTC	TCCTTTTCTT	ATTGAATTT	CTTTGGTGTG	GTAGAAAAACA	AAAAAAGAAA	5880
	AATATATATT	CATAAAAAAT	ATGGTGCTCA	TTCTCATCCA	TCCAGGATGT	ACTAAAACAG	5940
	TGTGTTTAA	AAATTGTAA	TATTTGTGT	ACAGTTCTAT	ACTGTTATCT	GTGTCCATT	6000
	CCAAACTTG	CACGTGTCCC	TGAATTCGCG	TGACTCTAAT	TTATGAGGAT	GCCGAAGTCT	6060
	GATGGCAATA	ATATATGTAT	TATGAAAATG	AAGTTATGAT	TTCCGATGAC	CCTAAGTCCC	6120
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Seq ID NO: 361 Protein sequence
Protein Accession #: NP_001845

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	EHGIQIQIGVE	VGRSPVFLFE	DHTGKPAPE	YPLFRVTNIA	DGKWHRVVIA	VEKKTVTMIV	180
50	DCKKKTTPKL	DRSERAIVD	NGITVPGTRI	LDEEVFEGDI	QQFLITGDPK	AAYDYCEHYV	240
	PDCSSAPKA	AQAQEPQIDE	YAPEDIIEYD	YBYGEAEYKE	AESVTEGPTV	TEETIAQTEA	300
	NIVDDFQYEN	YGTMESYQTE	APRHVSGTNE	PNPVEEILFE	EYLTGEDYDS	QRKNSEDTLY	360
	ENKEIDGRDS	DLVLDGDLGE	YDFYKEYE	DKPTSPPNEE	FGPGVPAETD	ITETSINGHG	420
	AYGEKGQKE	PAVVEPQMLV	EGPFGPAGPA	GIMGPPGLQG	PTGPPGDPGD	RGPFGPRPGL	480
55	GADGLPGPPG	TMLMLPFRYG	GDGSKGPTIS	AQEAQAQAIL	QQAIALRGP	PGPMGLTRFP	540
	GFVGGPGSSG	AKGESGDPGP	QGPFGVQGGP	GPTGKPGKRG	RPGADGGRGM	PGEPGAKGDR	600
	GFDGLPLPLP	DKHGRGERGP	QGPFGPPGDD	GMRGEDGEIG	PRGLPGEAGP	RGLLGPRTGP	660
	GAPGQPGMAG	VDGPPGPKGN	MGPQGEFPGP	QQQGNFGPQG	LPFGPQGPFG	PGKGPQGGK	720
	GLAGLPGADG	PPGHPPGKEG	SGEKGALGPP	GPQGPIGXPG	PRGVKADGV	RGLKGSKEGK	780
60	GEDGPPGPKG	DMGLKGRDGE	VQIGPRGX	GPGEKPKRAG	PTGDPGPGSQ	AGEKGLGVFP	840
	GLPGYFGRQG	PKGSTGPFPG	PGANGKGRAR	GVAGKPGPRG	QRGPTGPRGS	RGARGFTGKP	900
	GPKGTSGGDG	PPGPPGGRGP	QGPQGPVGGP	GPKGPPGPPG	RMGCPGHPGQ	RGETGFQGKT	960
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	GPAGLRGFP	ERGLPGAQGA	PGLKGGEGPQ	GPPGVPVSPG	ERGSAGTAGP	IGLRGRPGFP	1080
65	GPPGPAGEKG	APGEGKPGQP	AGRDGVQGPV	GLPGPAGPAG	SPGEDGDKGE	IGEPGQKGSK	1140
	GGKGENGPPG	PPGLQGPVGA	PGIAGGDGEP	GPRGQGMFGP	QKGDGARGF	PGPPGPIGLQ	1200
	GLPGPPGEGK	ENGDVGPWGP	PGPPGPRGPQ	GPNGADGPPG	PPGSGVSGVG	VGEKGEPEGA	1260
	GNPFGPPGAG	VGGPKGERGE	KGEAGPPGAA	GPPGAKGPPG	DDGPKGNPGP	VGFPDGPDPG	1320
	GELGPAGDGG	VGGDKGEDGD	PGQGPFGPFS	GEAGPPGPPG	KRGFPGAAGA	EGRQGEKGA	1380
70	GEAGAEPPG	KTGPVGPQGP	AGKPGPEGLR	GIPGVPGEQG	LPGAAGQDGP	PGPMGPPGLP	1440
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	GPPGLPQPQ	PKGNKSGTGP	AGQKGDGSLP	GPPGPPGPPG	EVIQPLPILS	SKKTRRRHTG	1560
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	EYWIDPNQGC	SGDSFKVYCN	FTSGGETCIY	PDKKSEGVRI	SSWPKEKPGS	WFSEFKRGKL	1680
75	LSYLDVEGNS	INMVQMTFLK	LLTASARQNF	TYHCHQSAAM	YDVSSGSYDK	ALRFLGSNDE	1740
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	PVCFLG						

Seq ID NO: 362 DNA sequence
Nucleic Acid Accession #: NM_003107
Coding sequence: 351-1775

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	GGAATATATA	CTCCTCTGCG	AGAGGCGGAG	AACCTCTTCC	CCAAATCTTT	TGGGGACTTT	180

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Seq ID NO: 363 Protein sequence
 Protein Accession #: NP_003098

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 ADYDPYKYRP RKIKVKSNNAN SSSSAAASSK PGEKGDKVGG SGGGGHGGGG GGGSSNAGGG 180
 GGGASGGGAN SKPAQKKSCG SKVAGGAGGG VSKPHAKLIL AGGGGGGKAA AAAAAAFABE 240
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Seq ID NO: 365 Protein sequence

Protein Accession #: AAA60331

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 SKLYVGAQFH PEVGLTENGL VILKNFLYDI AGCSGTFTVQ NRELECIRESI KERVGTSKVL 240
 VLLSGGVDSV VCTALLNRAL NQEQVIAVHI DNGPFRKRES QSVEEALKKL GIQVKVINAA 300
 HSPYNGTTTL PISDEDRTPR KRISKLTNMT TSPEEKRII GDTFVKIANE VIGEMNLKPE 360
 30 EVFLAQTGLR PDLIESASLV ASGKAELIKT HNDTELIRK LRBEQVIEP LKDPHKDEVR 420
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 BSLIFLARLI PRMCHNVNRV VYIFGPFVKE PFTDVTPTFL TTGVLSLRLQ ADFEAHNILR 600
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 35 VVLKMTVEIK KIPGISRIMY DLTSKPPGTT EWE

Seq ID NO: 366 DNA sequence

Nucleic Acid Accession #: NM_004219

Coding sequence: 46-654

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 GAGAGTTTTG ACCTGCCTGA AGAGCACCAG ATTGCGCACC TCCCTTGTAG TGGAGTGCCT 480
 CTATGATCC TTGACGAGGA GAGAGAGCTT GAAAAGCTGT TCGAGCTGGG CCCCCTTCA 540
 CCTGTGAAGA TGCCCTCTCC ACCATGGGAA TCCAATCTGT TGCAGTCTCC TTCAAGCATT 600
 CTGTGCGACC TGGATGTTGA ATTGCCACCT GTTTGCTGTG ACATAGATAT TTAATTTCT 660
 55 TAGTGCTTCA GAGTTTGTGT GTATTGTAT TAATAAGCA TTCTTCAACA GAAAAAAA 720
 AAAAAAA

Seq ID NO: 367 Protein sequence

Protein Accession #: NP_004210

1 11 21 31 41 51
 | | | | |
 MATLIYVDKE NGEPTGTRVVA KDGLKLGSGP SIKALDGRSQ VSTPRFGKTF DAPPALPKAT 60
 65 RKALGTVNRA TEKSVTKGFP LKQKQPSFSA KMTTEKTVKA KSSVPASDDA YPEIEKFFFP 120
 NPLDFESFDL PEHQIAHLP LSGVPLMILD EERELEKLFQ LGPPSPVKMP SPPWESNLLQ 180
 SPSSILSTLD VELPPVCCDI DI

Seq ID NO: 368 DNA sequence

Nucleic Acid Accession #: NM_000597

Coding sequence: 118-1104

1 11 21 31 41 51
 | | | | |
 75 ATTCGGGGCG AGGGAGGAGG AAGAAGCGGA GGAGGGCGCT CCCGCTCGCA GGGCCGTGCA 60
 CTGCGCCGCC CGCCCGCTCG CTGCTCGGCC CGCCGCGCCG CGCTGCCGAC CGCCAGCATG 120
 CTGCCGAGAG TGGCTGCCCC CGCGCTGCGG CTGCGCGCCG CGCGCTGCTG GCGCTGCTG 180
 CGCGTGTCTG TGCTGCTACT GGGCGCGAGT GCGCGCGCGG GCGGGGCGCG CGCGGAGGTG 240
 CTGTTCCGCT GCCCGCCCTG CACACCCGAG CGCCTGGCCG CCTGCGGGCC CCGCGCGGTG 300
 80 GCGCGCGCCG CCGCGGTGGC CGCAGTGGCC GGAGGCGCCC GCATGCCATG CGCGGAGCTC 360
 GTCCGGGAGC CGGGCTGCGG CTGCTGCTCG GTGTGCGCCC GCTGTGAGGG CGAGGCGTGC 420
 GGCGTCTACA CCCCGCGCTG CGGCCAGGGG CTGCGCTGCT ATCCCCACCC GGGCTCCGAG 480
 CTGCCCTTGC AGGCGCTGGT CATGGGCGAG GGCACCTGTG AGAAGCGCCG GGACGCGGAG 540
 TATGGCGCCA GCCCGCGTGA GGTTCAGAGC AATGGCGATG ACCACTCAGA AGGAGGCCCTG 600
 85 GTGGAGAACC ACGTGGACAG CACCATGAAC ATGTTGGGCG GGGGAGGCGA TGCTGGCCGG 660
 AAGCCCTTCA AGTGGGTAT GAAGGAGCTG GCCGTGTTCC GGGAGAAGGT CACTGAGCAG 720
 CACCGGCAGA TGGCAAGGG TGGCAAGCAT CACTTGGCC TGGAGGAGCC CAAGAAGCTG 780
 CGACCACCCC CTGCCAGGAC TCCTGCCAA CAGGAACCTG ACCAGGTCTT GGAGCGGATC 840

TCCACCATGC GCCTTCCGGA TGAGCGGGGC CCTCTGGAGC ACCTCTACTC CCTGCACATC 900
 CCCAAGTGTG ACAAGCATGG CCTGTACAAC CTCAAAACAGT GCAAGATGTC TCTGAACGGG 960
 CAGCGTGGGG AGTGTCTGGTG TGTGAACCCC AACACCGGGA AGCTGATCCA GGGAGCCCCC 1020
 ACCATCCGGG GGGACCCCGA GTGTCACTTC TTCTACAATG AGCAGCAGGA GGCTTGCCGG 1080
 GTGCACACCC AGCGGATGCA GTAGACCGCA GCCAGCCGGT GCCTGGCGCC CCTGCCCCCC 1140
 GCCCTCTCC AAACACCGGC AGAAAACGGA GAGTGCTTGG GTGGTGGGTG CTGGAGGATT 1200
 TTCCAGTTCT GACACACGTA TTTATATTGG GAAAGAGACC AGCACCAGAGC TCGCACCTTC 1260
 CCCGCCCTCT CTCTTCCAGC CTGCAGATGC CACACCTGCT CCTTCTTGCT TCCCCCGGG 1320
 GAGGAAGGGG GTTGTGGTGG GGGAGCTGGG GTACAGGTTT GGGGAGGGGG AAGAGAAATT 1380
 TTTATTTTGG AACCCCTGTG TCCCTTTTGC ATAAGATTAA AGGAGGAGAA AGT

Seq ID NO: 369 Protein sequence
 Protein Accession #: NP_000588

1 11 21 31 41 51
 MLPRVGCPL PLPPPLLLPL LPLLLLGLLA SGGGGGARAE VLFRCPPTCTP ERLAACGFPF 60
 VAPPAVAAV AGGARMPCAE LVREPGCGCC SVCARLEGEA CGVYTPRCGQ GLRCYPHFGS 120
 ELPLQALVMG EGTCEKRRDA EYGASPEQVA DNGDDHSEGG LVENHVDSTM NMLGGGGSAG 180
 RKPLKSGMKE LAVFREKVTG QHRQMGKGGK HHLGLEBPKK LRPPPARTPC QQELDQVLER 240
 ISTMLPDER GPLEHLYSLH IPNCDKHGLY NLKQCKMSLN GQRGECWCVN PNTGKLIQGA 300
 PTIRGDPECH LFINEQQEAC GVHTQRMQ

Seq ID NO: 370 DNA sequence
 Nucleic Acid Accession #: NM_004264
 Coding sequence: 6-440

1 11 21 31 41 51
 GGAACATGGC GGATCGGCTC ACGCAGCTTC AGGACGCTGT GAATTCGCTT GCAGATCAGT 60
 TTTGTAATGC CATTTGAGTA TTGCAGCAAT TTGGTCTCTC TGCTCTTTTC AATAATATTC 120
 AGACAGCAAT TAACAAAGAC CAGCCAGCTA ACCCTACAGA AGAGTATGCC CAGCTTTTTC 180
 CAGCATGTAT TGACAGAACCA GCAAAAGACA TTGATGTTTT GATAGATTCC TTACCCAGTG 240
 AAGAATCTAC AGCTGCTTTA CAGGCTGCTA GCTTGATATA GCTAGAAGAA GAAAACCATG 300
 AAGCTGCTAC ATGTGTGGAG GATGTTGTTT ATCGAGGAGA CATGCTTCTG GAGAAGATAC 360
 AAAGCGCACT TGCTGATATT GCACAGTCAC AGCTGAAGAC AAGAAGTGGT ACCCATAGCC 420
 AGTCTCTTCC AGACTCATAG CATCAGTGGG TACCATGTGG CTGAGAAAAG AACTGTTTGA 480
 GTGCCATTAA GAATCTTGCA TCAGACTTAG ATACAAGCCT TACCAACRAA TACAGAAACA 540
 TTAACACTA TGACACATTA CCTTTTATAG TATTTTAAAT AGTCTTCTAT TTTCACTCTT 600
 GATAAGCTTA TAAATCATGA TTGAATCAGC TTTAAAGCAT CATACCATCA TTTTAACT 660
 GAGTGAATTT ATTAAGGCAT GTAATACATT AATGAACATA ATATAAGGAA ACATATGTAA 720
 AATTCTGTGA TGACATAAAT TATGTCTCCA TTTGTTGTGA TTGGCCAGTA CTTTACAAAT 780
 C

Seq ID NO: 371 Protein sequence
 Protein Accession #: NP_004255

1 11 21 31 41 51
 MADRLTQLQD AVNSLADQFC NAIGVLQCCG PPASFNNIQT AINKDQFANP TEEYAQLFAA 60
 LIARTAKDID VLIDSLPSEE STAAALQAASL YKLEENHEA ATCEDVVYR GDMLEKIQS 120
 ALADIAQSQL KTRSGTHSQS LPDS

Seq ID NO: 372 DNA sequence
 Nucleic Acid Accession #: AJ271091
 Coding sequence: 1-1113

1 11 21 31 41 51
 ATGGAGAATC AGGTGTTGAC GCCGCATGTC TACTGGGCTC AGCGACACCG CGAGCTATAT 60
 CTGCGCGTGG AGCTGAGTGA CBTACAGAAC CCTGCCATCA GCATCACTGA AAACGTGCTG 120
 CATTTCAAAG CTCAGGACA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG 180
 TTCTTAGACC TTGTGAAACC AGAGCCTGTT TACAAACTGA CCCAGAGGCA GGTAAACATT 240
 ACAGTACAGA AGAAAGTGAG TCAGTGGTGG GAGAGACTCA CAAAGCAGGA AAAGCGACCA 300
 CTGTTTTTGG CTCTGACTT TGATCGTTGG CTGGATGAAT CTGATCGGGA AATGGAGCTC 360
 AGAGCTAAGG AAGAAGAGCG CCTAAATAAA CTCGACTGG AAAGCGAAGG CTCTCTGAA 420
 ACTCTTACAA ACTTAAGGAA AGGATACCTG TTTATGTATA ATCTTGTGCA ATTCTTGGGA 480
 TTCTCCTGGA TCTTTGTCAA CCTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCCITT 540
 TATGACACAT TCCATACTGT GGCTGACATG ATGTATTICT GCCAGATGCT GGCAGTTGTG 600
 GAAACTATCA ATGCAGCAAT TGGAGTCACT ACGTCACCGG TGCTGCCTTC TCTGATCCAG 660
 CTTCTTGGAA GAAATTTTAT TTTGTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC 720
 AAAGCTGTGG TTTTCTTTGT GTTTTATTG TGGAGTGCAA TTGAAATTTT CAGGTACTCT 780
 TTCTACATGC TGACGTGCAT TGACATGGAT TGGAAAGTGC TCACATGGCT TCGTTACACT 840
 CTGTGGATTC CCTTATATCC ACTGGGATGT TTGGGGGAG CTGTCTCAGT GATTCACTCC 900
 ATTCCAATAT TCAATGAGAC CGGACGATTC AGTTTCACAT TGCCATATCC AGTGAAATC 960
 AAAGTTAGAT TTTCTTTTTT TCTTCAGATT TATCTTATAA TGATATTTTT AGGTTTATAC 1020
 ATAAATTTTC GTCACTTTTA TAAACAGCGC AGACTGAAAA TGAGGGCAGG CGCAGTGGCT 1080
 CATGCCGTGT ATCCACGCGC TTTGGGAGGC TGA

Seq ID NO: 373 Protein sequence
 Protein Accession #: CAB69070

1 11 21 31 41 51
 MENQVLTPHV YWAQRHRELY LRVELSDVQN PAISITENVL HFKAQGHGAK GDNVYEFHLE 60
 FLDLVKPEPV YKLTQRQVNI TVQKKVSQWW ERLTKQEKRP LFLAPDFDRW LDESDAEMEL 120
 RAKEBERLNK LRLESBGSPE TLTNLRKGYL FMYNLVQFLG FSWIFVNLTV RFCILGKESF 180

YDTFHTVADM MYPCQMLAVV ETINAAIGVT TSPVLPSLIQ LLGRNFILFI IPGTMEEQN 240
 KAVVFFVFFYL WSAIEIFRYS FYMLTCIDMD WKVLTWLRYS LWIPLYPLGC LAEAVSVIQS 300
 IPIFNETGRF SFTLPYPVKI KVRFSFPLQI YLIMIFLGLY INFRHLYKQR RLKMRAGAVA 360
 HACDPSALGG

Seq ID NO: 374 DNA sequence
 Nucleic Acid Accession #: NM_016395
 Coding sequence: 1-1113

1 11 21 31 41 51
 | | | | |
 ATGGAGAATC AGTGTGTGAC GCCGCATGTC TACTGGGCTC AGCGACACCG CGAGCTATAT 60
 CTGCGCGTGG AGCTGAGTGA CGTACAGAAC CCTGCCATCA GCATCACTGA AAACGTGCTG 120
 CATTTCAAAG CTCAAGGACA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG 180
 TTCTTAGACC TTGTGA AAC AGAGCCTGTT TACAACTGA CCCAGAGGCA GGTAAACATT 240
 ACAGTACAGA AGAAAGTGAG TCAGTGGTGG GAGAGACTCA CAAAGCAGGA AAAGCGACCA 300
 CTGTTTTTGG CTCTGACTT TGATCGTTGG CTGGATGAAT CTGATGCGGA AATGGAGCTC 360
 AGAGCTAAGG AAGAAGAGCG CCTAAATAAA CTCCGACTGG AAAGCGAAGG CTCTCCTGAA 420
 ACTCTTACAA ACTTAAGGAA AGGATACCTG TTTATGTATA ATCTTGTGCA ATTCTTGGGA 480
 TTCTCCTGGA TCTTGTCAA CCTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCTTTT 540
 TATGACACAT TCCATACTGT GGCTGACATG ATGTATTCTT GCCAGATGCT GGCAGTTGTG 600
 GAAACTATCA ATGCAGCAAT TGGAGTCACT ACGTCACCGG TGCTGCCTTC TCTGATCCAG 660
 CTTCTTGGAA GAAATTTTAT TTTGTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC 720
 AAAGCTGTGG TTTTCTTTGT GTTTTATTTG TGGAGTGCAA TTGAAATTTT CAGGTACTCT 780
 TTCTACATGG TGACGTGCAT TGACATGGAT TGGAAAGTGC TCACATGGCT TCGTTAAGT 840
 CTGTGGATTC CCTTATATCC ACTGGGATGT TTGGCGGAAG CTGTCTCAGT GATTCACTCC 900
 ATTCCAATAT TCAATGAGAC CGGACGATTC AGTTTCACAT TGCCATATCC AGTGAAATC 960
 AAAAGTTAGT TTTCTCTTTT TCTTCAGATT TATCTTATAA TGATATTTT AGGTTTATAC 1020
 ATAAATTTTC GTACCTTTA TAAACAGCGC AGACTGAAAA TGAGGCGCAG CGCAGTGGCT 1080
 CATGCCGTGG ATCCAGCGC TTTGGGAGG TGA

Seq ID NO: 375 Protein sequence
 Protein Accession #: NP_057479

1 11 21 31 41 51
 | | | | |
 MENQVLTPHV YWAQRHRELY LRVELSDVQN PAISITENVL HFKAQGHGAK GDNVYEFHLE 60
 FLDLVKPEPV YKLTQRQVNI TVQKVSQW ERLTKQEKRP LPLAPDFDRW LDESDAEMEL 120
 RAKEERLNK LRLESRSPE TLTNLRKGYL FMYNLVQFLG FSWIFVNLTV RFCILGKESF 180
 YDTFHTVADM MYPCQMLAVV ETINAAIGVT TSPVLPSLIQ LLGRNFILFI IPGTMEEQN 240
 KAVVFFVFFYL WSAIEIFRYS FYMLTCIDMD WKVLTWLRYS LWIPLYPLGC LAEAVSVIQS 300
 IPIFNETGRF SFTLPYPVKI KVRFSFPLQI YLIMIFLGLY INFRHLYKQR RRRYKGRKR 360
 STKKKDLDF LPV

Seq ID NO: 376 DNA sequence
 Nucleic Acid Accession #: NM_005987
 Coding sequence: 1-270

1 11 21 31 41 51
 | | | | |
 ATGAATTCCT AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA GCAGCAGCAG 60
 GTGAAACAAC CTTGCCAGCC TCCACCCGAG GAACCATGCA TCCCCAAAAC CAAGGAGCCC 120
 TGCCAAACCA AGGTGCTCTGA GCCCTGCCAC CCCAAAGTGC CTGAGCCCTG CCAGCCCAAG 180
 ATTCAGAGC CCGCCAGGCC CAAGGTGCCT GAGCCCTGCC CTTCAACGGT CACTCCAGCA 240
 CCAGCCGAGC AGAAGACCAA GCAGAAGTAA

Seq ID NO: 377 Protein sequence
 Protein Accession #: NP_005978

1 11 21 31 41 51
 | | | | |
 MNSQQKQKPC TPPPQPQQQQ VKQPCQPPPO EPCIPKTKER CQPKVPEPCH PKVPBPQPK 60
 IPEPCQPKVP EPCPSTVTPA PAQKTKKQK

Seq ID NO: 378 DNA sequence
 Nucleic Acid Accession #: NM_002105
 Coding sequence: 74-505

1 11 21 31 41 51
 | | | | |
 ACAGCAGTTA CACTGCGGCG GCGCTCTGTT CTAGTGTGTT AGCCGTCGTG CTTACCCGGT 60
 CTACCTCGCT AGCATGTGCG GCGCGGCGCA GACTGGCGGC AAGGCCGCGG CCAAGGCCAA 120
 GTCGCGCTCG TCGCGCGCGG GCCTCCAGTT CCCAGTGGGC CGGTATACAC GGCTGCTGCG 180
 GAAGGGCCAC TACGCGAGC GCGTTGGCGC CGGCGCGCCA GTGTACCTGG CGGCAGTGCT 240
 GGAGTACCTC ACCGCTGAGA TCTTGGAGCT GCGGGGCAAT GCGGCCGCGG ACAACAAGAA 300
 GACGCGAATC ATCCCCGCC ACCTGCAGCT GGCCATCCGC AACGACGAGG AGCTCAACAA 360
 GCTGCTGGGC GGCCTGACGA TCGCCAGCG AGGCGTCTGT CCAACATCC AGGCGGTGCT 420
 GCTGCCAAG AAGACCAGCG CACCCGTGGG GCCGAAGGCG CCCTCGGGCG GCAAGAAGGC 480
 CACCCAGGCC TCCAGAGGT ACTAAGAGGG CCCGCGCGCG GCGCGGCGCG CCCAGCTCCC 540
 CATGCCACCA CAAAGGCCCT TTTAAGGGCC ACCACCGCCC TCATGGAAAG AGCTGAGCGC 600
 CTTCAAGCTG CGGGGCAAGC GGGCGCGGCG TCCCTTCCCC TCCCTTCCCC TCGCCCGGCT 660
 TCGCCGCGCG GCCTCGAGTC CCGCCGCGCG CCGCTCCCG TCCCGCACCG CCGCGCGGT 720
 CGGCTCGGG CCGCTCGGT CCGCCGCGCG CCCTCGGTA GGGTTCGGGC CTTCCGAGT 780
 CGGCTTGGGC GCTCTCGGG GACCTCGGT GCGCGGAAGA CCCGAGCCTG CCGGGGGGAG 840

GCCGGCGGGC CCGCACCTGC CCGCCTCGGC GTTCGTGACT CAGCCGCCCC ATCCCAGTGC 900
 GCTAAGGGGC TCGCGGGAGG CCGCAGCACC TTCTGGAAGA CTGGCCCTTC CGCTCTGAGC 960
 CAGGGCCGAG GTGGGCAGTC CAGGCCGAGA GCCGGCGGCC CTGAAGGTGA GTGAGGCCCT 1020
 CGGCAGCTGC AGCCGGGGTG TCTGGTACCC CCCCGGCGTG GTGCTTAGCC CAGGACTTTC 1080
 AGACGCGCGC TGGCGGGAGG GCCTTTGGTG GAGAGACCGG ATCGCGGATT TCGGTCTGGC 1140
 GCCCCTTCTG CGGCCGGGAC CCAGGCCTTT CACATCAGCT CTCCTTCCAT CTTCACTCAT 1200
 AGGTCTGCGC TGGGGCCGGG ACGAAGCACT TGGTAACAGG CACATCTTCC TCCCGAGTGA 1260
 CTGCTCTCTA GGAGGACATT TAGGGGAGGG CAGAGGCCTG CAGTTTGGCT TCACGGCTGG 1320
 CTATGTGGAC AGCAAGAGTC GTTTTTCGGA ACGCGACTGG CAGCCAGGCC TGTCCGGCCC 1380
 CCGACGCCGC CCAATTTCCC TTCCAGCAA CTCAACTCGG CAATCCAGC ACCTAGATAC 1440
 CAGCAACAAGT CGGTAAATCC CTGTCTGGAC TGAGCCTCCG TTGGCTTCTG AACTGGAATT 1500
 CTGCAGCTAA CCCTTCCAG ACTAGAACCT TAGGCATTGG GGAGTTTATG ATGACTAAT 1560
 TTTATTAAAG GATTGTTTTT TTTT

Seq ID NO: 379 Protein sequence
Protein Accession #: NP_002096

1 11 21 31 41 51
 | | | | |
 MSGRGKTGK ARAKAKSRSS RAGLQFPVGR VHRLLRKGHY AERVGAGAPV YLAADVLEYLT 60
 AEILELAGNA ARDNKKTII PRHLQLAIRN DEELNKLGG VTIAQGGVLP NIQAVLLPKK 120
 TSATVGPAPK SGGKKATQAS QEY

Seq ID NO: 380 DNA sequence
Nucleic Acid Accession #: AL136942
Coding sequence: 184-864

1 11 21 31 41 51
 | | | | |
 ACGCGTCCGG CAGAAGCTCG GAGCTCTCGG GGTATCGAGG AGGCAGGCCCG CGCGGGCGCAC 60
 GGGCGAGCGG GCCGGGAGCC GGAGCGCGCG AGGAGCCGCG AGCAGCGCGC CGCGGGGCTC 120
 CAGGCGAGGC GGTGCGACGCT CCTGAAGAACT TGCAGCGCGC CTGCGCCAC TGCAGCCGGA 180
 GCGATGAAGA TGGTGCAGCC CTGGACGCGG TTCTACTCCA ACAGCTGCTG CTTGTGCTGC 240
 CATGTCCGCA CCGGCACCAT CCGTCTCGCG GTCTGTGATC TGATCATCAA TGCTGTGGTA 300
 CTGTGTGATT TATTGAGTGC CCGGCTGAT CCGGACTAGT ATAACCTTTC AAGTTCTGAA 360
 CTGGGAGGTG ACTTTGAGTT CATGGATGAT GCCAACATGT GCATTGCCAT TGGGATTCT 420
 CTCTCATGA TCCTGATATG TGCTATGGCT ACTTACGGAG CGTACAAGCA ACGCGCAGCC 480
 TGGATCATCC CATTCTCTCG TTACCAGATC TTTGACTTTG CCCTGAACAT GTTGGTTGCA 540
 ATCACTGTGC TTATTATGCC AAATCCATT CAGGAATACA TACGGCAACT GCCTCCTAAT 600
 TTTCCCTACA GAGATGATGT CATGTCACTG AATCCTACCT GTTTGGTCCT TATTATTCTT 660
 CTGTTTATTA GCATTATCTT GACTTTTAA GGTACTTGA TTAGCTGTGT TTGGAAGTGC 720
 TACCGATACA TCAATGGTAG GAATCCTCT GATGTCTCGG TTTATGTTAC CAGCAATGAC 780
 ACTACGGTGC TGCTACCCCG GTATGATGAT GCCACTGTGA ATGGTCTGTC CAAGGAGCCA 840
 CCGCCACCTT ACGTGTCTGC CTAAGCCTTC AAGTGGGCGG AGCTGAGGGC AGCAGCTTGA 900
 CTTTGCAGAC ATCTGAGCAA TAGTTCTGTT ATTCTACTTT TGCATGAGC CTCTCTGAGC 960
 TTGTTTGTG CTGAAGTACT ACTTTTAAAT ATTAGATGT TAGATTGAAA ACTGTAGTTT 1020
 TCAACATATG CTTTGTCTGA ACATGTGAT AGATTAACTG TAGAATTCTT CCGTACGAT 1080
 TGGGGATATA ACGGGCTTCA CTAACCTTCC CTAGGCATTG AAATTTCCCC CAAATCTGAT 1140
 GGACCTAGAA GTCTGCTTTT GTACCTGCTG GGGCCCAAAG TTGGGCATTT TTCTCTCTGT 1200
 TCCCTCTCTT TTGAAAATGT AAAATAAAAC CAAAAATAGA CAATTTTTC TTGAGCCATT 1260
 CCAGCATAGA GAACAAACCT TTATGGAAAC AGGAATGTCA ATTGTGTAAT CATGTGTCTA 1320
 ATTAGGTAAA TAGAAGTCTT TATGTATGTG TTACAAGAA TCCCCCACA ACATCCTTTA 1380
 TGAAGTAACT TCAATGACAG TTTGTGTTTG GTGGTAAAGG ATTTTCTCCA TGGCCTGAAT 1440
 TAAGACCAT AGAAAGCACC AGGCGGTGGG AGCAGTGACC ATCTACTGAC TGTCTCTGTG 1500
 GATCTGTGT CAGGAGGACAT GGGGTGACAT GCCTCGTATG TGTTAGAGGG TGGAAATGGAT 1560
 GTGTTTGGCG CTGCTAGGGA TCTGGTCCCC CTCTCTCTCT GGATTCACAT CCCCACCCAG 1620
 GGGCCGCTGT TACTAGTGT TCTGCCCTAG ATTGGTTCAA GGAGGTCATC CAACTGACTT 1680
 TATCAAGTGG AATTGGGATA TATTGATAT ACTTCTGCTT AACACATGG AAAAGGGTTT 1740
 TCTTTTCCCT GCAAGCTACA TCCTACTGCT TTGAACCTCC AAGTATGTCT AGTACGCTTT 1800
 TAAATGTAA ACATTTTCAG AAAAATGAGG ATTGCCCTCC TTGATGCGC TTTTACCTT 1860
 GACTACCTGA ATTGCAAGGG ATTTTATAT ATTCAATATG TACAAAGTCA GCAACTCTCC 1920
 TGTGGTTTCA TTATTGAATG TGCTGTAAAT TAAGTCGTTT GCAATTAATA CAAGGTTTGC 1980
 CCACATCCAA AAAAAAAAAA AAAAA

Seq ID NO: 381 Protein sequence
Protein Accession #: CAB66876

1 11 21 31 41 51
 | | | | |
 MKMVPWTRF YNSNCLCCH VRTGTLILGV WYLIINAVVL LILLSALADP DQYNFSSSEL 60
 GGDPEFMDDA NMCIAIAISL LMILICAMAT YGAYQRAAW IIPFFCYQIF DPAIINMLVAI 120
 TVLIYPNSIQ EYIRQLPPNF PYRDDVMSVN PTCVLVLIIL FISIIITFKG YLISCVWNKY 180
 RYINGRNSD VLVVYTSNDT TVLLEPYDDA TVNGAAKEPP PPYVSA

Seq ID NO: 382 DNA sequence
Nucleic Acid Accession #: NM_002510
Coding sequence: 92-1774

1 11 21 31 41 51
 | | | | |
 CAGATGCCAG AAGAACACTG TTGCTCTTGG TGGACGGGCC CAGAGGAATT CAGAGTTAAA 60
 CCTTGAGTGC CTGCGTCCGT GAGAAATCAG CATGGAATGT CTCTACTATT TCCTGGGATT 120
 TCTGCTCTG CTGCGAAGAT TGCCACTTGA TGCCGCCAAA CGATTTCATG ATGTGCTGGG 180
 CAATGAAAGA CTTCTGCTTT ACATGAGGGA GCACAATCAA TTAATGGCT GGTCTTCTGA 240
 TGAATATGAC TGAATGAAA AACTCTACCC AGTGTGGAAG CGGGAGACA TGAGGTGGAA 300
 AAATCTCTGG AAGGGAGGCC GTGTGCAGGC GGTCTGTACC AGTGACTCAC CAGCCCTCGT 360

GGGCTCAAAAT ATAACATTGG CGGTGAACCT GATATTCCCT AGATGCCAAA AGGAAGATGC 420
 CAATGGCAAC ATAGTCTATG AGAAGAAGCTG CAGAAATGAG GCTGGTTTAT CTGCTGATCC 480
 ATATGTTTAC AACTGGACAG CATGGTCAGA GGACAGTGAC GGGGAAAATG GCACCGGCCA 540
 AAGCCATCAT AACGCTCTCC CTGATGGGAA ACCTTTTCCT CACCACCCCG GATGGAGAAG 600
 ATGGAATTTT ATCTACGTCT TCCACACACT TGGTCAGTAT TTCCAGAAAT TGGGACGATG 660
 TTCAGTGAGA GTTCTCTGTA ACACAGCCAA TGTGACACTT GGGCCTCAAC TCATGGAAGT 720
 GACTGTCTAC AGAAGACATG GACGGGCATA TGTTCCTATC GCACAAGTGA AAGATGTGTA 780
 CGTGGTAACA GATCAGATTTC CTGTGTTTGT GACTATGTTC CAGAGAAGCG ATCGAAATTC 840
 ATCCGACGAA ACCTTCCTCA AAGATCTCCC CATTATGTTT GATGTCCTGA TTCATGATCC 900
 TAGCCACTTC CTCAATTATT CTACCATTA CTACAAGTGG AGCTTCGGGG ATAATACTGG 960
 CCTGTTTGTG TCCACCAATC ATACTGTGAA TCACACGTAT GTGCTCAATG GAACCTTCAG 1020
 CCTTAACCTC ACTGTGAAAG CTGCAGCACC AGGACCTTGT CCGCCACCCG CACCACCACC 1080
 CAGACCTTCA AAACCCACCC CTTCTTTAGG ACCTGCTGGT GACAAACCCC TGGAGCTGAG 1140
 TAGGATTCTC GATGAAACT GGCAGATTAA CAGATATGGC CACTTTCAG CCACCATCAC 1200
 AATTGTAGAG GGAATCTTAG AGGTTAATCAT CATCCAGATG ACAGACGTCC TGATGCCGGT 1260
 GCCATGGCCT GAAAGCTCCC TAATAGACTT TGTGCTGACC TGCCAAGGGA GCATTCCCAC 1320
 GGAGGTCTGT ACCATCATT CTGACCCACC CTGCGAATC ACCCAGAAC CAGTCTGCAG 1380
 CCTGTGGATG GTGGATGAGA TGTGTCTGCT GACTGTGAGA CGAACCTTCA ATGGGTCTGG 1440
 GAGTACTGTG GTGAACTTCA CCCTGGGGGA TGACACAAGC CTGGCTCTCA CGAGCACCTC 1500
 GATTTCTGTT CCTGACAGAG ACCCAGCCTC GCCTTTAAGG ATGGCAAACA GTGCCCTGAT 1560
 CTCGTTTGGC TCTTGGGCA TATTGTCTAC TGTGATCTCC CTCTTGGTGT ACAAACAAACA 1620
 CRAGGAATAC AACCCAATAG AAAATAGTCC TGGGAATGTG GTCAAGACA AAGGCTGTAG 1680
 TGTCTTTCTC AACCGTGCAA AAGCCGTGTT CTTCGCGGGA AACCAAGGAA AGGATCCGCT 1740
 ACTCAAAAAC CAAGAATTAA AAGGAGTTTC TTAATTTTCG ACCTTGTTC TGAAGCTCAC 1800
 TTTTCAGTGC CATGATGTG AGATGTGCTG GAGTGGCTAT TAACCTTTT TTCTTAAAGA 1860
 TTATTGTTAA ATAGTGTATG TGGTTTGGGG AAGTTGAATT TTTTATAGT TAAATGTCT 1920
 TTTAGAGATG GGGAGAGGGA TTATACTGCA GGCAGCTTCA GCCATGTTGT GAAACTGATA 1980
 AAAGCAACTT AGCAAGGCTT CTTTTCATTA TTTTATATGT TTCATTATA AAGTCTTAG 2040
 TAACTAGTAG CATAGAAACA CTGTGTCCCG AGAGTAAGGA GAGAAGCTAC TATGATTAG 2100
 AGCCTAACCC AAGTTAACTG CAAGAAGAGG CGGGATACTT TCAGCTTTC ATGTAACCTG 2160
 ATGCATAAAG CCAATGTATG CCAGTTTCTA AGATCATGTT CCAAGCTAAC TGAATCCCAC 2220
 TTCAATACAC ACTCATGAAC TCCTGATGGA ACAATAACAG GCCCAAGCCT GTGATGATG 2280
 GTGCACACTT GCTAGACTCA GAAAAATAC TACTCTCATA AATGGGTGGG AGTATTTTGG 2340
 TGACAACCTA CTTTCTTGG CTGAGTGAAG GAATGATATT CATATATTCA TTTATTCCAT 2400
 GGACATTTAG TTAGGCTTTT TTATATACCA GGCATGATGC TGAGTGACAC TCTTGTGAT 2460
 ATTTCCAAAT TTTTGTATAG TCGCTGCACA TATTGAAAT CATATATTAA GACTTTCCAA 2520
 AGATGAGGTC CCTGCTTTT CATGGCAACT TGATCAGTAA GGATTTCACC TCTGTTTGT 2580
 ACTAAACCA TCTACTATAT GTTAGACATG ACATTCTTT TCTCTCCTC CTGAAAAATA 2640
 AAGTGTGGGA AGAGACAAAA AAAAAAAA

Seq ID NO: 383 Protein sequence
 Protein Accession #: NP_002501

1 11 21 31 41 51
 MECLYYFLGF LLLAARLPLD AAKRFHDVLG NERPSAYMRE HNQLNGWSSD ENDWNEKLYP 60
 VWRKGDNRWK NSWKGGRVQA VLTGSDSPALV GSNITFAVNL IPRCQKEDA NGNIVYEKNC 120
 RNEAGLSADP VYVNTWANE DSDGENTGQ SHNVFPDGK PPHHPGWRN WNFYVFTL 180
 GQYFQKLGRS SVRVSVNTAN VTLGPQLMEV TVYRRHGRAY VPLAQKVDVY VVTDQIPVFV 240
 TMFQKNDNRN SDTEFLKDLF IMPDVLHDP SHFLNYSTIN YKWSFGDNTG LFTVSTNHTVN 300
 HTYVLNGTFS LNLTVKAAAP GPCPPPPPPP RPSKPTPSLG PAGDNPLELS RIPDENQIN 360
 RYGHFQATIT IVEGLEVNI IQMTDVLMPV WPPESSLIDF VVTCQGSIPT EVCTIISDPT 420
 CEITQNTVCS FVDVDEMCLL TVRRTFNGSG TYCVNLTLGD DTSALTSTL ISVDFRDFAS 480
 PLRMANSALI SVGCLAIFVT VISLLVYKXH KEYNPIENSP GNVVRSKGLS VFLNRKAVF 540
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Seq ID NO: 384 DNA sequence
 Nucleic Acid Accession #: NM_001134
 Coding sequence: 48-1877

1 11 21 31 41 51
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 TGGAGAAAGTA CGGACATTCA GACTGCTGCA GCCAAAGTGA AGAGGGAAGA CATAACTGTT 420
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 ATGACAAAAT AATTCCATCT TGCTGCAAG CTGAAATGTC AGTTGAATGC TTCCAAACAA 660
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 GCCAGGAACA GGAAGCTGTC TTGCTGAAAG AGGGACAAAA ACTGATTTC AAAACTCGTG 1860
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Seq ID NO: 385 Protein sequence
 Protein Accession #: NP_001125

1 11 21 31 41 51
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 KEVSKMVKDA LTAIEKPTGD EQSSGCLENO LPAPLEELCH EKEILEKYGH SDCCSQSEEG 120
 RHNCFLAHKK PTPASIPLFQ VPEPVTSCFA YEEDRETFMN KFIYEIARRH PPLYAPTILL 180
 WAARYDKIIP SCCKAENAVE CPQTKAATVT KELRESSLLN QHACAVMKNF GTRTFQAITV 240
 TKLSQKFTKV NFTEIQKLVL DVAHVHEHCC RODVLDCLQD GEKIMSYICS QQDTLSNKIT 300
 ECCKLTTLER GQCIHAEND EKEPGLSPNL NRFLGDRDFN QFSSGEKNIF LASFVHEYSR 360
 RHPQLAVSVI LRVAQYQEL LEKCFQTENP LECQDKGEE LQYIQESQA LAKRSCGLFQ 420
 KLGEYYLQNA FLVAYTKKAP QLTSSSELMAI TRKMAATAAT CQQLSEDKLL ACGEGAADII 480
 IGHLCIRHEM TFPNPGVGQC CTSYANRRP CFSLLVDET YVPPAFSDDK FIFHKDLCA 540
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Seq ID NO: 386 DNA sequence
 Nucleic Acid Accession #: NM_002205.1
 Coding sequence: 1..3149

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 ATTGCAGAA TCTATTACCC CAGGTACCTG ATCAACCTGG TTCAAGGGGA GCTGCAGACT 780
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 TACAAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGGCA CCGCCATGGA AAAAGCTCAG 3120
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Seq ID NO: 387 Protein sequence
Protein Accession #: NP_002196.1

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LESSLSSEEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCTYLS 180
10 DNFTRILEYA PCRSDFSWAA GGGYCQGGFS AEFTKTGRVV LGGPGSYFQW QGILSATQEQ 240
IAESVYPEYL INLVQQLQT RQASSIYDDS YLGYSVAVGE FSGDDTEDFV AGVPKGNLTY 300
GYVTILNGSD IRSLYNPSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRFQ 360
EVGRVYVYLQ HPAGIEPTPT LTLTGHDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFPGET 420
15 QGGVVVFPFG GPGLGSKPS QVLQPLWAAS HTPDFFGSAL RGRDLDDGNG YPDLVGSPG 480
VDKAVVVRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540
GFTVELQLDW QKQKGGVRRR LPLASRQATL TOTLLIONGA REDCREMKIY LRNESEFRDK 600
LSPIHIALNF SLDPQAPVDS HGLRPLAHYQ SKSRIEDKAQ ILDCGEDI NI CVPLQLQEVF 660
GEQNHVYLG D KNALNLTFHA QNVGEGGAYE AELRVTPAPE AEYSGLVVRHP GNFSSLSCDY 720
20 FAVNQSRLLV ADLGNPMKAG ASLWGLRFT VPHLRDTKKT IQDFQILSK NLNNSQSDVV 780
SFRLSVAEQA QVTLNGVSKP EAVLFVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSII 840
SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGLSHH QOKREAPRSI 900
SASSGPQILK CPEAECEFLR CELGPLHQOE SQSLQLHFRV WAKTFPLQREH QPFLQCEAV 960
YKALIMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IITLAILFGL LLLGLLIYIL 1020
YKLGFFPKRSL PYGTAMEKAQ LKPPATSDA

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Seq ID NO: 388 DNA sequence
Nucleic Acid Accession #: NM_002425
Coding sequence: 26..1453

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35 TGCCAGACAA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG 180
AAAGGACAGT AATCTCATTT TTAATAAAAT CCAAGGAATG CAGAAGTTC TGGGTGGA 240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCCTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATTCGTCCAT 420
40 TGAGAAAGCT CTGAAAGTCT GGAAGAGAGT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
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TGATGGCCCA GGCACAGATT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGAGA 600
TATTCACTTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCTT 660
CGTTGCTGCT CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA ACCTGGAAGC 720
45 TTTGATGTAC CCACCTTACA ACTCATTCAC AGAGCTCGCC CAGTTCGCC TTTGCAAGA 780
TGATGTGAAT GGCATTCAGT CTCTCTACGG ACCTCCCTCT GCCTCTACTG AGGAACCCCT 840
GGTGCCCACT AATCTGTTT TCTCGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT 900
GTCCTTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTAAAG ACAGATATT 960
TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTTTCA TTGATTTCTG CATTTTGGCC 1020
50 CTCTCTTCCA TCATATTGG ATGCTGCATA TGAAGTTAAG AGCAGGGACA CCGTTTTTAT 1080
TTTTAAAGGA AATGATTTCT GGGCCATCAG AGGAAATGAG GTACAAGCAG GTTATCCAAG 1140
AGGCATCCAT ACCCTGGGTT TTCTCCAAAC CATAAGGAAA ATTGATGCAG CTGTTTCTGA 1200
CAAGGAAAAG AAGAAAACAT ACTTCTTTCG AGCGGACAAA TACTGGAGAT TTGATGAAAA 1260
TAGCCAGTCC ATGGAGCAAG GTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
55 GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTTTTC TACTTCTTCA GTGGATCATC 1380
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GTTACATTGC TAGCCAGAGT AGGGGGAAGA CAGATATGGG TGTTTTAAAT AAATCTAATA 1500
ATTATTATC TAATGTATTA TGAGCCAAAA TGGTTAATTT TTCTGCTGAT TTCTGTGACT 1560
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60 ACTTGCTTTT GAATTGCACT GAACAGAAAT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
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Seq ID NO: 389 Protein sequence
Protein Accession #: NP_002416

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70 PDLPRDAVDS AIEKALKVWE EVTPLTFPSRL YEGEADIMIS FAVKEHGDYF SFDGPHSLA 180
HAYPPGPGLY GDIFHDDDEK WTEDASGTNL FLVAAHELGH SLGLFHSANT EALMYPLYNS 240
FTELAQFRLS QDDVNGIQSL YGFPFPASTE PLVPTKSVPS GSEMPAKCDF ALSFDAISTL 300
RGEYLFKKDR YFWRRSHWNP EPEFHLISAF WPSLPSYLD AYEVSNSRDTV FIFKGNFENA 360
75 IRGNEVQAGY PRGHTLGLFP PTIRKIDAAV SDKEKKKTYF FAADKYWRFD ENSQSMEQGF 420
PRLIADDFPG VEPKVDVAVLQ AFGFFYFPFG SSQFEFDPNA RMVTHILKSN SWLHC

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Seq ID NO: 390 DNA sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1409

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85 TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAGAGC GGAGAAATAG TGGCCAGTGG 180
GTTGAAAAAT TGAAGCAAA GCAGGAATTC TTTGGGCTGA AAGTGAAGTG GAAACAGAT 240
GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCTGATGT GGCTCAGTTT 300

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5
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15
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GTCTCTACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT 360
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TGGAGTAATG TCACACCTCT GACATTACAC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
CTTGCTCATG CTTTTCACAC AGGCCCAAGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
GAAAGGTGGA CCAACAATT TACAGAGTAC AACTTACATC GTGTTGCGGC TCATGAACTC 660
GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC 720
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Seq ID NO: 391 Protein sequence
Protein Accession #: NP_002412.1

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1 11 21 31 41 51
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YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGQADIM ISFVRGDHRD NSPFDGPGGN 180
LAHAFFQPGPG IGGDAHFEDD ERWNTNPFREY NLHRVAAHAL GHSLGLSHST DIGALMYPST 240
TFSGDVQLAQ DDIDIGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300
FYMRNPFYF EVELNPFISV WPQLPNGLEA AYEFPADRDEV RFFKGNKYWA VQGNVNLHGY 360
PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWRV DEYKRSMDPG YPKMIAHDFP 420
GIGHKVDVAV MKDGFYFFPH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

Seq ID NO: 392 DNA sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1409

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GATGAATATA AAGATCTAT GATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTTCT 1260
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Seq ID NO: 393 Protein sequence
Protein Accession #: NP_002412.1

70
75
80

1 11 21 31 41 51
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LAHAFFQPGPG IGGDAHFEDD ERWNTNPFREY NLHRVAAHAL GHSLGLSHST DIGALMYPST 240
TFSGDVQLAQ DDIDIGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300
FYMRNPFYF EVELNPFISV WPQLPNGLEA AYEFPADRDEV RFFKGNKYWA VQGNVNLHGY 360
PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWRV DEYKRSMDPG YPKMIAHDFP 420
GIGHKVDVAV MKDGFYFFPH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

Seq ID NO: 394 DNA sequence
Nucleic Acid Accession #: NM_014331.2
Coding sequence: 1..1506

85

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	ATGGTCAGAA	AGCCTGTTGT	GTCCACCATC	TCCAAAGGAG	GTTACCTGCA	GGGAAATGTT	60
	AACGGGAGGC	TGCCTTCCTT	GGGCAACAAG	GAGCCACCTG	GGCAGGAGAA	AGTGCAGCTG	120
	AAGAGGAAAG	TCACCTTTACT	GAGGGGAGTC	TCCATTATCA	TTGGCACCAT	CATTGGAGCA	180
5	GGAAATCTTCA	TCTCTCTTAA	GGCGGTGCTC	CAGAACACGG	GCAGCGTGGG	CATGTCCTCG	240
	ACCATCTGGA	CGGTGTGTGG	GGTCTGTGCA	CTATTGGAG	CTTTGTCTTA	TGCTGAAATG	300
	GGAAACAAC	TAAAGAAATC	TGGAGGTCAT	TACACATATA	TTTGGGAAGT	CTTGGTCCA	360
	TTACCAGCTT	TTGTACGAGT	CTGGGTGGAA	CTCCTCATAA	TACGCCCTGC	AGCTACTGCT	420
	GTGATATCCC	TGGCATTG	ACGCTACATT	CTGGAACCAT	TTTTTATTCA	ATGTGAAATC	480
10	CCTGAACCTG	CGATCAAGCT	CATTACAGCT	GTGGGCATAA	CTGTAGTGAT	GGTCTTAAT	540
	AGCATGAGTG	TCAGCTGGAG	CGCCCGGATC	CAGATTTTCT	TAACTTTTGG	CAAGCTCACA	600
	GCAATTTCTG	TAATTATAGT	CCCTGGAGTT	ATGCAGCTAA	TAAAGGTCA	AACGCAGAAC	660
	TTTAAAGACG	CGTTTTTCAG	AAGAGATTCA	AGTATTACGC	GGTGGCCACT	GGCTTTTTAT	720
	TATGGAATGT	ATGCATATGC	TGGCTGGTTT	TACCTCAACT	TTGTTACTGA	AGAAGTAGAA	780
	AACCTTGAAA	AAACCATTC	CCTTGCAATA	TGTATATCCA	TGGCCATTGT	CACCATTTGG	840
15	TATGTGCTGA	CAATGTGGG	CTACTTTACG	ACCATTAAATG	CTGAGGAGCT	GCTGCTTTCA	900
	AATGCAGTGA	CAGTGTGGCT	CTACTGGGAA	ATTCTCTATT	AGCAGTTCGG		960
	ATCTTTGTTG	CCCTCTCTCG	CTTTGGCTCC	ATGAACGGTG	GTGTGTTTGC	TGTCTCCAGG	1020
	TTATTCTATG	TTGCGTCTCG	AGAGGGTCAC	CTTCCAGAAA	TCTCTCTCAT	GATTTCATGTC	1080
20	CGCAAGCACA	CGCTCTTACC	AGCTGTTATT	GTTTTGCACC	CTTGACAAT	GATAATGCTC	1140
	TTCTCTGGAG	ACCTCGACAG	TCTTTTGAAT	TTCCCTCAGTT	TTGCCAGGTT	GCTTTTATT	1200
	GGGCTGGCAG	TTGCTGGGCT	GATTATCTT	CGATACAAAT	GCCCAGATAT	GCATCGTCTC	1260
	TTCAAGGTGC	CACGTTCAT	CCCAGCTTTG	TTTTCTTCA	CATGCCCTCT	CATGGTTGCC	1320
	CTTTCCCTCT	ATTCGGACCC	ATTTAGTACA	GGGATTGGCT	TCGTCATCAC	TCTGACTGGA	1380
25	GTCCCTGGGT	ATTATCTCTT	TATTATATGG	GACAAGAAAC	CCAGGTGGTT	TAGAATAATG	1440
	TCAGAGAAAA	TAACCAAGAAC	ATTACAAATA	ATACTGGAAG	TTGTACCAGA	AGAAGATAAG	1500
	TTATGAACAT	ATGGACTTGA	GATCTTGCCA	ATCTGCCCAA	GGGGAGACAC	AAAATAGGGA	1560
	TTTTTACTTC	ATTTTCTGAA	AGTCTAGAGA	ATTACAACCT	TGGTGATAAA	CAAAAGGAGT	1620
	CAGTTATTTT	TATTCTATATA	TTTTAGCATA	TTCCGAACATA	TTTCTAAGAA	ATTTAGTTAT	1680
30	AACTCTATGT	AGTTATAGAA	AGTGAATATG	CAGTTATTCT	ATGAGTCGCA	CAATTCTTGA	1740
	GTCTCTGATA	CCTACCTATT	GGGGTTAGGA	GAAGAAGACTA	GACAATTACT	ATGTGGTCAT	1800
	TCTCTACACA	ATCTGTTAGC	ACGGCAAAGA	ACCTTCAAAAT	TGAAGACTGA	GATTTTCTG	1860
	TATATATGGG	TTTTGTAAAG	ATGGTTTAC	ACACTACAGA	TGTCTATACT	GTGAAAAGTG	1920
	TTTTCAATTC	TGAAAAAAG	CATACATCAT	GATTATGGCA	AAGAGGAGAG	AAAGAAATTT	1980
35	ATTTTACATT	GACATTGCAT	TGCTTCCCTT	TAGATACCAA	TTTAGATAAC	AAACACTCAT	2040
	GCTTTAATGG	ATTATACCCA	GAGCACTTTG	AACAAGAGTC	AGTGGGGATT	GTGTAATACA	2100
	TTAAAGAAGA	TTTCTAGGG	GCTACTGTTT	ATGAGACACA	TCCAGGAGTT	ATGTTTAAGT	2160
	AAAAATCCTT	GAGAAATTAT	TATGTCAGAT	GTTTTTCAT	TCATTATCAG	GAAGTTTATG	2220
	TTATCTGTCA	TTTTTTTTTT	TCACATCAGT	TTGATCAGGA	AAGTGATATA	CACATCTTAG	2280
40	AGCAAGAGTT	ATTTTGTGAT	TAAATCTCA	TTAGAACAAAC	CACCTGTTTC	ACTAATAACT	2340
	TACCCTGAT	GAGTCTATCT	AAACATATGC	ATTTTAAAGCC	TTCAAAATTAC	ATTATCAACA	2400
	TGAGAGAAAT	AACCAACAAA	GAAGATGTTT	AAAAATATAG	TCCCATATCT	GTAATCATAT	2460
	CTACATGCAA	TGTTAGTAAT	TCTGAAGTTT	TTTAAATTTA	TGGCTATTTT	TACACGATGA	2520
	TGAATTTTGA	CAGTTTGTGC	ATTTTCTTTA	TACATTTTAT	ATTCTTCTGT	TAAATATCT	2580
45	CTTCAGATGA	AACGTGTCAG	ATTAATTAGG	AAAAGGCATA	TATTAACATA	AAAATTGCAA	2640
	AAGAAATGTC	GCTGTAAATA	AGATTTACAA	CTGATGTTTC	TAGAAAATTT	CCACTTCTAT	2700
	ATCTAGGCTT	TGTCAGTAAT	TTCCACACCT	TAATTATCAT	TCAACTTGCA	AAAGAGACAA	2760
	CTGATAAGAA	GAAATTTGAA	ATGAGAATCT	GTGGATAAGT	GTTTGTGTTC	AGAAGATGTT	2820
	GTTTGTCCAG	TATTAGAAAA	TACTGTGAGC	CGGGCATGGT	GGCTTACATC	TGTAATCCCA	2880
50	GCACCTTGGG	AGGCTGAGGG	GGTGGATCAC	CTGAGGTCGG	GAGTTCCTAGA	CCAGCCTGAC	2940
	CAACATGGAG	AAACCCCATC	TCTACTAAAA	ATACAAAATT	AGCTGGGCAT	GGTGGCACAT	3000
	GCTGTGAATC	TCAGCTATTG	AGGAGGCTGA	GGCAGGAGAA	TTGCTTGAAC	CCGGGAGGCG	3060
	GAGGTTGCAG	TGAGCCAAAG	TTGCACCAC	GTACTCCAGC	CTGGGTGACA	AAGTCAGACT	3120
	CCATCTCCAA	AAAAAAAAAA	AAAA				

Seq ID NO: 395 Protein sequence
Protein Accession #: NP_055146.1

	1	11	21	31	41	51	
60	MVRKPVVSTI	SKGGYVQGNV	NGRLPSLGNK	EPPGQEKVQL	KRKVTLLRGV	SIIIGTIIGA	60
	GIFISPKGVV	QNTGSVGMSL	TIWTVCGVLS	LFGALSYAEL	GTTIKKSGGH	YTYILEVFGP	120
	LPAFVRVWVE	LLIIRPAATA	VISLAFGRVI	LEPFFIQCEI	PELAIKLITA	VGITVVMVLN	180
	SMSVSWASRI	QIFLTFCKLT	AILIIIVPGV	MQLIKGQTON	FKDAPSGRDS	SITRLPLAFY	240
65	YGMVYAGWPF	YLVFVTEEVE	NPEKTIPLAI	CISMAITIGV	YVLTVNAVYFT	TINAEELLLS	300
	NAVAVTFPSR	LLGNFSLAVP	IFVALSCFPG	MNGGVFAVSR	LFVVASREGH	LPEILSMIHV	360
	RKHTPLPAVI	VLHPLTMIML	FSGDLDSLNL	FLSFARWLFI	GLAVAGLIYL	RYKCPDMHRP	420
	FKVPLFIPAL	FSFTCLFMVA	LSLYSDPFST	GIGFVITLTG	VPAYYLFIIW	DKPKRWFIRM	480
	SEKIIRTLQI	ILEVVEEDK	L				

Seq ID NO: 396 DNA sequence
Nucleic Acid Accession #: NM_006528
Coding sequence: 57..764

	1	11	21	31	41	51	
75	GCCGCCAGCG	GCTTTCTCGG	ACGCCCTTGCC	CAGCGGGCCG	CCCGACCCCC	TGCACCATGG	60
	ACCCCGCTCG	CCCCCTGGGG	CTGTGCAATC	TGCTGCTTTT	CCTGACGGAG	GCTGCACTGG	120
80	GCGATGCTGC	TCAGGAGCCA	ACAGGAAATA	ACGCGGAGAT	CTGTCTCCTG	CCCCTAGACT	180
	ACGGACCTCG	CCGGGCCCTG	CTTCTCCGTT	ACTACTACGA	CAGGTACACG	CAGAGCTGCC	240
	GCCAGTTCCT	GTACGGGGGC	TGCGAGGGCA	ACGCCAACAA	TTTCTACACC	TGGGAGGCTT	300
	GCGACGATGC	TGTCTGGAGG	ATAGAAAAAG	TTCCCAAAGT	TTGCCGGCTG	CAAGTGAGTG	360
	TGGACGACCA	GTGTGAGGGG	TCCACAGAAA	AGTATTTCTT	TAATCTAAGT	TCCATGACAT	420
85	GTGAAAAATT	CTTTCCGGGT	GGGTGTCAAC	GGAAACCGGAT	TGAGAACAGG	TTTCCAGATG	480
	AAGCTACTTG	TATGGGCTTC	TGCGACCCAA	AGAAAAATTCC	ATCATTTTGC	TACAGTCCAA	540
	AAGATGAGGG	ACTGTGCTCT	GCCAAATGTA	CTCGCTATTA	TTTAAATCCA	AGATACAGAA	600
	CCTGTGATGC	TTTCACTTAT	ACTGGCTGTG	GAGGGAATGA	CAATAACTTT	GTTAGCAGGG	660

WO 02/086443

PCT/US02/12476

AGGATTGCAA ACGTGCATGT GCAAAAGCTT TGAAAAAGAA AAAGAAGATG CCAAAGCTTC 720
GCTTTGCCAG TAGAATCCGG AAAATTCCGA AGAAGCAATT TTAACATTC TTAATATGTC 780
ATCTTGTTTG TCTTTATGGC TTATTTGCCCT TTATGGTTGT ATCTGAAGAA TAATATGACA 840
GCATGAGGAA ACAATCATT GGTGATTTAT TCACCACTTT TTATTAATAC AAGTCACTTT 900
TTCAAAATT TGGATTTTAT TATATATAAC TAGCTGCTAT TCAAAATGTA GTCTACCACT 960
TTTAATTTAT GGTTCACCTG TTTGTGAGAC GAATTCCTGC AATGCATAAG ATATAAAGC 1020
AAATATGACT CACTCATTTT TGGGGTGGT ATTCCTGATT TCAGAAGAGG ATCATAACTG 1080
AAACAACATA AGACAATATA ATCATGTGCT TTAAACATAT TTGAGAATAA AAAGGACTAG 1140
CC

Seq ID NO: 397 Protein sequence
Protein Accession #: NP_006519

1 11 21 31 41 51
MDPARPLGLS ILLFLTEAA LGDAAQEPTG NNAEICLLPL DYGPCRALLL RYYYDRYTQS 60
CRQFLYGGCE GNANFNFTWE ACDDACWRIE KVPKVCRLQV SVDDQCEGST EKYFFNLSSM 120
TCEKFFSGGC HRNRIENRFP DEATCMGFCA PKKIPFCYS PKDEGLCSAN VTRYVFNPRY 180
RTCDAFYTYG CGNDNNFVS REDCKRACAK ALKXKKKMPK LRFASIRIKI RKKQF

Seq ID NO: 398 DNA sequence
Nucleic Acid Accession #: NM_001508.1
Coding sequence: 1..1361

1 11 21 31 41 51
ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60
CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCTTA TTCTGGTGT CCTGATCATC 120
TTCTGTATGG GCCTTCTGGG GAACAGCGTC ACCATTCGGG TCACCCAGGT GCTGCAGAG 180
AAAGGATACT TGCAGAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTGGACATC 240
TTGGTGTTC TCATCGGATG GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACC 300
ACGTCAGCT ACACCTGTCT CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC 360
GCTACGCTGC TGCAGTGTCT GACGCTCAGC TTTGAGCGCT ACATCGCCAT CTGTACCCCC 420
TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG 480
GTCACTCTCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTCG 540
GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCACGAG 600
CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660
CAGTCCAGCA TCTTCGGGCG CTTCGTGGTC TACCTCGTGG TCTGCTCTC CTAGCCTTC 720
ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC 780
ACGCGGCTCT CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840
ACCATCATCT TCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACGAG 900
ATTGCGAGGA TCATGCTCTG GGCCAAACCC AAGCACGACT GGACGAGGTC CTACTTCCGG 960
GCGTACATCA TCTCTGCCCT CTCTCGGAG ACGTTTTTCT ACCTCAGCTC GGTATCAAC 1020
CCGCTCTGT ACACGGTGTCT CTCGAGCAG TTTCCGGCGG TGTTCTGTGA GGTGCTGTGC 1080
TGCCGCTGT CGCTGCAGCA CGCCAAACCC GAGAAGCGCC TGCGCTTACA TGCGCACTCC 1140
ACCACGAGCA GCGCCCGCTT TGTGCAGCGC CCGTTGCTCT TCGCTGCCG CGCCAGTTC 1200
TCTGCAAGGA GAAGTGAAGA GATTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260
TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACGAGCC 1320
AATTCGTCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

Seq ID NO: 399 Protein sequence
Protein Accession #: NP_001499.1

1 11 21 31 41 51
MASPSLPGSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNV TIRVTQVLQK 60
KQYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNLPT TSSYTLSCKL HTFLFEACSY 120
ATLLHLVLTLS FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFMAGTEYPL 180
VNYPSHRGLT CNRSSTRHHE QPETSNNMSIC TNLSSRWTFV QSSIFGAFV YLVVLLSVAF 240
MCWNMMQVLM KSQKSLLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLIV TLAVCWMPNQ 300
IRIRIMAAKP KHDWTRSYFR AYMLLPFSE TFPYLSVIN PLLYTVSSQQ FRRVFVQVLC 360
CRLSLQHANH EKRLRVHAHS TTDSARFVR PLLFASRRQS SARTEKIFL STFQSEAEPP 420
SKSQSLSLES LEFNSGAKFA NSAAENGFOE HEV

Seq ID NO: 400 DNA sequence
Nucleic Acid Accession #: NM_006475.1
Coding sequence: 28..2538

1 11 21 31 41 51
AACAGAACTG CAACGGAGAG ACTCAAGATG ATTCCCTTTT TACCATGTT TTCTCTACTA 60
TTGCTGCTTA TTGTTAACCC TATAAACGCC AACAACTATT ATGACAAGAT CTGGGCTCAT 120
AGTCGTATCA GGGGTCGGGA CCAAGGCCCA AATGTCTGTG CCTTCAACA GATTTTGGGC 180
ACCAAAAGA AATACCTCAG CACTTGTAA GAACTGGTATA AAAAGTCCAT CTGTGGACAG 240
AAAAAGACTG TTTTATATGA ATGTTGCCCT GGTATATGA GAATGGAAGG AATGAAAGGC 300
TGCCAGCAG TTTTGCCCAT TGACCATGTT TATGGCACTC TGGGCATCGT GGGAGCCACC 360
ACAAAGCAGC GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATCGAGGG AAGGGATCC 420
TTCACTTACT TTGCACCGAG TAATGAGGCT TGGGACAACT TGGATTCTGA TATCCGTAGA 480
GGTTTGAGGA GCAACGTGAA TGTGGAATTA CTGAATGCTT TACATAGTCA CATGATTAAT 540
AAGAGAAATG TCACCAAGGA CTAAAAAAT GGCATGATTA TTCTTCAAT GTATAACAAT 600
TTGGGGCTTT TCATTAACCA TTATCCTAAT GGGGTGTGCA CTGTTAATTG TGCTCGAATC 660
ATCCATGGGA ACCAGATTGC AACAAATGGT GTTGTCCATG TCATTGACCG TGTGCTTACA 720
CAAAATGGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA 780
GCAAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGAA GAGACGGTCA CTTCACTC 840
TTTGTCTCCA CCAATGAGGC TTTTGAGAAA CTTCCACGAG GTGCTCTAGA AAGGTTCTAG 900
GGAGACAAAG TGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT 960
TCTGAGTCTA TTATGGGAGG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA 1020

	GGATGTGACG	GTGACAGTAT	AACAGTAAAT	GGAATCAAAA	TGGTGAACAA	AAAGGATATT	1080
	GTGACAAATA	ATGGGTGTGAT	CCATTGTGATT	GATCAGGTCC	TAATTCCTGA	TTCTGCCCAA	1140
	CAAGTTATTG	AGCTGGCTGG	AAAAACAGCAA	ACCACCTTCA	CGGATCTTGT	GGCCCAATTA	1200
5	GGCTTGGCAT	CTGCTCTGAG	GCCAGATGGA	GAATACACTT	TGCTGGCACC	TGTGAATAAT	1260
	GCATTTTCTG	ATGATACTCT	CAGCATGGTT	CAGCGCCTCC	TTAAATTAAT	TCTGCAGAAT	1320
	CACATATTGA	AAGTAAAGT	TGGCCTTAAT	GAGCTTTACA	ACGGGCAAAAT	ACTGGAACCC	1380
	ATCGGAGGCA	AACAGCTCAG	AGTCTTCGTA	TATCGTACAG	CTGTCTGCAT	TGAAAATTCA	1440
	TGCATGGAGA	AAGGGAGTAA	GCAAGGGAGA	AACGGTGCAG	TTACATATT	COGCGAGATC	1500
10	ATCAAGCCAG	CAGAGAAATC	CCTCCATGAA	AAGTTAAAC	AAGATAAGCG	CTTTAGCACC	1560
	TTCTCAGCC	TACTTGAAGC	TGCAGACTTG	AAAGAGCTCC	TGACACAACC	TGGAGACTGG	1620
	ACATTATTTG	TGCCAACCAA	TGATGCTTTT	AAGGGAATGA	CTAGTGAAGA	AAAAGAAATT	1680
	CTGATACGGG	ACAAAATATG	TCTTCAAAAC	ATCATTCTTT	ATCACCTGAC	ACCAGGAGTT	1740
	TTCAATTGGAA	AAGGATTTGA	ACCTGGTGTT	ACTAACATTT	TAAAGACCAC	ACAAGGAAGC	1800
15	AAAATCTTTC	TGAAAGAAGT	AAATGATACA	CTTCTGGTGA	ATGAATTGAA	ATCAAAAGAA	1860
	TCTGACATCA	TGACACAAA	TGGTGTAATT	CATGTTGTAG	ATAAACTCCT	CTATCCAGCA	1920
	GACACACCTG	TTGGAATGA	TCAACTGCTG	GAAATACCTA	ATAAAATTAAT	CAAATACATC	1980
	CAAAATTAAGT	TTGTTCTGGG	TAGCACCTTC	AAAGAAATCC	CGGTGACTGT	CTATACAACCT	2040
	AAAATTATAA	CCAAAGTTGT	GGAAACCAAAA	ATTAAAGTGA	TTGAAGGCAG	TCTTCAGCCT	2100
20	ATTATCAAAA	CTGGAAGACC	CACACTAACA	AAAGTCAAAA	TTGAAGGTGA	ACCTGAATTC	2160
	AGACTGATTA	AAGAAGGTGA	AACATAACT	GAAGTATCC	ATGGAGAGCC	AATTATTAAA	2220
	AAATACACCA	AAATCATTTA	TGGAGTGCCT	GTGGAATAAA	CTGAAAAAGA	GACACGAGAA	2280
	GAACGAATCA	TTACAGGTCC	TGAATAAAAA	TACACTAGGA	TTTCTACTGG	AGGTGGAGAA	2340
	ACAGAAGAAA	CTCTGAAGAA	ATTGTTACAA	GAAGAGGTCA	CCAAGGTGAC	CAAATTCATT	2400
25	GAAGGTGGTG	ATGGTCAATT	ATTTGAAGAT	GAAGAAATTA	AAAGACTGCT	TCAGGGAGAC	2460
	ACACCCGTGA	GGAAGTTGCA	AGCCCAACAA	AAAGTTCAAG	GTCTTAGAAG	ACGATTAAGG	2520
	GAAGGTGCTT	CTCAGTGAAT	ATCCAAAAAC	CAGAAAAAAA	TGTTTATACA	ACCCTAAGTC	2580
	AATAACCTGA	CCTTAGAAAA	TTGTGAGAGC	CAAGTTGACT	TCAGGAACCTG	AAACATCAGC	2640
	ACAAAGAACG	AATCATCAAA	TAATTTCTGAA	CACAAATTTA	ATATTTTITT	TTCTGAATGA	2700
30	GAACATGAG	GGAAATTTGG	GAGTTAGCCT	CCTGTGGTAA	AGGAATTTGA	GAAAATATAA	2760
	CACCTTACAC	CCTTTTTCAT	CTTGACATTA	AAAGTTCTGG	CTAACTTTGG	AATCCATTAG	2820
	AGAAAAATCC	TTGTCACCAAG	ATTCAATACA	ATTCAAAATG	AAGAGTTGTG	AACTGTTATC	2880
	CCATTGAAAA	GACCGAGCCT	TGTATGTATG	TTATGGATAC	ATAAAATGCA	CGCAAGCCAT	2940
	TATCTCTCCA	TGGGAAGCTA	AGTTATATAA	ATAGGTGCTT	GGTGTACAAA	ACTTTTTTATA	3000
35	TCAAAAGGCT	TGACCAATTT	CTATATGAGT	GGGTTTACTG	GTAATTTATG	TTATTTTTTA	3060
	CACTAATTT	TGTACTCTCA	GAATGTTTGT	CATATGCTTC	TTGCAATGCA	TATTTTTTAA	3120
	TCTCAACGT	TTCAATAAAA	CCATTTTTCA	GATATAAAGA	GAATTACTTC	AAATTGAGTA	3180
	ATTCAGAAAA	ACTCAAGATT	TAAGTTAAAA	AGTGGTTTGG	ACTTGGGAA		

Seq ID NO: 401 Protein sequence
Protein Accession #: NP_006466.1

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45	MIPFLPMFSL	LLLLIVNPIN	ANNHYDKILA	HSRIRGRDQG	PNVCALQQIL	GTKKKYFSTC	60
	KNWYKKSICG	QKTTVLYECC	PGYMRMEGMK	GCPAVLPIDH	VYGTGLGIVGA	TTTQRYSDAS	120
	KLREEIEGKG	SFTYFAPSNE	AWDNLDSDIR	RGLESNVNVE	LLNALHSHMI	NKRMLTKDLK	180
	NGMIIPSMYN	NLGLFINHYP	NGVVTVNCAI	IIHGNQIATN	GVVHVIVDRVL	TQIGTSIQDF	240
	IEAEDDLSSP	RAAAITSDIL	EALGRDGHFT	LPAPTNEAFE	KLPRGVLEBF	MGDKVASEAL	300
50	MKYHILNTLG	CSESMGGAV	FETLEGNTIE	IGCDGDSITV	NGIKMVNKKD	IVTNNGVIHL	360
	IDQVLIPDSA	KQVIELAGKQ	QTTFTDLVAQ	LGLASALRPD	GEYTLAPVN	NAFSDDTLSM	420
	VORILLKLIQ	NELLYKQVGL	NELYNGQILE	TIGGKQLRVF	VYRTAVCIEN	SCMEKGSKQG	480
	RNGAIHTFRE	IIKPAEKSLH	EKLKQDKRFS	TFLSLLEAAD	LKELLTQPGD	WTLFVPTNDA	540
	PKGMTSBEKE	ILIRDKNALQ	NIILYHLTPG	VFIGKGFEPG	VTNILKTTQG	SKIFLKEVND	600
55	TLVLNELKSK	ESDIMTNGV	IHVVDKLLYP	ADTPVGNQDL	LEILNKLIRY	IQIKFVRGST	660
	FKEIPVTVTT	TKIITKVVEP	KIKVIEGSLQ	PIIKTEGPTL	TKVKIEGEPE	FRLIKEGETI	720
	TEVIHGSPII	KYTKKIIDGV	PVEITEKETR	EERIITGPEI	KYTRISTGGG	STEETLKILL	780
	QEEVTKVTKF	IEGGDGHLEF	DEEIKRLLQG	DTPVRKLQAN	KKVQGSRRRL	REGRSQ	

Seq ID NO: 402 DNA sequence
Nucleic Acid Accession #: NM_002416
Coding sequence: 40..417

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65	ATCCAATACA	GGAGTGACTT	GGAATCCCAT	TCTATCACTA	TGAAGAAAAG	TGGTGTCTTT	60
	TTCTCTTTGG	GCATCATCTT	GCTGGTCTG	ATTGGAGTGC	AAGGAACCCC	AGTAGTGAGA	120
	AAGGGTCGCT	GTTCTCTGAT	CAGCACCAAC	CAAGGGACTA	TCCACCTACA	ATCCTTGAAA	180
	GACCTTAAAC	AATTTGCCCC	AAGCCCTTCC	TGCGAGAAAA	TTGAAATCAT	TGCTACACTG	240
70	AAGAATGGAG	TTCAAAACATG	TCTAAACCCA	GATTCAAGCAG	ATGTGAAGGA	ACTGATTAAA	300
	AAGTGGGAGA	AACAGGTGAC	CCAAAGAAAA	AAGCAAAAGA	ATGGGAAAAA	ACATCAAAAA	360
	AAGAAAGTTC	TGAAAGTTCC	AAAAATCTCA	CGTTCTCGTC	AAAAGAAGAC	TACATAAGAG	420
	ACCACTTCAC	CAATAAGTAT	TCTGTGTTAA	AAATGTTCTA	TTTAAATTAT	ACCCTATCA	480
	TTCCAAAGGA	GGATGGCATA	TAATACAAAG	GCTTATTAAT	TTGACTAGAA	AATTTAAAAA	540
75	ATTACTCTGA	AATTGTAACT	AAAGTTAGAA	AGTTGATTTT	AAGAATCCAA	ACGTTAAGAA	600
	TTGTTAAAGG	CTATGATTGT	CTTTGTTCTT	CTACCACCCA	CCAGTTGAAT	TTTCATGTC	660
	TTAAGGCCAT	GATTTTAGCA	ATACCCATGT	CTACACAGAT	GTTACCCCAA	CCACATCCCA	720
	CTCACAACAG	CTGCCCTGGA	GAGCAGCCCT	AGGCTTCCAC	GTACTGCAGC	CTCCAGAGAG	780
	TATCTGAGCG	ACATGTCAGC	AAGTCCTAAG	CCTGTTAGCA	TGCTGGTGAG	CCAAGCAGTT	840
80	TGAAATTGAG	CTGGAGCTCA	CCAAGCTGCT	GTGGCCATCA	ACCTCTGTAT	TTGAATCAGC	900
	CTACAGGCCT	CACACAAT	GTGCTGAGA	GATTCAATGCT	GATTGTTATT	GGGTATCACC	960
	ACTGGAGATC	ACCAGTGTGT	GGCTTTTCTA	GCCTCCTTTC	TGGCTTTGGA	AGCCATGTGA	1020
	TTCCATCTGT	CCCGCTCAGG	CTGACCACTT	TATTTCTTTT	TGTTCCCTTT	TGCTTCATTC	1080
	AAGTCAGCTC	TTCTCCATCC	TACCACAATG	CAGTGCCCTT	CTTCTCTCCA	GTGCACCTGT	1140
	CATATGCTCT	GATTTTCTCG	AGTCAACTCC	TTTCTCATCT	TGTCCCAAC	ACCCACAGAA	1200
85	AGTGTCTTCT	TCTCCCAATT	CATCTCACT	CAGTCCAGCT	TAGTTCAAGT	CCTGCCTCTT	1260
	AAATAAACCT	TTTTGGACAC	ACAAATTATC	TTAAACTCC	TGTTTCACTT	GGTTCACTAC	1320
	CACATGGGTG	AACACTCAAT	GGTTAACTAA	TTCTTGGGTG	TTTATCTAT	CTCTCCAACC	1380

AGATTGTGAG CTCCTTGAGG GCAAGAGCCA CAGTATATTT CCCTGTTTCT TCCACAGTGC 1440
 CTAATAATAC TGTGGAACTA GGTTTTAATA ATTTTAAAT TGATGTTGTT ATGGGCAGGA 1500
 TGGCAACACG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCATGTTGG 1560
 CTAGCCTCTG GTAACCTCTT ACTTATTATC TTCAGGACAC TCCTACAGG GACCAGGGAT 1620
 GATGCAACAT CCTGTCTTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA 1680
 GCACGTGTGA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740
 AAAATCATAT AATCTTACAA TGAAAAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800
 CCAACCATAC AAAAATTCCT TTTCCCGAAG GAAAAGGGCT TTCTCAATAA GCCTCAGCTT 1860
 TCTAAGATCT AACAGATAG CCACCGAGAT CCTTATCGAA ACTCATTTTA GGCAAAATAG 1920
 AGTTTTATAT TCCGTTTACT TGTTCAGAG TTTGTATTGT GATTATCAAT TACCACACCA 1980
 TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCGGT 2040
 TAGTGAAGC ATGATTGGTG CCCAGTTAGC CTCTGCAGGA TGTGGAAGC TCCTTCCAGG 2100
 GGAGGTTGAG TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTTAAA CCTATACTCA 2160
 CTTTCCCAA TCGAATCACT GCTCACACTG CTGATGATTT AGAGTGCTGT CCGGTGGAGA 2220
 TCCCACCGAA ACCTGTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG 2280
 AAAAATCTAA GTGTTTCTTA TAATTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340
 GTAGACAGTA TATAACTAAC AACCAAGAC TACATATTGT CACTGACACA CACGTATATA 2400
 TCATTATACA TATATATACA TACATGCATA CACTCTCAA GCAAATAATT TTTCACTTCA 2460
 AAACAGTATT GACTTGTATA CCTTGAATTT TGAAATATTT TCTTTGTATA AATAGAATGG 2520
 TATCAATAAA TAGACCATTA ATCAG

Seq ID NO: 403 Protein sequence
Protein Accession #: NP_002407

1 11 21 31 41 51
 MKKSGVLFLL GIILLVLIGV QGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCEK 60
 IEIIATLKNQ VQTCNLNPSA DVKELIKKWE KQVSQKKKQK NGKKHQKKKV LKVRKSQRSR 120
 QKKTT

Seq ID NO: 404 DNA sequence
Nucleic Acid Accession #: NM_006670
Coding sequence: 85..1347

1 11 21 31 41 51
 CCGGCTCGCG CCCTCCGGGC CCAGCCTCCC GAGCCTTCGG AGCGGGGGCC GTCCAGCCCC 60
 AGCTCCGGGG AAAACGCGAGC CGCGATGCCCT GGGGGGTGCT CCCGGGGGCC CGCGCGCGGG 120
 GACGGGGCTG TCGGGCTGGC GCGACTAGCG CTGGTACTCC TGGGCTGGGT CTCCTCGTCT 180
 TCTCCCACTT CCTCGGCATC CTCTCTCTCC TCCTCGGCGC CGTTCCTGGC TTCCGCGCGT 240
 TCCGCGCAGC CCGCGCTGCC GGACCACTGC CCGCGCTGCT GCGAGTGTCT CGAGGCAGCG 300
 CGCACAGTCA AGTGGCTTAA CCGCAATCTG ACCGAGGTGC CCACGACCT GCCCGCTTAC 360
 GTGCGCAACC TCTTCTTAC CGCAACCAG CTGGCCGTGC TCCTGCGCG CGCCTTCGCC 420
 CGCGGCGCGC CGCTGGCGGA GCTGGCCGCG CTCAACCTCA GCGGCAGCGC CTGGACGAG 480
 GTGCGCGCGG GCGCCTTCGA GCATCTGCCC AGCCTGGGCC AGCTCGACCT CAGCCACAA 540
 CCACCTGGCG ACCTCTTCTT CTTCGCTTTC TCGGGCAGCA ATGCCAGCGT CTCGGCCCCC 600
 AGTCCCTCTG TGAACCTGAT CCTGAACCAC ATCGTGCCCC CTGAAGATGA GCGGCAGAAC 660
 CGAGGCTCTG AGGCGATGGT GGTGGCGGCC CTGCTGGCGG GCGGTGCACT CGAGGGGCTC 720
 CGCGGCTTGG AGCTGGCCAG CAACCACTTC CTTTACCTGC CGCGGGATGT GCTGGCCCAA 780
 CTGCCCCAGC TCAGGCACCT GGACTTAAAT AATAATTCGC TGGTGAGCCT GACCTACGTG 840
 TCCCTTCGCA TCTGACACA TCTAGAAAGC CTCCACCTGG AGGACAAATG CCTCAAGGTC 900
 CTTCACAATG GCAACCTGGC TGAGTTGCAA GGTCTACCCC ACATTAGGGT TTTCTGGGAC 960
 AACCAATCCT GGCTCTGCGA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA 1020
 GAGGTAGTGC AGGCGAAAGA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG 1080
 GTCCTCTTGG AACTCAACAG TGCTGACCTG GACTGTGACC CGATTCTTCC CCCATCCCTG 1140
 CAAAACCTCT ATGTCTTCTT TTAGCTATTGTT TTAGCCCTGA TAGCCGCTAT TTTCTCTCTG 1200
 GTTTTGTATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCTGC 1260
 AGGGATCACA TGGAAGGGTA TCTTACAGA TATGAAATCA ATGCGGACCC CAGATTAACA 1320
 AACCTCAGTT CTAACCTGGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACTCTG 1380
 CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440
 TAGATACAAAC GGACTTTGAC TAAAAGCAGT GAAGGGGATT TGCTTCTCTG TTATGTAAAG 1500
 TTTCTCGGTG TGTCTCTTGA ATGTAAGACG ATGAACAGTT GTGTATAGTG TTTTACCCTC 1560
 TTTCTTTTCT TGGAACTCCT CAACACGTAT GGAGGGATT TTCAGGTTTC AGCATGAACA 1620
 TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
 ACAGATAGCA TTCAACAAAA GCTGCCTCAA CTTTTCGAG AAAAATACTT TATTATAAAA 1740
 TATCAGTTTT ATTCTCATGT ACCTAAGTTG TGGAGAAAAA AATTGCATCC TATAAACTGC 1800
 CTGCAGACGT TAGCAGGCTC TTCAAAATAA CTCCATGGTG CACAGGAGCA CCTGCATCCA 1860
 AGAGCATGCT TACATTTTAC TGTCTGTCAT ATTACAAAAA ATAACCTGCA ACTTCATAAC 1920
 TTTCTTGACA AAGTAAATTA CTTTTTTGAT TGCAGTTTAT ATGAAATGT ACTGATTTT 1980
 TTTTAATAAA CTGCATCGAG ATCCAACCGA CTGAATTGTT AAAAAAATAA AAAAAATAAG 2040
 ATTCCTAAAA GAA

Seq ID NO: 405 Protein sequence
Protein Accession #: NP_006661

1 11 21 31 41 51
 MPGGCSRGP AAGDRLRLAR LALVLLGWVS SSSPTSSASS FSSAPFLAS AVSAQPPLPD 60
 QCPALCEBSE AARTVKCVNR NLTEVPTDLP AYVRNLFTLG NQLAVLPAGA FARRPPLAEL 120
 AALNLSGSR LDEVRAFAEH LPSLRQLDLS HNPLADLSPF AFSGSNASVS APSPLVELIL 180
 NHIVPFEDER QNRSFEGMVV AALLAGRALQ GLRRLELASN HFLYLPDRVL AQLPSLRHLD 240
 LSNNSLVSLT YVSPRNLTSL ESHLEDNAL KVLHNGTLAE LQGLPHIRVF LDNNPWVDC 300
 HEMDMVTWLK ETEVVQKDR LTCAYPEKMR NRVLLELNSA DLDCLPLPP SLQTSYVPLR 360
 IVLALIGALF LLVLYLNRKG IKKWMHNIRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV

Seq ID NO: 406 DNA sequence
Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..927

	1	11	21	31	41	51	
5	ATGCCTGGGG	GGTGTCTCCG	GGGCCCCGCC	GCCGGGGACG	GGGCTCTGCG	GCTGGCGCGA	60
	CTAGGCGCTGG	TACTCTGTGG	CTGGGTCTCC	TCGTCTTCTC	CCACCTCCTC	GGCATCCTCC	120
	TTCTCTCTCT	CGCGCGCGTT	CCTGGCTTCC	GCGGTGTCCG	CCCAGCCCCC	GCTGCCGGAC	180
	CAGTGGCCCC	CGCTGTGCGA	GTGCTCCGAG	GCAGCGCGCA	CAGTCAAGTG	CGTTAACCGC	240
10	AATCTGACCG	AGGTGCCCCA	GGACCTGCCC	GCCTACGTGC	GCAACCTCTT	CCTTACCGGC	300
	AACCAGCTGG	CCAGCAACCA	CTTCCTTTAC	CTGCCGCGGG	ATGTGCTGGC	CCAACTGCCC	360
	AGCCTCAGGC	ACCTGGACTT	AAGTAATAAT	TCGCTGGTGA	GCCTGACCTA	CGTGTCTTTC	420
	CGCAACCTGA	CACATCTAGA	AAGCCTCCAC	CTGGAGGACA	ATGCCCTCAA	GGTCTTTCAC	480
	AATGGCACCC	TGGCTGAGTT	GCAAGGTCTA	CCCCACATTA	GGGTTTTCCT	GGACAACAAT	540
15	CCCTGGGTCT	CGACTGTGGC	CATGGCAGAC	ATGGTGACCT	GGCTCAAGGA	AACAGAGGTA	600
	GTGCAAGGCA	AAGACCGGCT	CACCTGTGCA	TATCCGGAAG	AAATGAGGAA	TCGGGTCTTC	660
	TTGGAATCA	ACAGTGTCTG	CTGGACTGT	GACCCGATTC	TTCCCCATC	CCTGCAAAAC	720
	TCTTATGTCT	TCCTGGGTAT	TGTTTATAGC	CTGATAGGCG	CTATTTTCTT	CCTGGTTTTC	780
	TATTTGAACC	GCAAGGGGAT	AAAAAGTGG	ATGCATAACA	TCAGAGATGC	CTGCAGGGAT	840
20	CACATGGAAG	GGTATCATTA	CAGATATGAA	ATCAATGCGG	ACCCAGGATT	AACAAACCTC	900
	AGTTCTAACT	CGGATGTCTT	CGAGTGA				

Seq ID NO: 407 Protein sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
25	MPGGCSRGPA	AGDGRRLRLAR	LALVLLGWVS	SSSPTSSASS	FSSSAPFLAS	AVSAQPPLEP	60
	QCPALCECSE	AARTVKCVNR	NLTVPTDLP	AYVRNLFPTG	NQLASNHFLY	LPRDVLQQLP	120
30	SLRHLDSLNN	SLVSLTYVSF	RNLTHLESLH	LEDNALKVLH	NGTLABELQL	PHIRVFLDNN	180
	PWVDCDHMAD	MVTWLKETEV	VQGDRLTCA	YPEKMRNRVL	LELNSADLDC	DFILPPSLQT	240
	SYVFLGIIVLA	LIGAILLLVL	YLNKRGIKKW	MEINIRDACRD	HMEGYHYRYE	INADPRLTNL	300
	SSNSDVLE						

Seq ID NO: 408 DNA sequence
Nucleic Acid Accession #: NM_000095.1
Coding sequence: 26..2299

	1	11	21	31	41	51	
40	CAGCACCCAG	CTCCCCGCCA	CGGCCATGGT	CCCCGACACC	GCCTGCGTTC	TTCTGCTCAC	60
	CCTGGCTGCC	CTGGGCGCGT	CGCGACAGGG	CCAGAGCCCG	TTGGGCTCAG	ACCTGGGCCC	120
	GCAGATGCTT	CGGAACTGCT	AGGAAACCAA	CGCGGCGCTG	CAGGACGTGC	GGGACTGGCT	180
	GCGGCAGCAG	GTCAAGGAGA	TCACGTTCTT	GAAAAACACG	GTGATGGAGT	GTGACGCGTG	240
45	CGGGATGCAG	CAGTCAGTAC	GCACCGGCTT	ACCCAGCGTG	CGGCCCTCTG	TCCACTGCGC	300
	GCCCGGCTTC	TGCTTCCCGG	CGGTGGCCTG	CATCCAGACG	GAGAGCGGCG	GCCGCTGCGG	360
	CCCTGCGCCC	GCGGGCTTCA	CGGGCAACGG	CTCGCACTGC	ACCGACGTCA	ACGAGTGCAA	420
	CGCCCCACCC	TGCTTCCCGG	GAGTCCGCTG	TATCAACACC	AGCCCGGGGT	TCCGCTGCGA	480
	GGCTTGCCCG	CGGGGTGACA	CGGGCCCCAC	CCACCAGGGC	GTGGGCTTGG	CTTTCGCCAA	540
50	GGCCAAACAAG	CAGGTTTGCA	CGGACATCAA	CGAGTGTGAG	ACCGGGCAAC	ATAACTGCGT	600
	CCCCAACTCC	GTGTGCATCA	ACACCCGGGG	CTCCTTCCAG	TGCGGCCCCG	GCCAGCCCGG	660
	CTTCTGGGGC	GACCAAGGCT	CGGGCTGCCA	GCGCGGCGCA	CAGCGCTTCT	GCCCGGACGG	720
	CTCGCCGAGC	GAGTGCACAG	AGCATGCAGA	CTGCGTCTTA	GAGCGCGATG	GCTCGCGGTC	780
	GTGCGTGTGT	CGCGTTGGCT	CGGCGGCGAA	CGGGATCCTC	TGTGGTTCGG	ACACTGACCT	840
55	AGACGGCTTC	CCGACGAGA	AGCTGCGCTG	CCCGGAGCCG	CAGTGCCTGA	AGGACAACCT	900
	CGTGACTGTG	CCCAACTCAG	GGCAGGAGGA	TGTGGACCGC	GATGGCATCG	GAGACGCTCG	960
	CGATCCGAGT	CCGCGAGGGG	ACGGGCTCCC	CAATGAAAAG	GACAACTGCC	CGCTGGTGCG	1020
	GAACCCAGAG	CACCGCAACA	CGGACGAGGA	CAAGTGGGGC	GATGCGTGCG	ACAACCTCCG	1080
	GTCCCAGAAG	AACGAGGAC	AAAAGGACAC	AGACCAGGAC	GGCCGGGGCG	ATGCGTGCGA	1140
60	CGACGACATC	GACGGCGACC	GGATCCGCAA	CCAGGCCGAC	AACTGCCCTA	GGGTACCCAA	1200
	CTCAGACCAG	AAGGACAGTG	ATGGCGATGG	TATAGGGGAT	GCCTGTGACA	ACTGTCCCCA	1260
	GAAGAGCAAC	CCGATGCAGG	CGGATGTGGA	CCACGACTTT	GTGGGAGATG	CTTGTGACAG	1320
	CGATCAAGAG	CAGGATGGAG	ACGGACATCA	GGACTCTCGG	GACAACTGTC	CCACGGTGCC	1380
	TAACAGTGCC	CAGGAGGACT	CAGACACAGA	TGGCCAGGGT	GATGCCCTGC	ACGACGACGA	1440
65	CGACAATGAC	GGAGTCCCTG	ACAGTCGGGA	CAACTGCCGC	CTGGTGCTTA	ACCCCGGCCA	1500
	GGAGGACCGG	GACAGGACCG	GCGTGGGCGA	CGTGTGCCAG	GACGACTTTG	ATGCAGACAA	1560
	GGTGGTAGAC	AAGATCGAGC	TGTGTCCGGA	GAACGCTGAA	GTACAGCTCA	CCGACTTCAG	1620
	GGCCTTCCAG	ACAGTCTGTC	TGGACCCGGA	GGGTGACCGG	CAGATTGACC	CCAACTGGGT	1680
	GGTGCTCAAC	CAGGGAAGGG	AGATCGTGCA	GACAATGAAC	AGCGACCCAG	GCCTGGCTGT	1740
70	GGGTACACT	GCCTTCAATG	GCGTGGACTT	CGAGGGCACG	TTCCATGTGA	ACACGGTCAC	1800
	GGATGACGAC	TATGCGGGCT	TCATCTTTGG	CTACCAAGAC	AGCTCCAGCT	TCTACGTGGT	1860
	CATGTGGAAG	CAGATGGAGC	AAACGTATTG	GCAGGCGAAC	CCCTTCCGTC	CTGTGGCCGA	1920
	GCCTGGCATC	CAACTCAAGG	CTGTGAAGTC	TTCCACAGGC	CCCGGGGAAC	AGTGCAGGAA	1980
	CGCTCTGTGG	CATACAGGAG	ACACAGAGTC	CCAGGTGCGG	CTGCTGTGGA	AGGACCCCGG	2040
75	AAACGTGGGT	TGGAAGGACA	AGAAGTCCTA	TCGTGGTTTC	CTGCAGCACC	GGCCCCAAGT	2100
	GGGCTACATC	AGGGTGCGAT	TCTATGAGGG	CCCTGAGCTG	GTGGCCGACA	GCAACGTGGT	2160
	CTTGACACAC	ACCATGCGGG	GTGGCCGCCT	GGGGGTCTTC	TGCTTCTCCC	AGGAGAACAT	2220
	CATCTGGGCG	AACTGCGCTT	ACCGCTGCAA	TGACACCATC	CCAGAGGACT	ATGAGACCCA	2280
	TCAGCTGCGG	CAGCCTTAGG	GACCAAGGTC	AGGACCCGCG	GGATGACAGC	CACCTCACC	2340
80	GCGGCTGGAT	GGGGGCTCTG	CACCCAGCCC	AAGGGGTGGC	CGTCTGAGG	GGGAGTGAG	2400
	AAGGGCTCAG	AGAGGACAAA	ATAAGTGTG	TGTGCAGGG			

Seq ID NO: 409 Protein sequence
Protein Accession #: NP_000086.1

85	1	11	21	31	41	51	
	MVPDTACVLL	LTALALGASG	QGSPLGSDL	GPQMLRELQE	TNAALQDVDR	WLRQVREIT	60

WO 02/086443

PCT/US02/12476

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FLKNTVMECD ACQMQQSVRT GLPSVRPLLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG 120
NGSHCTDVNE CNAHPCFPRV RCINTSPGFR CEACFPFGYSG PTHQGVGLAF AKANKQVCTD 180
INECTGQHN CVNSVCINT RGSFQCGPCQ PGFVGDAQSG CQRGAQRFCP DGSPSECEH 240
5 ADCVLERDGS RSCVCRVWGA GNGILCGRDT DLDGFFDEKL RCEPQCRKD NCVTVFNSGQ 300
EDVDRDGIAD ACDDPADGDG VPNEKDNCPV VRNPQQRNTD EDKWDGACDN CRSQKNDQK 360
DTDQDGRGDA CDDIDIDRI RNQADNCPRV PMSDQKDSBG DGIQDADCN PQKSNPDQAD 420
VDHDFVGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQDQDAD DDDNDGVFDS 480
RDNCLRVNFP GQEDADRDGV GDVQDDFDA DKVVDKIDVC PENAETVLT D FRAFTVVL D 540
PEGDAQIDPN WVLNQGREGI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI 600
10 FGQDSSSFY VVMWQMEQT YWQANPFRV AEPGILQKAV KSSTGPGQEL RNALWHTGDT 660
ESQVRLWKD PRNVGWKK SYRNPLQHRF QVGYIRVRFY EGPELVADSN VVLDTTMRGG 720
RLGVFCFSQE NIWANLRYR CNDTIPEDYE THQLRQA

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Seq ID NO: 410 DNA sequence
Nucleic Acid Accession #: NM_001565.1
Coding sequence: 67..363

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1      11      21      31      41      51
|      |      |      |      |      |
20 GAGACATTCC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC 60
AGCACCATGA ATCAAACTGC GATTCTGATT TGCTGCCTTA TCTTTCTGAC TCTAAGTGSC 120
ATTCAAGGAG TACCTCTCTC TAGAACCCTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
CCTGTTAATC CAAGGTCTTT AGAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240
CCTGTGAGA TCATTGTCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
25 TCGAAGGCCA TCAAGAATTT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT 360
TAAACACAGA GGGAGGCAAA ATCGATGCAG TGCTTCCAAAG GATGGACCAC ACAGAGGCTG 420
CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTC TTAGTTTGCA 480
GTTACACTAA AAGGTGACCA ATGATGGTCA CCAATCAGC TGCTACTACT CCTGTAGGAA 540
30 GGTAAATGTT CATCATCTTA AGCTATTGAG TAATAACTCT ACCCTGGCAC TATAATGTAA 600
GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTTCGACC CTGCTTCAA TATTTCCTC 660
ACCTTTCCCA TCTTCCAAAG GTACTAAGGA ATCTTTCTGC TTTGGGGTTT ATCAGAAATC 720
TCAGAAATCT AAATAACTAA AAGGTATGCA ATCAAATCTG CTTTTTAAAG AATGCTCTTT 780
ACTTCATGGA CTCTCACTGC CATCCTCCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA 840
35 CATACAATTC CAAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGAAGTATT 900
CTTATTTAAT GAAAGACTGT ACAAAGTATA AGTCTTAGAT GTATATATT CCTATATTGT 960
TTTCAGTGTG CATGGAATTA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
TTTAAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080
TTTTCAAATA AAAATGAGGT ACTCTCTCGG AAATATTAAG

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Seq ID NO: 411 Protein sequence
Protein Accession #: NP_001556.1

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1      11      21      31      41      51
|      |      |      |      |      |
45 MNQTAILICC LIPLTLGSIQ GVPLSRTVRC TCISISNQPV NPRSLEKLEI IPASQFCPRV 60
EIIATMKKKG EKRCNLPESK AIKNLLKAVS KEMSKRSP

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Seq ID NO: 412 DNA sequence
Nucleic Acid Accession #: XM_057014
Coding sequence: 143..874

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1      11      21      31      41      51
|      |      |      |      |      |
55 GGGAGGGAGA GAGGCGGCGG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG 60
CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCCTCGGT CTCCTCCGCC TCCAGCTCCG 120
CGCTGCCCGG CAGCCGGGAG CCATGCGACC CCAGGGCCCC GCGGCTCCCG CGCAGCGGCT 180
CGCGGCGCTC CTGCTGCTCC TGCTGTGCA GCTGCCCCGG CCGTCGAGCG CCTCTGAGAT 240
CCCCAAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG 300
AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360
60 CATTCGGGTG ACACCTGGGA TCCAGGTGCG GGATGGATTC AAAGGAGAAA AGGGGGAATG 420
TCTGAGGGAA AGCTTTGAGG AGTCTGGAC ACCCAACTAC AAGCAGTGTT CATGGAGTTC 480
ATTGAATTAT GGCATAGATC TTGGGAAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC 540
AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACTTCGG CTAAAATGCA GAAATGCATG 600
CTGTGAGCGT TGGTATTCCA CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATGTA 660
65 AGCTATAATT TATTTGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTATCG 720
CACTTCTTCT GTGGAAGGAC TTGTGTAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT 780
CTGGGTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
TTCTCGATC ATTATTGAAG AACTACCAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900
TTTTTTTATT ATGCTTGGGA ATGGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA 960
70 CATCTGAATG AAAAGCAAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020
TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTTCATAT TTTTCTTAGT 1080
TGGTTAGAAT ACTTCTTCTA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTGT 1140
GGTCTTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAAA ATATAAAGC TACCAATCTT 1200
75 GTACAAATT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTCCAA 1260
CAACCTTAAA AAAAAA AAAA

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Seq ID NO: 413 Protein sequence
Protein Accession #: XP_057014

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1      11      21      31      41      51
|      |      |      |      |      |
80 MRPQGPASP QRLRGLLLLL LLQLPAPSSA SEIPKQKQKA QLRQREVVDL YNGMCLQGPA 60
GVPRDGSFG ANGIPGTPGI PGRDGFKEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120
GKIAECTFTK MRSNSALRLV FSGSLRLKCR NACCQRWYFT FNGAECSGPL PIEAIYLDQ 180
85 GSPMNSTIN IHRSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIITE 240
LPK

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WO 02/086443

Seq ID NO: 414 DNA sequence
Nucleic Acid Accession #: XM_084007
Coding sequence: 138..2405

PCT/US02/12476

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      CTCGTGCCGA ATTCGGGCACG AGACCGCGTG TTCGCGCCTG GTAGAGATT TCTCGAAGACA 60
      CCGTGTGGGCC CGTGTGGGAAC CAAACCTGCG CGCGTGGCCG GGCCGTGGGA CAACGAGGCC 120
      GCGGAGACGA AGGCGCAATG GCGAGGAAGT TATCTGTAAT CTTGATCCTG ACCTTTGGCC 180
10     TCTCTGTAC AAATCCCTT CATGAACTAA AAGCAGCTGC TTTCCCCCAG ACCACTGAGA 240
      AAATTAGTCC GAATTGGGAA TCTGGCAITTA ATGTTGACTT GGCAATTTCC ACACGGCAAT 300
      ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAAATA TTCTTTGTCA GTTGAAGGGT 360
      TCAGAAAAAT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG 420
      ACCACGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG 480
15     AGCATCACTC AGACCAACGAG CATCACTCTG ACCATGATCA TCACTCCCAC CATATATCATG 540
      CTGCTTCTGG TAAATAAAG CGAAAAGCTC TTTGCCCAGA CCAATGACTCA GATAGTTTCTAG 600
      GTAAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA 660
      GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG 720
      TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACCTCTTCC 780
20     CCAAGATGAT AAGCAGCTCC ACTCCACCCA GTGTACATC AAAGAGCCCG GTGAGCCCGC 840
      TGGCTGGTGA GAAACCAAAAT GAATCTGTGA GTGAGCCCGG AAAAGGCTTT ATGATTTCGA 900
      GAAACACAAA TGAATACTCT CAGGAGTGT TCAATGATC AAAGCTACTG ACATCTCATG 960
      GCATGGGCAT CCAGGACAGT TGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA 1020
      TCAACCAAAAT TGATGCTAGA TCTTGTCTGA TTCATACAAG TGAAGAAGAG GCTGAAATCC 1080
25     CTCCAAAGAC CTATTCATTA CAAATAGCCT GGGTGTGGT TTTTATAGCC ATTTCCATCA 1140
      TCACTTTTCT GTCTCTGCTG GGGGTTATCT TAGTGCCCTC CATGAATCGG GTGTTTTTCA 1200
      AATTTCTCTT GAGTTTCTCT GTGGCACTGG CCGTGGGAC TTTGAGTGTG GATGCTTTT 1260
      TACACCTTCT TCACACTTCT CATGCAAGTC ACCACATAG TCATAGCCGT GAAGAACAG 1320
      CAATGGAAAT GAAAGAGGGA CCACTTTTCA GTCATCTGTC TTCTCAAAAC ATAGAAGAAA 1380
30     GTGCTATATT TGATTCACAG TGAAGGGTTC TAACAGCTCT AGGAGGCCCTG TATTTTATG 1440
      TTCTTGTGTA ACATGCTCTC ACATGTATCA AACAATTTAA AGATAAGAAG AAAAAGAATC 1500
      AGAAGAAACC TGAATAATGAT GATGATGTGG AGATAAGAA GCAGTTGTCC AAGTATGAAT 1560
      CTCAACTTCT AACAAATGAG GAGAAAGTAG ATACAGATGA TCGAACTGAA GGTATTTTAC 1620
      GAGCAGACTC ACAAGAGCCC TCCCACTTTG ATTCTCAGCA GCCTGCAATC TTGGAAGAAG 1680
35     AAGAGGTGAT GATAGTCTAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG 1740
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Seq ID NO: 415 Protein sequence
Protein Accession #: XP_084007

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Seq ID NO: 416 DNA sequence
Nucleic Acid Accession #: NM_015419.1
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Seq ID NO: 417 Protein sequence
Protein Accession #: NP_056234.1

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	QTLQGLSNLM	RLHIDHNKIE	FIHPQAFNGL	TSRLRLHLEG	NLLHQLHPST	FSTFTFLDYF	180
	RLSTRHLYL	AENMVRTLPA	SMLRNMPLLE	NLYLQGNPWT	CDCMRWFLE	WDAKSRGILK	240

	CKKDKAYEGG	QLCAMCFSPK	KLYKHEIHLK	KDMTCLKPSI	ESPLRQNRSR	SIEEEQEQEE	300
	DGGSQLELEK	FQLPQWSISL	NMTDEHGMV	NLVCDIKKPM	DVYKIHNLQT	DPPDIDINAT	360
	VALDFECFMT	RENYEKLWKL	IAYSEVPVK	LHREMLSKD	PRVSYQYRQD	ADEEALYYTG	420
5	VRQILAEPE	WVHQPSIDIQ	LNRRQSTAKK	VLLSYTYQYS	QTISTKDTKQ	ARGRSWVMIE	480
	PSGAVQRDQT	VLEGGPCQLS	CNVKASESPS	IFWVLPDGS	LKAPMDDDPS	KFSILSSGWL	540
	RIKSMEPSDS	GLYQCIAQVR	DEMDRMVYRV	LVQSPSTQPA	EKDTVTIGKN	PGESVTLPCN	600
	ALAIPEAHL	WILPNRRIIN	DLANTSHVYM	LPNGTLSIPK	VQVSDSGYYR	CVAVNQGGAD	660
	HFTVGTITVK	KGSGLPKSRG	RRFGAKALSR	VREDIVEDEG	GSGMGDEENT	SRLLHLPKQD	720
10	EVFLKTKDDA	INGDKKAKKG	RRKLKLWKHS	EKEPETNVAE	GRRVFESRRR	INMANKQINP	780
	ERWADILAKV	RGKNLPKGTE	VPPLIKTTSF	PSLSLEVTTP	FPAVSPSPAS	PVQVTSAAE	840
	SSADVLLGE	EEHVLGTISS	ASMGLEHNNH	GVILVEPEVT	STPLEEVVDD	LSEKTEEITS	900
	TEGDLKGTA	FTLISEPYEP	SPTLHTLDTV	YEKPTHETA	TEGWSAADVG	SSPEPTSSEY	960
	EPFLDAVSLA	ESEFMQYFDP	DLETSKSPDE	DKMKEDTFAH	LTPPTIWN	DSSTSOLFED	1020
	STIGEPGVP	QSHLQGLTDN	IHLVKSLSL	QDTLLIKKGM	KEMSQTLQGG	NMLEGDPHDS	1080
15	RSESEGGES	KSTLTPDSTL	KFSSMSFPVK	KPAETTVGTL	LKDDTTVT	TPRQKVAPSS	1140
	TMSTHPSRR	PNRRHRLRPN	GPRHRHKQTP	PTTFAPSETF	STQPTQAPDI	KISSQVESSL	1200
	VPTAWVDNTV	NTPKQLEMEK	NAEPTSKGTP	RRKHGKRFNK	HRYPSTVSS	RASGSKSPSP	1260
	PENKRNIVT	PSSETILLPR	TVSLKTEGYP	DSLDMYTTTR	KIYSSYPKVQ	STLPVITYKPT	1320
20	SDGKEIKDDV	ATNVDRKXSD	ILVTGESITN	AIPTSRSLVS	TMGEFKEESS	PVGFPPTPTW	1380
	NPSRTAQFGR	LQTDIPVTTT	GENLTDPLL	KELEDVDFTS	EFLSSLTSTV	PFHQEAGSS	1440
	TTLSSIKVEV	PDQLPAPVTL	DDHLETTVA	ILLSETRPQN	HTPTAARMKE	PASSSPSTIL	1500
	MSLGQTITTK	PALPSPRISQ	ASRDSKENVF	LMYVGNPETE	ATPVNNEGTO	HMSGPNELST	1560
	PSSDRDAFNL	STKLELEKQV	FGSRSLPRGP	DSQRQDGRVH	ASHQLTRVPA	KPILPTATVR	1620
25	LEPMSTQAS	RYFVTSQSPR	HWTKNKEITT	YPSGALPENK	QFTTPTLSS	TIPLPLHMSK	1680
	PSIPSKFTDR	RTDQFNYSK	VFGNNNIPEA	RNPVGKPPSP	RIPHYNGLR	PFPTNKTLSP	1740
	POLGVTTRP	IPTSPAPVPM	ERKVIPIGSY	RIHSHSTFHL	DFGPPAPPLL	HTPQTGSPS	1800
	TNLQNIPIVS	STQSSISFIT	SSVQSSGSPH	QSSSKFFAGG	PPASKFWSLG	EKPQILTKSP	1860
	QTVSVTAETD	TVFPCEATGK	PKPFVTWTKV	STGALMTPTN	RIQRFEVLKN	GTILVIRKVP	1920
30	QDRGQYMC	SNLHGLDRMV	VLLSVTVQPP	QILASHYQDV	TVYLGDTIAM	ECLAKGTAPV	1980
	QISWTFPDR	VWQTVSPVES	RTLHENRTL	SIKEASFSDR	GVYKCVASNA	AGADSLAIRL	2040
	HVAALPVIH	KTYLAVQVPY	PGLSIHIHCT	AKAAPLPSVR	WVLGDTQIR	PSQFLHGNL	2100
	VFPNGTYLIR	NLAPKDSGRY	ECVAANLVGS	ARRTVQLNVQ	RAAANARITG	TSPRRTDVRY	2160
	GGTLKLDCA	SGDPWPRILW	RLPSKRMDA	LFSFDSRIKV	FANGTLVVKS	VTDKDAGDYL	2220
35	CVARNKVGD	VNVLKVDVVM	KPAKIEHKEE	NDHKVYFGGD	LKVDVCATGL	PNPEISWSLP	2280
	DGSLVNSFMQ	SDSSGGRTKR	YVVFNNGLTY	FNEVGMRREG	DYTCFAENQV	GKDEMVRVVK	2340
	VUTAPATIRN	KTYLAVQVPY	GDVVTVACEA	XGEPMPKVTV	LSPTNKVIPT	SSEKYQIYQD	2400
	GTLLIQKAQR	SDSGNYTCLV	RNSAGEDRKT	VMIHVNVPFP	KINGNPNPIT	TVREIAAGGS	2460
	RKLIDCKAEG	IPTPRVLWAF	PEGVVLPAFY	YGNRITVHGN	GSLDIRSLRK	SDSVQLVCM	2520
40	RNEGGEARLI	VQLTVLEPME	KIPFHDPISE	KITAMAGHTI	SLNCSAAGTP	TPSLVWVLPN	2580
	GTDLQSGQQL	QRFYHKADGM	LHISGLSSVD	AGAYRCVARN	AAGHTERLVS	LKVGKPEAN	2640
	KQYHNLVSI	ITLTKLPCT	PGAGQGRFS	WTLPNGMHLE	GPQTLGRVIR	LDNGTLTVRE	2700
	ASVFDRTGYV	CRMETEYGPS	VTSIPVIVIA	YPPRITSEPT	PVIYTRPGNT	VKLNCMAMGI	2760
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45	KTTYIHVF						

Seq ID NO: 418 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..5001

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	ACCTCTCAAG	AGGACGAATT	GGATGTACCT	GACGACATCA	GCGTCCGGGT	TATGTCATCT	120
55	CAGTCTGTGC	TTGTGCTCTG	GGTGGATCCT	GTTCTGGAAA	AACAGAAGAA	AGTTGTTGCA	180
	TCAAGACAGT	ACACCGTGCG	CTATCGAGAG	AAGGGGGAA	TGGCCAGGTG	GGATTATAAG	240
	CAGATCGCTA	ACAGGCGGTG	GCTGATTGAG	AACCTGATTC	CAGACACTGT	GTATGAATTT	300
	GCAGTCCGTA	TTTCACAGGG	TGAAAGAGAT	GGCAAAATGGA	GTACGTCAGT	CTTCCAAAGA	360
	ACACCAAGAT	CTGCCCCTAC	CACAGCTCCT	GAAAACCTGA	ACGTCGTGGC	AGTCAATGGC	420
60	AAACCTACAG	TTGTGCTGTC	ATCTTGGGAT	GCGCTACCAG	AGACTGAGGG	GAAAGTGAAA	480
	GTCTGTCTGC	TGGACACAGG	ACTGTTTTCA	GTTTCTCTCT	TCCAACCATC	TGCCAAATCA	540
	TTTCAGAATA	CATCTTTTCA	TACGCCCCGG	CTCTCAAACC	ATTGGAGAGT	AAGTCCCTCA	600
	CCTATCCTGG	AGACACTACT	CTGCCCCCTG	TGGATGGTCT	GCAGCCTGGG	GAAACGCTATC	660
	TTTTCAAAAT	CCGGGCCACA	AACAGGAGAG	GCCTGGGACC	TCACTCCAAA	GCCTTCATG	720
65	TGGCTATGCC	AACAGAATG	CAGCTGTACC	CAGAAGGATT	TCAGTTGTCT	AGCTTACCTG	780
	ATCGATATCC	AAACCAACA	AGTTAATAAA	GATCCACAAC	TGGAAGGGAG	TGTTTTTGGA	840
	CCATGTTTTT	TTTTCTACTT	CCTCACATTT	ATGCTGGATA	TTGGCGGCTT	TTCTTCATT	900
	ATGTGCTATG	AAGACCCANN	TGTTTCTTCT	TTGACAGGCA	ATTCTTTAAA	ATCTGTTGCA	960
	GCCAGTAAGG	CGGATGTTCA	CGAGAACACG	GAGGACAATG	GGAAACCCGA	AAAACTGTAG	1020
70	CCTTCTCTAC	CTTCTCCCAG	AGCTCCAGCT	TCCTCCCAAC	ACCCCTCTGT	GCCTGCTTCT	1080
	CCCCAAGGGA	GAAATGCCAA	GGACCTTCTT	CTTGACTTGA	AGAACAAAAT	ATTGGCTAAT	1140
	GGTGGGGGCG	CCGAAAACCC	CCAGCTTCGC	GCCAGAAGAG	CAGAGGAGCT	GGATCTTCAG	1200
	TCGACAGAAA	TCACTGGGGA	GGAGGAGCTG	GGTTCGCCGG	AGGACTCGCC	CATGTCACCC	1260
	TCAGACACCC	AAGACCAGAA	ACGGACCCCT	AGGCGGCCAA	GAGACACCGG	CCAATCGGTG	1320
75	GTTGCTCCCG	GCAGGACTGC	AGTGAGGGCC	CGGATGCCAG	CGCTGCCCGG	AAGGGAAGGC	1380
	GTAGATAAGC	CTGGCTTTTC	CCTGGCCACG	CAGCCCCGCC	CAGGGGCGCC	CCCCTCGGCT	1440
	TCGGCTCTCT	CTGCCACCCA	CGCGTCCACC	CAGGGCACCT	CTCATGCTCC	TTCCCTCGCT	1500
	GCCAGCTTGA	ATGACAAACG	CTTGGTGGAC	TCAGACGAGG	ATGAGCGCGC	TGTGGGCTCC	1560
	CTCCACCCCA	AGGCGGCTTT	CGCCAGCCCG	CGGCCAGCCC	TGTCCCCCAG	CGCCAGTCC	1620
	CGGTCCAGCG	TTCTCCGCGA	CAGAAGCTCT	GTGCAACCCG	CGCAGAAAGC	AGCCTCGCCG	1680
80	GCGCGGAGGA	CCCCCATTC	AGGGGCCGCA	GAGGAAGATT	CCAGTGCTCT	AGCCCCACCC	1740
	TCAAGACTTT	CTCCACCCCA	TGGGGGATCA	TCTCGGCTGC	TGCCACCCCA	GCCACACCTG	1800
	AGCTCTCCAC	TTTCCAAGGG	CGGGAAGGAT	GGTGAGGACG	CCCCAGCCAC	CAACTCCAAT	1860
	GCGCATCAC	GCTCCACCAT	GTCTCTCTCT	ATCTCTCTGC	CAGGACGCGC	CAGGACGCGC	1920
	GTCTCTGAGG	GAGCGGAGGC	TTCTGATGGT	GAAAGCCACG	GATGACGCGA	TAGGGAAGAC	1980
85	GGCGGAAGGC	AGGCGGAGGC	CACGGGCCAG	ACGCTGCGGG	CCCGGCTCTG	CTCTGGACAC	2040
	TTCCATTGTC	TCAGACACAA	ACCCCTTTGCT	GCCAACGGGA	GGTCTCCAAG	CAGGTTCCAG	2100
	ATTGGGCGGG	GACCTCGGCT	GCAGCCCTCC	AGCTCCCCAC	AGTCAGACTGT	GCCCTCCCGA	2160

Seq ID NO: 419 Protein sequence
Protein Accession #: Eos sequence

70	1	11	21	31	41	51	
	MPG TKL TRTG	APADYRVILK	TSQEDEL DVP	DDISVRVMSS	QSVLVSVNDP	VLEKQKKVVA	60
	SRQTYTYVRE	KGELARWDYK	QIANNRVLIE	NLIPDTVYEF	AVRTSQGERD	GKWSTVSVQR	120
	TPESAPTATP	ENLNVNVPNG	KPTVVAASVD	ALNETPEGKVK	VCLLDLTGLFS	VSSFPQSAKS	180
75	FQNTFTFPTP	LSNHLQSPSS	PILSTLLLPV	WMVCSLGNAI	FSKSGPQTGE	ANDLTPKPSL	240
	SLCQCCECTP	KQDFSLCLAY	IDIQTKQVKN	DDQLEGSVFG	PCFLFYFLTF	MLDIGGFSFI	300
	MCYEDPVSSL	TGNSLKSVAA	SKADVPQONTE	DNGKPEKPEP	SSPSRPAPAS	SOHSPVPASP	360
	QQRNAKDL LL	DLKXKILANG	GAPRKPQLRA	KKAEELDLQS	TEITGEEELG	SREDSFMPSS	420
80	QDRNQDKRTL	PPSRHGHSVV	APGRATAVRAR	MPALPRRREGV	DKPGFSLATL	PRFGAPFPAS	480
	ASPAHHAOST	GTSHRPSPSLA	SLNDNDLVDS	DEDERAVAGSL	HPKGAPQAQPR	PALSPSRSPQ	540
	SSVLDRSSSV	HPGAKPASPA	PLRTPHSGAAE	EDSSASAPVS	RLSPFPHGGSS	RLLPQTQPHLS	600
	SPLSKGGKGD	EDAPATNSNA	PSLRSTMSSSV	SSHLSSRTQV	SEGAEASDGE	SHAGDGRDGE	660
	GRQAEATAQT	LLRAPASGHG	HLRLHXPFPAA	NGRSPERFSI	GRPGRLQPSL	SPQSTVPSPA	720
	HPRVVPHSPD	HPKLSSSGIGH	DEEDEKPLPA	TVVNDHVPSG	SRQPSIRSGVE	DLARSPQRGA	780
85	SLHRKEPISD	NPKSTGADTH	PQGGYKLSLAS	KADQDVQSTQ	ADTBGHSFSA	QPGSTDRHAS	840
	PARPFAARSQ	QHPSPVRMR	PGRAPEQQPP	PPVATSQHIF	GFQSRDAGRS	PQSPRLSLPTQ	900
	AGDPRPRTSOG	RSHSSSDPYT	ASRGMLFTA	LNQODEDAOG	QNDSDSTEVE	AQDVRAASLHA	960

ARAKEAAASL PKHQVQVESPT GAGAGGDHRS QRGHAASPAR PSRPGGQPSR ARVPSRAAPG 1020
 KSEPPSKRPL SSKSQQSVSA EDEEEDAGF PKGGKEDLLS SSVPKWBSST TPRGGKDADG 1080
 SLAKEEREPAL IALAPRGSL APVKRPLPPP PGSSPRASHV PSRPPPSRAA TVSPVAGTHP 1140
 WPRYTTRAPP GHFTSTPMLS LRQRMHARF RNPLSRQPAR PSYRQGYNGR PNVEGKVLPG 1200
 SNGKFNQGR IINGPQGTWKV VLDLDRGLVLN AEGRYLDQSH GNPLRIKLGG DGRITVDLEG 1260
 TPVVSFQDLF LFGQGRHGT LANAQDKPIL SLGGKPLVGL EVIKKTTHPP TTTMQPTTTT 1320
 TPLPTTTTPR PTTATTMQPT TTTTLPPTTT PRPTATTTRR TTTTRRPTTV RTTTTPTTTT 1380
 TPKPTTPIPT CPPGTLESHD DGNLIMSSN GIPECYAEED EFSGLETDTA VPTTEAYVIY 1440
 DEDYEFETSR PPTTTEPSTT ATTPRVIEE GAISFPPEEE FDLAGRKRKF APYVTVLNKD 1500
 PSAPCSLTDAL LDHFQVDSLD EIIIPNDLKKS DLPPQHAPRN ITVVAVEGCH SFVIVDWDKA 1560
 TPGDLVTGYL VYSASYEDFI RNKFSTQASS VTHLPIENLK PNTRYVFKVQ AQNPBGYGF I 1620
 SPVSFVFTES DNPLLVVRPP GGELSGSHSL SNMIPATRTA MDGNM

Seq ID NO: 420 DNA sequence
 Nucleic Acid Accession #: NM_022743
 Coding sequence: 128..1237

1 11 21 31 41 51
 GTGGATTGA GAGATACCTC CCCTCCTTCT GCTCAGCTGC CTTGCAGTAA TTAAACTCTT 60
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 AAAAGCTGAT CGATGCTCTC AGTGCCGCGT CGCCAAATAC TGTAGTGCTA AGTGTGAGAA 180
 AAAAGCTTGG CCAGACACCA AGCGGGAAAT CAAATGCCTT AAAAGCTGCA AACCCAGATA 240
 TCTCCAGAG TCGTTTGAC TTCTTGGCAG AGTTGTCTTC AAACCTATGG ATGGAGCACC 300
 TTCAGAAATC AAGAGAGCTT ACTCATTTTA TGATCTGGAG TCAATATTA ACAAACTGAC 360
 TGAAGATAAG AAGAGGGGCC TCAGGCAACT CGTAATGACA TTTCAACATT TCATGAGAGA 420
 AGAAATACAG GATGCTCTC AGCTGCCACC TGCCCTTGAC CTTTGTGAAG CCTTTGCAAA 480
 AGTGTCTGC AACTCTTTCA CCATCTGTAA TGCGGAGATG CAGGAAGTTG GTGTTGCCCT 540
 ATATCCAGT ATCTCTTTGC TCAATCACAG CTGTGACCCC AACTGTTTGA TTGTGTTCAA 600
 TGGGCCCCAC CTCTTACTGC GAGCAGTCCG AGACATCGAG GTGGGAGAGG AGCTCACCAT 660
 CTGCTACCTG GATATGCTGA TGACCAAGTGA GGAGCGCCGG AAGCAGCTGA GGGACCAGTA 720
 CTGCTTTGAA TGTGACTGTT TCCGTTGCCA AACCCAGGAC AAGGATGCTG ATATGCTAAC 780
 TGGTGATGAG CAAGTATGGA AGGAAGTTCA AGAATCCCTG AAAAAAATTG AAGAACTGAA 840
 GGCACACTGG AAGTGGGAGC AGGTTCTGGC CATGTGCCAG GCGATCATAA GCAGCAATTC 900
 TGAACGGCTT CCCGATATCA ACATCTACCA GCTGAAGGTG CTCGACTGCG CCATGGATGC 960
 CTGCATCAAC CTCGGCCTGT TGGAGGAAGC CTTGTTCTAT GGTACTCAGA CCATGGAGCC 1020
 ATACAGGATT TTTTCCCAG GAAGCCATCC CGTCAGAGGG GTTCAAGTGA TGAAGTTGG 1080
 CAAACTGCAG TCATACCAAG GCATGTTTCC CCAAGCAATG AAGAATCTGA GACTGGCTTT 1140
 TGATATTATG AGATGTACAC ATGGCAGAGA ACACAGCCTG ATTGAAGATT TGATTCTACT 1200
 TTTAGAAGAA TGCAGCCCA ACATCAGAGC ATCCTAAGGG AACGCAGTCA GAGGGAAATA 1260
 CGGCGTGTGT TTTTGTGAA TGCCCTATTG AGGTACACA CTCTATGCTT TGTAGCTGT 1320
 GTGAACCTCT CTTATTGAA ATTCTGTTCC GTGTTGTGT AGGTAATAA AGGCAGACAT 1380
 GGTTTGCAAA CCACAAGAA CATTAGTTGT AGAGAAGCAC GATTATAATA AATTCAAAAC 1440
 ATTTGGTTGA GGATGCCAAA AAAAAAAAAA AAAAAA

Seq ID NO: 421 Protein sequence
 Protein Accession #: NP_073580

1 11 21 31 41 51
 MRCSQCRVAK YCSAKCKKA WPDHKRECK LKSKCPRYPP DSVRLLRVV FKLMDGAPSE 60
 SEKLYSPYDL ESNINKLTED KKEGLRLQVM TPOHFMREEI QDASQLPPAF DLFEAFKVI 120
 CNSFTICNAE MQEVGVGLYP SISLNHSCD PNCISVFNPG HLLLRVRDI EVGEELTICY 180
 LDMLMTSEER RKQLRDQYCP ECDPCRCQTO DKDADMLTGD BQVWKEVQES LKKIEELKAI 240
 WKWEQVLAMC QAISSNSER LPDINIYQLK VLDCAAMDACI NLGLLEBALF YGTRTMEPYR 300
 IFPPGSHFVR GVQVMKVGKL QLRQGMFFQA MNLRILAFDI MRVTHGREHS LIEDLILLLE 360
 ECDANIRAS

Seq ID NO: 422 DNA sequence
 Nucleic Acid Accession #: NM_003014.2
 Coding sequence: 238..648

1 11 21 31 41 51
 GGCGGTTCC GCGCCCGAAG GCTGAGAGCT GGCGCTGCTC GTGCCCTGTG TGCCAGACGG 60
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 AAACCTCTCT GCGCCCCAGA AGATTTCTTC CTCGGGGAAG GGACAGCGAA AGATGAGGGT 180
 GGCAGGAAGA GAAGGCGCTT TCTGTCTGCC GGGGTGCGAG CGCGAGAGGG CAGTGCCATG 240
 TTCTCTCCA TCCTAGTGGC GCTGTGCTG TGGCTGCACC TGGCGCTGGG CGTGCAGGCG 300
 GCGCCCTGCG AGGCGGTGCG CATCCCTATG TGCCCGCACA TGCCCTGGAA CATCACGCGG 360
 ATGCCCAACC ACCTGCACCA CAGCACGCAG GAGAACGCCA TCCTGGCCAT CGAGCAGTAC 420
 GAGGAGCTGG TGGACGTGAA CTGCAGCGCC GTGCTGCGCT TCTTCTCTG TGCCATGTAC 480
 GCGCCCATTT GCACCTTGGG GTTCCTGCAC GACCCTATCA AGCCGTGCAA GTCGGTGTGC 540
 CAACGCGCGC GCGACGACTG CGAGCCCTTC ATGAAGATGT ACAACACAG CTGGCCCGAA 600
 AGCCTGGCCT GCGACGAGCT GCCTGTCTAT GACCGTGGCG TGTGCATTTC GCCTGAAGCC 660
 ATCGTACCGG ACCTCCCGGA GGATGTTAAG TGGATAGACA TCACACAGA CATGATGGTA 720
 CAGGAAGAAG CTCTTGATGT TGACTGTAAA CGCCTAAGCC CCGATCGGTG CAAGTGTAAA 780
 AAGGTGAAGC CAACTTTGGC AACGTATCTC AGCAAAAACT ACAGCTATGT TATTATGCC 840
 AAAATAAAG CTGTGCAGAG GAGTGGCTGC AATGAGGTCA CAACGCTGGT GGATGTAAAA 900
 GAGATCTTCA AGTCTCATC ACCCATCCCT CGAATCTAAG TCCCGCTCAT TACAAATTCT 960
 TCTTGCCAGT GTCCACACAT CCTGCCCATC CAAGATGTTT TCATCATGTG TTACAGAGTG 1020
 CGTTCAAGGA TGATGCTTCT TGAATAATGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080
 AAAAGATCCA TACAGCTGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAGA 1140
 AAGAAACAG CCGGCGCAC CAGTCGTAGT AATCCCCCA AACCAAGGG AAAGCCTCCT 1200
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 AACCCGAAAA GAGTGTGAGC TAACTAGTTT CCAAGCGGA GACTTCCGAC TTCTTACAG 1320
 GATGAGGCTG GGCATTGCCCT GGCACAGCCT ATGTAAGGCC ATGTGCCCTT TGCCTAAC 1380

	ACTCACTGCA	GTGCTCTTCA	TAGACACATC	TTGCAGCATT	TTTCTTAAGG	CTATGCTTCA	1440
	GTTTTTCTTT	GTAAGCCATC	ACAAGCCATA	GTGGTAGGTT	TGCCCTTTGG	TACAGAAGGT	1500
	GAGTTAAAGC	TGGTGGAAAA	GGCTTATTGC	ATTGCATTCA	GAGTAACCTG	TGTGCATACT	1560
5	CTAGAAGAGT	AGGGAAAAATA	ATGCTTGTTA	CAATTGCGACC	TAATATGTGC	ATTGTAAAAAT	1620
	AAATGCCATA	TTTCAAACAA	AACACGTAAT	TTTTTTACAG	TATGTTTTAT	TACCTTTTGA	1680
	TATCTGTGGT	TGCAATGTTA	GTGATGTTTT	AAAAATGTAT	GAAAAATATA	TGTTTTTAAG	1740
	AAGGAACAGT	AGTGAATGA	ATGTTAAAAAG	ATCTTTATGT	GTTTATGGTC	TGCAGAAGGA	1800
	TTTTTGTGAT	GAAAGGGGAT	TTTTTGAAAA	ATTAGAGAAG	TAGCATATGG	AAAAATTATA	1860
10	TGTGTTTTTT	TACCAATGAC	TTGAGTTTCT	GTTTTTAGCT	AGAAACTTAA	AAACAAAAAT	1920
	AAATAATAAG	AAAAATAAAT	AAAAAGGAGA	GGCAGACAAT	GTCTGGATTG	CTGTTTTTTG	1980
	GTTACCTGAT	TTCCATGATC	ATGATGCTTC	TTGTCAACAC	CCTCTTAAGC	AGCACCAGAA	2040
	ACAGTGAGTT	TGTCTGTACC	ATTAGGAGTT	AGGTACTAAT	TAGTTGGCTA	ATGCTCAAGT	2100
	ATTTTATACC	CACAAGAGAG	GTATGTCACT	CATCTTACTT	CCCAGGACAT	CCACCCTGAG	2160
	AATAATTTGA	CAAGCTTAAA	AATGGCCTTC	ATGTGAGTGC	CAAATTTTGT	TTTTCTTCAT	2220
15	TTAAATATTT	TCTTTGCTTA	AATACATGTG	AGAGGAGTTA	AATATAAATG	TACAGAGAGG	2280
	AAAGTTGAGT	TCCACCTCTG	AAATGAGAAT	TACTTGACAG	TTGGGATACT	TTAATCAGAA	2340
	AAAAAGAAGT	TATTTGCAGC	ATTTTATCAA	CAAATTTTAT	AATTTGTGAC	AATTGGAGGC	2400
	ATTTATTTTA	AAAAACAATT	TTATTGGCCT	TTTGCTAACA	CAGTAAGCAT	GTATTTTATA	2460
20	AGGCATTCAA	TAACTGGACA	ACGCCCAAGG	GAAATAAAAT	CCTATCTAAT	CCTACTCTCC	2520
	ACTACACAGA	GGTAACTACT	ATTAGTATTT	TGGCATATTA	TTCTCCAGGT	GTTTGCTTAT	2580
	CACATTATGA	AATGATTTGA	ACAAATAAAA	CTAGGAACCT	GTATACATGT	GTTTCATAAG	2640
	CTGCTCTCTT	TGCTTGGCCC	TTTATTGAGA	TAAGTTTTCC	TGTCAGAGAA	GCAGAAACCA	2700
	TCTCATTTCT	AACAGCTGTG	TTATATTCCA	TAGTATGCAT	TACTCAACAA	ACTGTTGTGC	2760
25	TATTGGATAC	TTAGGTGGTT	TCTTCACTGA	CAATACTGAA	TAAACATCTC	ACCGGAATTC	

Seq ID NO: 423 Protein sequence
Protein Accession #: NP_003005.1

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	YEELVDVNC	AVLRFFPCAM	YAPICTLEPL	HDPIKPKCKSV	QQRARDCEP	LMKMYNHSWP	120
	ESLACDELFP	YDRGVCSIFE	AIUTDLPELV	KWIDITPDM	VQERPLDVDC	KRLSPDRCKC	180
	KVKKPTLATY	LSKNYSYVIH	AKIKAVQRS	CNEVTTVVDV	KEIFKSSSPI	PRTQVPLITN	240
35	SSQCQPHILP	HQDVLIMCYE	WRSRMMLLEN	CLVEKWRDQL	SKRSIQWEER	LQEQRRVTQD	300
	KKKTAGRTSR	SNPPKPKGKP	PAPKPAAPKK	NIKTRSAQKR	TNPKRV		

Seq ID NO: 424 DNA sequence
Nucleic Acid Accession #: BC010423
Coding sequence: 248..1780

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45	AGCTACGGCT	GGGTGTGTAG	AACGGGGCCG	GGGCTGGGGC	TGGGTCCCTT	AGTGGAGACC	120
	CAAGTGCAGG	AGGCAAGAAC	TCTGCAAGCT	CCTGCTTCTT	GGGTCAAGTT	CTTATTCAAG	180
	TCTGCAAGCG	GCTCCAGGGG	AGATCTCGGT	GGAACCTCAG	AAACGCTGGG	CAGTCTGCCT	240
	TTCAACCATG	CCCCTGTCCC	TGGGAGCCGA	GATGTGGGGG	CCTGAGGCCT	GGCTGTGCTT	300
50	GCTGCTACTG	CTGGCATCAT	TTACAGGCCG	GTGCCCCGGG	GGTGAGCTGG	AGACCTCAGA	360
	CGTGGTAAC	GTGGTGTGCG	GCCAGGACGC	AAAACCTGCC	TGCTTCTACC	GAGGGGACTC	420
	CGGCGAGCAA	GTGGGGCAAG	TGGCATGGGC	TGCGGTGGAC	GCGGGCGAAG	GCGCCGAGGA	480
	ACTAGCGCTA	CTGCACTCCA	AATACGGGCT	TGATGTGAGC	CCGGCTTACG	AGGGCCGCGT	540
	GGAGCAGCCG	CCGCCCCCAC	GCAACCCCTT	GGACGGCTCA	GTGCTCTGTC	GCAACGCACT	600
55	GCAGGCGGAT	GAGGGCGAGT	ACGAGTGCCG	GGTCAGCACC	TTCCCCCGCG	GCAGCTTCCA	660
	GGCGCGGCTG	CGGCTCCGAG	TGCTGGTGCC	TCCCCCTGCC	TCAGTGAATC	TGGTCCAGC	720
	ACTAGAAGAG	GGCCAGGCCC	TGACCTTGCC	AGCCTCTGCG	ACAGCTGAGG	GCAGCCGAGC	780
	CCCCAGCGTG	ACCTGGGACA	CGGAGGTCAA	AGGCACAACG	TCCAGCGGTT	CCTTCAAGCA	840
	CTCCCCGCTT	GCTGCGGTCA	CCTCAGAGTT	CCACTTGGTG	CCTAGCCGCA	GCATGAATGG	900
60	GCAGCCACTG	ACTTGTGTGG	TGTCCCATCC	TGGCCTGCTC	CAGGACCAAA	GGATCAACCA	960
	CACTCTCCAC	GTGTCTCTCC	TGTCTGAGGC	CTCTGTGAGG	GGCCTTGAAG	ACCAAAATCT	1020
	GTGGCACATC	TGGCAAGAAC	GAGCTATGCT	CAAGTGCCGT	AGTGAAGGGC	AGCCCCCTCC	1080
	CTCATACAAC	TGGACACGGC	TGGATGGGCC	TCTGCCAGAT	GGGGTACGAG	TGGATGGGGA	1140
	CACCTTGGGC	TTTCCCCCAC	TGACCACTGA	GCACAGCGGC	ATCTACGTCT	GCCATGTCTC	1200
65	CAATGAGTTC	TCCTCAAGGG	ATTCTCAGGT	CACGTGTGAT	GTTCTTGACC	CCCAGGAAGA	1260
	CTCTGGGAAG	CAGGTGGAGC	TAGTGTGAGC	CTCGGTGGTG	GTGGTGGGTG	TGATCGCCGC	1320
	ACTCTTGTTC	TGCTTCTTGG	TGGTGGTGCT	GGTGCTCATG	TCCCGATACC	ATCGGGCGCA	1380
	GGCCAGCAGC	ATGACCCAGA	AATATGAGGA	GGAGCTGACC	CTGACCCAGG	AGAACTCCAT	1440
	CCGGAGGCTG	CATTCCCATC	ACACGGACCC	CAGGAGCCAG	CCGGAGGAGA	GTGTAGGGCT	1500
70	GAGAGCCGAG	GGCCACCCTG	ATAGTCTCAA	GGACAACAGT	AGCTGCTCTG	TGATGAGTGA	1560
	AGAGCCGAG	GGCCGCGAGT	ACTCCAGGCT	GACCACGGTG	AGGGAGATAG	AAACACAGAC	1620
	TGAACCTGCT	TCTCCAGGCT	CTGGGCGGGC	CGAGGAGGAG	GAAGATCAGG	ATGAAGGCAT	1680
	CAACAGGGCC	ATGAACCAAT	TTGTTCAAGG	GAATGGGACC	CTACGGGCCA	AGCCACCGGG	1740
	CAATGGCATC	TACATCAATC	GGCGGGGACA	CCTGGTCTGA	CCCAGGCCTG	CCTCCCTTCC	1800
75	CTAGGCCTGG	CTCCTTCTGT	TGACATGGGA	GATTTTAGCT	CATCTTGGGG	GCCTCCTTAA	1860
	ACACCCCAT	TTCTTGGGGA	AGATGCTCCC	CATCCCACTG	ACTGCTTGAC	CTTTACTCTC	1920
	AAACCTTCTG	TTCTTGGGGA	GGGCTCCACC	AATTGAGTCT	CTCCCACTAT	GCATGCAGGT	1980
	CACCTGTGTG	GTGCATGTGT	GCCTGTGTGA	GTGTGAGTCT	ACTGTGTGTG	TGTGGAGGGG	2040
	TGACTGTCCG	TGGAGGGGTG	ACTGTGTCCG	TGGTGTGTAT	TATGCTGTCA	TATCAGAGTG	2100
	AAGTGAACCT	TGGTGTATGT	GCCACGGGAT	TTGAGTGGTT	GCGTGGGCAA	CACGTGTGAG	2160
80	GTTTGGCGTG	TGTGTCAATG	GGCTGTGTGT	GACCTCTGCC	TGAAAAAGCA	GGTATTTTCT	2220
	CAGACCCGAG	AGCAGTATTA	ATGATGCAGA	GGTTGGAGGA	GAGAGGTGGA	GACTGTGGCT	2280
	CAGACCCGAG	TGTGCGGGGA	TAGCTGGAGC	TGGAATCTGC	CTCCGGTGTG	AGGGAACCTG	2340
	TCTCCTACCA	CTTGGAGGCC	ATGGGGGCAA	GTGTGAAGCA	GCCAGTCCCT	GGGTGAGCCA	2400
	GAGGCTTGAA	CTGTATACAGA	AGCCCTCTGC	CCTCTGGTGG	CCTCTGGGCC	TGCTGCATGT	2460
85	ACATATTTTC	TGTAATATATA	CATGCGCCGG	GAGCTTCTTG	CAGGAATACT	GCTCCGAATC	2520
	ACTTTTAATT	TTTTTCTTTT	TTTTTCTTCT	CCCTTTCAT	TAGTGTGATT	TTTTATTTAT	2580
	TTTTATTTT	ATTTTTTTTT	AGAGTTTGAG	TCCAGCCTGG	ACGATATAGC	CAGACCTGT	2640

CTGTAAAAAA ACCAAAACCC AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 425 Protein sequence
Protein Accession #: AAH10423

5

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QVGQVAWARV	DAGEGAQELA	LLHSKYGLHV	SPAYEGRVEQ	PPPPRNPLDG	SVLLRNAVQA	120
DEGEYECRV	TFPAGSFQAR	LLRLVLPPL	PSLNPFPAL	EGQGLTLAAS	CTAEGSPAPS	180
VTWDTVEKGT	TSSRSFKHSR	SAAVTSEFHL	VPSRSMNGQP	LTCVVSHPL	LQDQRITHIL	240
HVSFLAEASV	RGLEDQNLWH	IGREGAMKLC	LSEGGPPPSY	NWTRLDGFLP	SGVRVDGDTL	300
GFPPLTTEHS	GIYVCHVNE	FSSRDSQVTV	DVLDPQEDSG	KQVDLVASV	VVGVIAALL	360
FCLLVVVVL	MSRYHRRKAQ	QMTQKYEEL	TLTRENSRR	LHSHHTDPRS	QPEESVGLRA	420
EGHPDLSKDN	SSCSVMSSEP	EGRSYSTLTT	VREIETQTEL	LSPGSGRAEE	EEDQDEGIKQ	480
AMNHPVQENG	TLRAKPTGNG	IYINGRGHLV				

Seq ID NO: 426 DNA sequence
Nucleic Acid Accession #: NM_003474.2
Coding sequence: 37..3036

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CTTTTAAAG	AATGAAAGGC	TAGAAAGAGCT	CAGCGGCGCG	CGGGGCGCTG	CGCGAGGGCT	180	
CCGGAGCTGA	CTCGCGGAGG	CAGGAAATCC	CTCCGGTGGC	GAGCGCGGCG	CCCGCTCGGC	240	
GCCCCGCTGG	GATGGTGACG	CGCTCGCCGC	CGGGCCCGAG	AGCTGCTGCA	CTGAAGGCCG	300	
GCGACGATGG	CAGCGCGCCC	GCTGCCCGTG	TCCCCCGCCC	CGCCCTCTCT	GCTCGCCCTG	360	
GCCCGTGCTC	TGCTCGCGCC	CTGCGAGGCC	CGAGGGGTGA	GCTTATGGAA	CGAAGGAAGA	420	
GCTGATGAAG	TTGTGATGTC	CTCTGTTCCG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC	480	
TTGCACTCCA	AGAATCATCC	AGAAGTGCTG	AATATTGAC	TACAACGGGA	AAGCAAGAAA	540	
CTGATCATAA	ATCTGGAAG	AAATGAAGGT	CTCATTGCCA	GCAGTTTCAC	GGAAACCCAC	600	
TATCTGCAAG	ACGGTACTGA	TGTCTCCCTC	GCTCGAAATT	ACACGGTAAT	TCTGGGTAC	660	
TGTTACTACC	ATGACATGAT	ACGGGATAT	TCTGATTCAG	CAGTCAGTCT	CAGCACGTGT	720	
TCTGCTCTCA	GGGACTATTG	TGTGTTTGA	AATGAAAGCT	ATGTCTTAGA	ACCAATGAAA	780	
AGTGCAACCA	ACAGATACAA	ACTCTTCCA	GCGAAGAAGC	TGAAAGCGT	CCGGGGATCA	840	
TGTGGATCAC	ATCACAACAC	ACCAAACCTC	GCTGCAGAAG	ATGTGTTTCC	ACCAACCTCT	900	
CAGACATGGG	CAAGAAGGCA	TAAAAGAGAG	ACCCTCAAGG	CAACTAAGTA	TGTGGAGCTG	960	
GTGATCGTGG	CAGACAACCG	AGAGTTTCAG	AGGCAAGGAA	AAGATCTGGA	AAAAGTTAAG	1020	
CAGCGATTAA	TAGAGATTGC	TAACTACGTT	GACAAGTTT	ACAGACCACT	GAACATTGG	1080	
ATCGTGTGG	TAGCGTGGGA	AGTGTGGAAT	GACATGGACA	AATGCTCTGT	AAGTCAGGAC	1140	
CCATTCCACA	GCCTCCATGA	ATTTCTGGAC	TGGAGGAAGA	TGAAGCTTCT	ACCTCGCAAA	1200	
TCCCATGACA	ATGCGCAGCT	TGTCAGTGGG	GTTTATTTCC	AAGGGACCAC	CATCGGCATG	1260	
GCCCCAATCA	TGAGCATGTG	CACGGCAGAC	CAGTCTGGGG	GAATTGTCT	GGACCATTC	1320	
GACAATCCCC	TTGGTGGAGC	CGTGACCTG	GCACATGAGC	TGGGCCACAA	TTTCGGGATG	1380	
AATCATGACA	CATGAGACAG	GGGCTGTAGC	TGTCAAATGG	CGGTGAGAA	AGGAGGCTGC	1440	
ATCATGAACG	CTTCCACCGG	GTACCCATT	CCCATGGTGT	TCAGCAGTTG	CAGCAGGAAG	1500	
GACTTGGAGA	CCAGCCTGGA	GAAAGGAATG	GGGGTGTGCC	TGTTTAACT	GCCGGAAGTC	1560	
AGGGAGTCTT	TGGGGGGCCA	GAAGTGTGGG	AACAGATTGG	TGGAAGAAGG	AGAGGAGTGT	1620	
GACTGTGGGG	AGCCAGAGGA	ATGTATGAAT	CGCTGCTGCA	ATGCCACCAC	CTGTACCTCG	1680	
AAGCCGAGCG	CTGTGTGCGC	ACATGGGCTG	TGCTGTGAAG	ACTGCCAGCT	GAAGCCTGCA	1740	
GGAAACAGCG	GCAAGGACTC	CAGCAACTCC	TGTGACCTCC	CAGAGTTCTG	CACAGGGGCC	1800	
AGCCCTCACT	GCCCAGCCAA	CGTGTACCTG	CACGATGGGC	ACTCATGTCA	GGATGTGGAC	1860	
GGCTACTGCT	ACAATGTCAT	CTGCCAGACT	CACGAGCAGC	AGTGTGTCT	ACTCTGGGGA	1920	
CCAGGTGCTA	AACCTGCCCC	TTGGATCTGC	TTTGAGAGAG	TCAATTCTGC	AGGTGATCCT	1980	
TATGGCAACT	GTGGCAAGAT	CTCGAAGAGT	TCCTTTGCCA	AATGCGAGAT	GAGAGATGCT	2040	
AAATGTGAAA	AAATCCAGTG	TCAAGGAGGT	GCCAGCGGCG	CAGTCATTGG	TACCAATGCC	2100	
GTTTCCATAG	AAACAACAT	CCCCCTGCAG	CAAGGAGGCC	GGATTCTGTG	CCGGGGGACC	2160	
CACGTGTACT	TGGGCGATGA	CATGCCGGAC	CCAGGGCTTG	TGCTTGCAGG	CACAAAGTGT	2220	
GCAGATGGAA	AAATCTGCCT	GAATCGTCAA	TGTCAAAATA	TTAGTGTCTT	TGGGGTTCAC	2280	
GAGTGTGCAA	TGCAGTGCCA	CGGCAGAGGG	GTGTGCAACA	ACAGGAAGAA	CTGCCACTGC	2340	
GAGGCCCAT	CCTACCCATG	GAAGGACAAT	CCCAGGAGAT	TGCTGCAGTG	TCAGAAATGTT	2400	
GGCCCATATC	GGCAAGCAGA	TAACCAAGGT	TTAACCATAG	GAATCTGGT	GACCATCTGT	2460	
TGTCTTCTTG	CTGCCGGATT	TGTGGTTTAT	CTCAAAAGGA	AGACCTTGAT	ACGACTGCTG	2520	
TTTACAAATA	AGAAAGACCAC	CATTGAAAAA	CTAAGGTGTG	TGCGCCCTTC	CCGGCCACCC	2580	
CGTGGCTTCC	AACCTGTCTA	GGCTCACCTC	GGCCACCTTG	GAAAAGGCCT	GATGAGGAAG	2640	
CCGCCAGATT	CCTACCCATG	GAAGGACAAT	CCCAGGAGAT	TGCTGCAGTG	TCAGAAATGTT	2700	
GACATCAGCA	GACCCCTCAA	CGGCCTGAAT	GTCCCTCAGC	CCAGTCAAC	TCAGCAGATG	2760	
CTTCTCTCCC	TCCACCGGGC	CCCACGTGCA	CCTAGCGTCC	CTGCCAGACC	CCTGCCAGCC	2820	
AAGCCTGCAC	TTAGGCAAGG	CCAGGGGACC	TGTAAGCCAA	ACCCCTCTCA	GAAGCCTCTG	2880	
CCTGCAGATC	CTCTGGCCAG	AACAACCTCG	CTCACTCATG	CCTTGGCCAG	GACCCAGGAA	2940	
CAATGGGAGA	CTGGGCTCGG	CCTGGCACCC	CTCAGACCTG	CTCCACAATA	TCCACACCAA	3000	
GTGCCCAGAT	CCACCCACAC	CGCCTATATT	AAGTGAGAAG	CCGACACCTT	TTTCAACAG	3060	
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	CCAGTAGGTT	ATTAGGTTG	GGAAGGTGG	TGTTTCTGTA	AGAAACCTAC	TGCCCAGGCA	3900
	CTGCAAAACCG	CCACCTCCCT	ATACTGCTTG	GAGCTGAGCA	AATCACCACA	AACTGTAATA	3960
	CAATGATCCT	GTATTCAGAC	AGATGAGGAC	TTTCCATGGG	ACCACAACTA	TTTTCAGATG	4020
5	TGAACCAITA	ACCAGATCTA	GTCAATCAAG	TCTGTTTACT	GCAAGGTTCA	ACTTATTAAC	4080
	AATTAGGCAG	ACTCTTTATG	CTTGCAAAAA	CTACAACCAA	TGGAATGTGA	TGTTTCATGGG	4140
	TATAGTTTCAT	GTCTGCTATC	ATTATTGCTA	GATATTGGAC	AAAGAACCTT	CTCTATGGGG	4200
	CATCCTCTTT	TTCCAACCTG	GCTGCAGGAA	TCTTTAAAG	ATGCTTTTAA	CAGAGTCTGA	4260
	ACCTATTCT	TAAACACTTG	CAACCTACCT	GTGAGCATC	ACAGAATGTG	ATAAGGAAAT	4320
10	CAACTTGCTT	ATCAACTTCC	TAAATATTAT	GAGATGTGGC	TTGGGCAGCA	TCCCCTTGAA	4380
	CTCTTCACTC	TTCAAATGCC	TGACTAGGGA	GCCATGTTTC	ACAAGGTCTT	TAAAGTGACT	4440
	AATGGCATGA	GAATAACAAA	AATACTCAGA	TAAGGTAAAA	TGCCATGATG	CCTCTGTCTT	4500
	CTGGACTGGT	TTTCACATTA	GAAGACAATT	GACAACAGTT	ACATAATTCA	CTCTGAGTGT	4560
	TTTATGAGAA	AGCCTTCTTT	TGGGGTCAAC	AGTTTTCCTA	TGCTTTGAAA	CAGAAAAATA	4620
15	TGTACCAAGA	ATCTTGTTT	GCCTTCCAGA	AAACAAAAC	GCATTTCACT	TTCCCGGTGT	4680
	TCCCCACTGT	ATCTAGGCAA	CATAGTATTC	ATGACTATGG	ATAAACTAAA	CACGTGACAC	4740
	AAACACACAC	AAAAGGGAAC	CCAGCTCTAA	TACATTCCAA	CTCGTATAGC	ATGCATCTGT	4800
	TTATTCTATA	GTTATTAGT	TCTTTAAAT	GTAAGCCAT	GCTGAAAAAT	AATACTGCTG	4860
	AGATACATAC	AGAATTACTG	TAAGTGATTA	CACTTGGTAA	TTGTACTAAA	GCCAAACATA	4920
20	TATATACTAT	TAAAAAGGTT	TACAGAAATT	TATGGTGAT	TACGTGGGCA	TTGCTTTTTT	4980
	AGATGCCCAA	ATCCTTAGAT	CTGGCATGTT	AGCCCTTCCT	CCAATTATAA	GAGGATATGA	5040
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Seq ID NO: 427 Protein sequence

Protein Accession #: NP_003465

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30	SKNHPEVLNI	RLQRESKELI	INLERNEGLI	ASSFTETHYL	QDGTVDVSLAR	NYTVILGHY	120
	YHGHVRGYS	SAVSLSTCSG	LRGLIVFENE	SVVLEPMKSA	TNRYKLPFAK	KLKSVRSGCG	180
	SHHNTFNLA	KNVFPFPPSQ	WARRHKRETL	KATKYVELVI	VADNREFORQ	GKDLKVKQR	240
	LIBIANHVDK	FYRPLNIRIV	LVGVEVWMDM	DKCSVSQDPF	TSLHEFLDWR	KMKLLPRKSH	300
	DNAQLVSGVY	FQGTITIGMAP	IMSCTADQS	GGIVMDHSDN	PLGAAVTLAH	ELGHNFGMNH	360
35	DTLDRGCSQ	MAVEKGGCIM	NASTGYFFPM	VFSSCSRKDL	ETSLEKMGV	CLFNLPEVRE	420
	FGGGQKCGNR	FVEEGEECD	GEPEECMNR	CNATCTLKPF	DAVCAHLGCC	EDQCLKPAGT	480
	ACRDSNSDC	LPEFTGASPF	HCPANVYLHD	GHSCQDVVDY	CYNGICQTHE	QQCVTLWPGS	540
	AKPAPGICFE	RVNSAGDPYG	NCGKVSXSS	AKCEMRDACC	GKIQCGGAS	RPVIGTNAVS	600
	IEINIPLOQ	GRILCRGTHV	YLGDMDPDP	LVLAGTKCAD	GKICLNROCC	NISVFGVHEC	660
40	AMQCHGRGVC	NNRNKNCHEA	HWAPPCDKF	FGGSGTDSGP	IRQADNQLGT	IGILVTILCL	720
	LAAGFVVYLK	RKTLIRLLFT	NKRTTIEKLR	CVRPSRPPRG	FQPCQALHGH	LKGLMRKFP	780
	DSYFPKDNPR	RLQCGGAGG	SRPLNGLNVP	PQSTQRLVLP	PLHRAPRAPS	VPARPLPAKP	840
	ALRQAGGTCK	PNPQKPLPA	DPLARTRLT	HALARTPGQW	ETGLRLAPLR	PAPQYPHQVP	900
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Seq ID NO: 428 DNA sequence

Nucleic Acid Accession #: NM_003714

Coding sequence: 135..1043

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	TAATACCAAG	AACCATGTGT	GCCGAGCGGC	TGGGCCAGTT	CATGACCTGT	GCTTTGGTGT	180
55	TGGCCACCTT	TGACCCGCGC	CGGGGACCCG	ACGCCACCAA	CCCACCCGAG	GGTCCCCAAG	240
	ACAGGAGCTC	CCAGCAGAAA	GGCCGCTGT	CCCTGCAGAA	TACAGCGGAG	ATCCAGCACT	300
	GTTTGGTCAA	CGCTGGCGAT	GTGGGGTGTG	GCCTGTTTGA	ATGTTTCGAG	AACAACTCTT	360
	GTGAGATTGG	GGGCTTACAT	GGGATTTGCA	TGACTTTTCT	GCACAACGCT	GGAAAAATTTG	420
	ATGCCCAGCG	CAAGTCATT	ATCAAGAGCG	CCTTGAAATG	TAAGGCCAC	GCTCTGCGGC	480
60	ACAGGTTCCG	CTGCATAAGC	CGGAAGTGCC	CGGCCATCAG	GGAAATGGTG	TCCCAGTTGC	540
	AGCGGGAATG	CTACCTCAAG	CACGACCTGT	GGCGGCTG	CCAGGAGAAC	ACCCGGGTGA	600
	TAGTGGAGAT	GATCCATTTC	AAGGACTTGC	TGCTGCACGA	ACCTTACGTG	GACCTCGTGA	660
	ACTTGTCTGT	GACCTGTGGG	GAGGAGGTGA	AGGAGGCCAT	CACCCACAGC	GTGCAGGTTT	720
	AGTGTGAGCA	GAACTGGGGA	AGCCTGTGCT	CCATCTTGAG	CTTCTGCACC	TCCGGCATCC	780
65	AGAAGCCTCC	CACGCGCGCC	CCCGAGCGCC	AGCCCCAGGT	GGACAGAAC	AAGCTCTCCA	840
	GGGCCCCACCA	CGGGGAAGCA	GGACATCACC	TCCCAGAGCC	CAGCAGTAGG	GAGACTGCGC	900
	GAGGTGCCAA	GGGTGAGCGA	GGTAGCAAGA	GCCACCCAAA	CGCCCATGCC	CGAGGCAGAG	960
	TCCGGGGCCT	TGGGGCTCAG	GGACCTTCCG	GAAGCAGCGA	GTGGGAAGAC	GAACAGTCTG	1020
	AGTATTCTGA	TATCCGAGG	TGAAATGAAA	GGCCTGGCCA	CGAAATCTTT	CCTCCACGCC	1080
70	GTCCATTTC	TTATCTATGG	ACATTCCAAA	ACATTTACCA	TTAGAGAGGG	GGGATGTAC	1140
	ACGCAGGATT	CTGTGGGGAC	TGTGGACTTC	ATCGAGGTGT	GTGTTCCGCG	AACGACAGG	1200
	TGAGATGGAG	ACCCCTGGGG	CCGTGGGGTC	TCAGGGGTGC	CTGGTGAATT	CTGCATTAC	1260
	ACGTACTCAA	GGGAGCGCGC	CCGCGTTATC	CTCGTACCTT	TGTCTTCTTT	CCATCTGTGG	1320
	AGTCAGTGGG	TGTCGGCGC	TCTGTTGTGG	GGGAGGTGAA	CCAGGGAGGG	GCAGGGCAAG	1380
75	GCAGGCCCC	CAGAGCTGGG	CCACACAGTG	GGTGCTGGGC	CTCGCCCGA	AGCTTCTGGT	1440
	GCAGCAGCCT	CTGGTGCTGT	CTCCGCGGAA	GTGAGGCGG	CTGATTCCA	GGACAGGAGT	1500
	GAATGTAAAA	ATAAATATCG	CTTAGAATGC	AGGAGAGGGG	TGGAGAGGAG	GCAGGGGCGG	1560
	AGGGGGTGCT	TGGTGCCAAA	CTGAAATTC	GTTTCTTGTG	TGGGGCCTTG	CGGTCAGAG	1620
	CTCTTGGCGA	GGGTGGAGGG	AGGAGTGTCA	TTTCTATGTG	TAATTTCTGA	GCCATTGTAC	1680
80	TGTCGCGGCT	GGGGGGGACA	CTGTCCAAGG	GAGTGGCCCC	TATGAGTTTA	TATTTAAACC	1740
	ACTGCTTCAA	ATCTCGATTT	CACTTTTTTT	ATTTATCCAG	TTATATCTAC	ATATCTGTCA	1800
	CTTAAATAAA	TGGCTTTCAA	ACAAAGCAAC	TGGGTCAATTA	AAACCAGCTC	AAAGGGGGTT	1860
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	TTAAAGCTA	TCAACACGCG	ACATAGCCAT	ACATCTGACT	GCCTGACATG	GACTCTCGCC	1980
	CACTTGGGGG	AAACCTTATA	CCCAGAGGAA	AATACACACC	TGGGGAGTAC	ATTTGACAAA	2040
85	TTTCCCTTAG	GATTTCTGTA	TCTCACCTTG	ACCCTCAGCG	AAGATTGGTA	AAGCTGCGTC	2100
	CTGGCGATT	CAGGAGACCC	AGCTGGAAC	CTGGCTTCTC	CATGTGAGGG	GATGGGAAAG	2160
	GAAAGAGAG	AATGAAGACT	ACTTAGTAAT	TCCCATCAGG	AAATGCTGAC	CTTTTACATA	2220

WO 02/086443

PCT/US02/12476

AAATCAAGGA GACTGCTGAA AATCTCTAAG GGACAGGATT TTCCAGATCC TAATTGGAAA 2280
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 GGGAGAGGAA GAAAGAAGAG AGAGAAAAGA GCCTCGTGCC

5 Seq ID NO: 429 Protein sequence
 Protein Accession #: NP_003705

1 11 21 31 41 51
 10 MCAERLQGM TLALVLATFD PARGTDATNP PEGPQDRSSQ QKGRLSLQNT AEIQHCLVNA 60
 GDVGGGVPEC FENNSEIRG LHGICMTFLH NAGKFDAGQK SFIKDALKCK AHALRHRFGC 120
 ISRKCPAIRE MVSQLQRECY LKHDLCAAAQ ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT 180
 CGEEVKCAIT HSVVQVCEQN WGSILCSILSF CTSAIQKPPT APPERQPVVD RTKLSRAHHG 240
 EAGHHLPEPS SRETGRGAKG ERGSKSHPNH HARGRVGGLG AQGPSGSSEW EDEQSEYSDI 300
 15 RR

Seq ID NO: 430 DNA sequence
 Nucleic Acid Accession #: NM_005940
 Coding sequence: 23..1489

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 25 AAGCCACGCA GCGCCGGGGC GGATGGCTCC GGCCGCGCTGG CTCCGCAGCG CGGCCGCGCG 60
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 TCTGCGCGCG GAGCTCCACC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCTGGCATGC 180
 AGCCCTGCCC AGTAGCCCGG CACCTGCCCC TGCCACGCGA GAAGCCCCCG GGCTGCGCAG 240
 CAGCCTCAGG CCTCCCGCT GTGGCGTGCC CGACCCATCT GATGGGTGA GTGCCGCGCA 300
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 30 CCTAAAGGTA TGGAGCGATG TGACGCCACT CACCTTTACT GAGGTGCAAG AGGGCCGTGC 480
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 TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACTT 600
 CGACTATGAT GAGACCTGGA CTATCGGGGA TGACCAAGGC ACAGACCTGC TGCAGGTGGC 660
 AGCCCATGAA TTTGGCCACG TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCCTGAT 720
 35 GTCCGCCTTC TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGATGACT GCAGGGGCGT 780
 TCAACACCTA TATGGCCAGC CTGGGCCACG TGTCACTCC AGGACCCGAG CCCTGGGCCC 840
 CCAGGCTGGG ATAGACACCA ATGAGATTGC ACGCTGGAG CCAGACGCCC CGCCAGATGC 900
 CTGTAGGGCC TCCTTTGAGC CGTCTCCAC CATCCGAGGC GAGCTCTTTT TCTTCAAAGC 960
 40 GGGCTTTTGG TGGCGCCTCC GTGGGGGCCA GCTGCAGCCC GGCTACCCAG CATTTGGCCTC 1020
 TCGCCACTGG CAGGACATGC CCAGCCCTGT GGAAGCTGCC TTGAGGATG CCCAGGGGCA 1080
 CATTGTGTTT ATCCAAAGTG CTGAGTACTG GGTGTACGAC GGTGAAAGC CAGTCTCTGG 1140
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 GGGTCCCGAG AAGAACAAGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTTCACACC 1260
 45 CAGCACCCGG CGTGTAGACA GTCCCGTGCC CGCAGGGGCC ACTGACTGGA GAGGGGTGCC 1320
 CTCTGAGATC GAGCTGCCTT TCCAGGATGC TGATGGCTAT GCCTACTTCC TGCGCGGCGG 1380
 CCTCTACTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCGTCTCGT 1440
 GGGTCTGAG TTCTTTGGCT GTGCCGAGCC TGCCAACTCT TTCTCTGAC CATGGCTTGG 1500
 ATGCCCTCAG GGGTGTCTGAC CCTGTCCAGG CCAAGAAATAT CAGGCTAGAG ACCCATGGCC 1560
 50 ATCTTTTGGG CTGTGGGCAC CAGGCATGGG ACTGAGCCCA TGCTCTCTGC AGGGGATGG 1620
 GGTGGGGTAC AACCACCATG ACAACTGCCG GGAGGGGCCA GCAGGTCTGT GTCCACTGCC 1680
 AGCGACTGTC TCAGACTGGG CAGGGAGGCT TTGGCATGAC TTAAGAGGAA GGGCAGTCTT 1740
 GGGACCCGCT ATGCAGTCTC TGGCAAACTT GGTGCCCCTG TCTCATCCCT GTCCCTCAGG 1800
 GTAGCACCAT GGCAGACTCG GGGGAACTGG AGTGTCTTTC CTGTATCCCT GTTGTGAGGT 1860
 55 TCCTTCCAGG GGTGCGCACT GAAGCAAGGG TGCTGGGGCC CATGGCCCTT CAGCCCTGGC 1920
 TGAGCAACTG GGTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCCTGC 1980
 ATCTGTCTGC CTCTGCTGCG ACAATCTTGG AAATCTGTTC TCCAGAAATC AGGCCAAAAA 2040
 GTTACAGTCT AAATGGGGAG GGGTATTTCT CATGCAAGAG ACCCCAGGCC CTGGAGGCTG 2100
 CAACATACCT CAATCTGTGC CCAGGCCGGA TCCTCTCTGA GCCCTTTTCG CAGCACTGCT 2160
 60 ATCTTCCAAA GCCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCTTTTTTT 2220
 TTTTAAACT GAGGATTGTC ATTAACACAA GTTGTTTTCT

Seq ID NO: 431 Protein sequence
 Protein Accession #: NP_005931

65 1 11 21 31 41 51
 70 MAPAAWLRS AARALLPPML LLLLQPPPLL ARALPPDVHH LHAERRGPQP WHAALPSSPA 60
 PAPATQEAPR PASSLRPPRC GVPDPSDGLS ARNRQKRFVL SGGRWEKTDL TYRILRFPWQ 120
 LVQEQVRQTM AEALKVWSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLFP DPGGILAHA 180
 75 PFPKTHREGD VHFYDETWT IGDDQGTDL QVAAHEFGHV LGLQHTTAAK ALMSAFYTFR 240
 YPLSLSPDDC RGVQHLVQGP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACBASFDA 300
 VSTIRGELFF FKAGFVWRLR GGQLQPGYPA LASRHWQGLP SPVDAAPEDA QGHIWFFQGA 360
 QYWWYDGEKP VLGPAPLTEL GLVRFPPVHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVD 420
 80 PVPRRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFDP VKVKALEGFP RLVGPDFFGC 480
 AEPANTFL

Seq ID NO: 432 DNA sequence
 Nucleic Acid Accession #: NM_024022
 Coding sequence: 202..1563

80 1 11 21 31 41 51
 85 ACCGGGCACC GGACGGCTCG GGTACTTTCG TTCTTAATTA GGTTCATGCC GTGTGAGCCA 60
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACGTGGGC TACTATCTCT TCCGCTGGTG 120
 CCATCTACAT TTTTGGGATC CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCGGATGTC 180
 AGAGTCTCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCTCTTC 240
 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCTGTGTGC ACCAGATGCA 300

	GATGCTGTTG	CTGCACAGAT	CCTGTCACTG	CTGCCATTGA	AGTTTTTTTC	AATCATCGTC	360
	ATTGGGATCA	TTGCATTGAT	ATTAGCACTG	GCCATTGGTC	TGGGCATCCA	CTTCGACTGC	420
	TCAGGGAAGT	ACAGATGTCT	CTCATCCTTT	AAGTGTATCG	AGCTGATAGC	TCGATGTGAC	480
5	GGAGTCTCGG	ATTGCAAGA	CGGGGAGGAC	GAGTACCGCT	GTGTCCGGGT	GGGTGGTCAG	540
	AATGCCGTGC	TCCAGGTGTT	CACAGCTGCT	TCGTGGAAGA	CCATGTGCTC	CGATGACTGG	600
	AAGGGTCACT	ACGCAAAATG	TGCCTGTGCC	CAACTGGGTT	TCCCAAGCTA	TGTGAGTTCA	660
	GATAACCTCA	GAGTGAGCTC	GCTGGAGGGG	CAGTTCCGGG	AGGAGTTTGT	GTCCATCGAT	720
	CACCTCTTGC	CAGATGACAA	GGTGACTGCA	TTACACCACT	CAGTATATGT	GAGGGAGGGA	780
10	TGTGCCCTCTG	GCCACGTGGT	TACCTTGACG	TGCACAGCCT	GTGGTCATAG	AAGGGGCTAC	840
	AGCTCACGCA	TCGTGGGTGG	AAACATGTCC	TTGCTCTCGC	AGTGGCCCTG	GCAGGCCAGC	900
	CTTCAGTTCC	AGGGCTACCA	CCTGTGCGGG	GGCTCTGTCA	TCAGCCCCCT	GTGGATCATC	960
	ACTGTGTCAC	ACTGTGTTTA	TGACTTGTAC	CTCCCCAAGT	CATGGACCAC	CCAGGTGGGT	1020
	CTAGTTTCCC	TGTTGGACAA	TCCAGCCCCA	TCCCACCTGG	TGGAGAAGAT	TGTCTACCA	1080
15	AGCAAGTACA	AGCCAAAGAG	GCTGGGCAAT	GACATCGCCC	TTATGAAGCT	GGCCGGGCCA	1140
	CTCACGTTCA	ATGAAATGAT	CCAGCCTGTG	TGCCCTGCCA	ACTCTGAAGA	GAACTTCCCC	1200
	GATGGAAAG	TGTGCTGGAC	GTGAGGATGG	GGGGCCACAG	AGGATGGAGG	TGACGCCCTC	1260
	CCTGTCTTGA	ACCACGGGGC	CGTCCCTTTG	ATTTCCAACA	AGATCTGCAA	CCACAGGGAC	1320
	GTGTACGGTG	GCACTGCTC	CCCTCCATG	CTCTGCGCGG	GCTACCTGAC	GGGTGGCGTG	1380
20	GACAGCTGCC	AGGGGGACAG	CGGGGGGCC	CTGGTGTGTC	AAGAGAGGAG	GCTGTGGAAG	1440
	TTAGTGGGAG	CGACCAGCTT	TGGCATCGGC	TGCGCAGAGG	TGAACAAGCC	TGGGGTGTAC	1500
	ACCCGTGTCA	CCTCCTTCTT	GGACTGGATC	CACGAGCAGA	TGGAGAGAGA	CCTAAAAACC	1560
	TGAAGAGGAA	GGGGACAAAT	AGCCACCTGA	GTTCCTGAGG	TGATGAAGAC	AGCCCGATCC	1620
	TCCCCTGGAC	AGAGACAGGT	GAACTTGCAC	ACGAGCAGAC	ACCCTTGGAG	CTCTGAGTTC	1680
25	CGGCACCACT	AGCAGGCCCG	AAAGAGGCAC	CCTTCCATCT	GATTCCAGCA	CAACCTTCAA	1740
	GCTGCTTTTT	GYTTTTTGT	TTTTTGAGGT	GGAGTCTCGC	TCTGTTGCC	AGGCTGGAGT	1800
	GCAGTGGCGA	AATCCCTGCT	CACGTGAGCC	TCCGCTTCCC	TGGTTCAAGC	GATTCTCTTG	1860
	CCTCAGCTTC	CCAGTAGCT	GGGACCAAG	GTGCGCCGCA	CCACACCCAA	CTAATTTTTG	1920
	TATTTTATGT	AGAGACAGGG	TTTACCAGTG	TTGGCCAGGC	TGCTCTCAA	CCCTGACCT	1980
30	CAAAATGATG	GCCTGCTTCA	GCCTCCACCA	GTGCTGGGAT	TACAGGCATG	GGCCACCACG	2040
	CCTAGCCTCA	CGCTCCTTTC	TGATCTTCAC	TAAGAACAAC	AGAAGCAGCA	ACTTGCAAGG	2100
	GGGGCCTTTC	CCACTGGTCC	ATCTGGTTTT	CTCTCCAGGG	GTCTTGCAAA	ATTCTGACG	2160
	AGATAAGCAG	TTATGTGACC	TCACGTGCAA	AGCCACCAAC	AGCCACTCAG	AAAAGACGCA	2220
	CAGGCCGAGA	AGTGACAGAC	TGCACTCACT	GCACGTTTTT	ATCTCTAGGG	ACCAGAACCA	2280
35	AACCCACCTT	TTCTACTTCC	AAGACTTATT	TTACATGTG	GGGAGGTTAA	TCTAGGAATG	2340
	ACTCGTTTAA	GGCCTATTTT	CATGATTTCT	TTGTAGCATT	TGGTGTGTTG	CGTATTATTG	2400
	TCCTTTGATT	CCAAATAATA	TGTTTCCTTC	CCTCAAAAAA	AAAAAATAAA	AAAAAATAAA	2460
	AAAAA						

Seq ID NO: 433 Protein sequence
Protein Accession #: NP_076927

	1	11	21	31	41	51	
45	MGENDPPAVE	APFSFRSLFG	LDDLKISPVA	PDADAVAAQI	LSLLFLKFFP	IIVIGIIALI	60
	LALAIGLTH	FDCSGKYRCR	SSPKCIELIA	RCDGVSDDCK	GEDEYRCVRV	GGQNAVQLQV	120
	TAASWKTMCS	DDWKGHYANV	ACAQLGFPSY	VSSDNLRVSS	LEQQFREEFV	SIDHLLPDDK	180
	VTALHHSYVY	REGGASGHVY	TLQCTACGHR	RGYSSRIVGG	NMSLLSQWPW	QASLQFPQYH	240
	LCGGSVITPL	WIITAAHCVY	DLXLPKSWTI	QVGLVSLLDN	PAPSHLVEKI	VYHSKYKPKR	300
50	LGNDIALMKL	AGPLTFNEMI	QPVCLPNSEE	NFPDQKVCWT	SGWGATEDGG	DASPLVNHAA	360
	VPLISNKKIN	HRDVGGLIIS	PSMLCAGYLT	GGVDSQQGDS	GGPLVCQERR	LWKLVGATSF	420
	GIGCAEVNKP	GVYTRVTSFL	DWIHEQMERD	LKT			

Seq ID NO: 434 DNA sequence
Nucleic Acid Accession #: NM_000493.2
Coding sequence: 97..2139

	1	11	21	31	41	51	
60	CACCTTCTGC	ACTGCTCATC	TGGGCAGAGG	AAGCTTCAGA	AAGCTGCCAA	GGCACCATCT	60
	CCAGGAATCT	CCAGCAGGCA	GAATCCATCT	GAGAATATGC	TGCCACAAT	ACCCTTTTTC	120
	CTGCTAGTAT	CCTTGAACCT	GGTTCATGGA	GTGTTTTACG	CTGAACGATA	CCAAATGCCC	180
	ACAGGCATAA	AAGGCCCACT	ACCCAAACACC	AAGACACAGT	TCTTCATTCC	CTACACCATA	240
	AAGAGTAAAG	GTATAGCAGT	AAGAGGAGAG	CAAGGTACTC	CTGGTCCACC	AGGCCCTGCT	300
65	GGACCTCGAG	GGACCCAGG	TCCTTCTGGA	CCACCAAGGA	AACCAGGCTA	CGGAAGTCCT	360
	GGATCCCAAG	GAGAGCCAGG	GTTGCCAGGA	CCACCGGGAC	CATCAGCTGT	AGGGAAACCA	420
	GGTGTGCCAG	GACTCCACAG	AAAACCAAGG	GAGAGAGGAC	CATATGGACC	AAAAGGAGAT	480
	GTTGGACCA	CTGGCCTACC	AGGACCCCGG	GGCCACCCAG	GACCACTTGG	AATCCCTGGA	540
	CCGGCTGGAA	TTTCTGTGCC	AGGAAAACCT	GGACAAACAG	GACCCACAGG	AGCCCCAGGA	600
70	CCCAGGGGCT	TTCCTGGAGA	AAAGGGTGCA	CCAGGAGTCC	CTGGTATGAA	TGGACAGAAA	660
	GGGGAAATGG	GATATGGTGC	TCCTGGTGGT	CCAGGTGAGA	GGGGTCTTCC	AGGCCCTCAG	720
	GGTCCCACAG	GACCATCTGG	CCCTCCTGGA	GTGGGAAAAA	GAGGTGAAAA	TGGGGTTCCA	780
	GGACAGCCAG	GCATCAAAGG	TGATAGAGGT	TTTCCGGGAG	AAATGGGACC	AATTGGCCCA	840
	CCAGGTCCCC	AAGGCCCTCC	TGGGGAACGA	GGGCCAGAAG	GCATTGGAAA	GCCAGGAGCT	900
75	GCTGGAGCCC	CAGGCCAGCC	AGGGATTCCA	GGAAACAAAG	GTCTCCCTGG	GGCTCCAGGA	960
	ATAGCTGGGC	CCCCAGGGCC	TGCTGGCTTT	GGGAAACCA	GCTTGGCAGG	CCTGAAAGGA	1020
	GAAAGAGGAC	CTGCTGGCCT	TCCTGGGGGT	CCAGGTGCCA	AAGGGGAACA	AGGGCCAGCA	1080
	GGTCTTCTTG	GGAAGCCAGG	CTGACTGGA	CCCCCTGGGA	ATATGGGACC	CCAAGGACCA	1140
80	AAAGGCATCC	CGGGTAGCCA	TGGTCTCCCA	GGCCCTAAAG	GTGAGACAGG	GCCAGCTGGG	1200
	CCTGCAAGAT	ACCTTGGGGC	TAAGGGTGAA	AGGGGTTCCT	CTGGGTGAGA	TGGAAAAACA	1260
	GGGTACCCAG	GAAACACAGG	TCTCGATGGT	CCTAAGGGTA	ACCCAGGGTT	ACCAGGTCCA	1320
	AAAGGTGATC	CTGAGTTTGG	AGGACCTCCT	GGTCTCCACG	GCCCTGTGGG	CCCAGCAGGA	1380
	GCAAGGGGAA	TGCCCGGACA	CAATGGAGAG	GCTGGCCCAA	GAGGTGCCCC	TGGAATACCA	1440
85	GGTACTAGAG	GCCCTATTGG	GCCACCAAGC	ATTCCAGGAT	TCCCTGGGTC	TAAAGGGGAT	1500
	CCAGGAAGTC	CGGTCTCTCC	TGGCCACAGT	GGCATAGCAA	CTAAGGGGCT	CAATGGACCC	1560
	ACCGGGCCAC	CAGGTCTCTCC	AGGTCCAAGA	GGCCACTCTG	GAGAGCCTGG	TCTTCCAGGG	1620
	CCCCCTGGGC	CTCCAGGCC	ACCAGGTCAA	GCAGTCATGC	CTGAGGGTTT	TATAAAGGCA	1680
	GGCCAAAGGC	CCAGTCTTTC	TGGGACCCCT	CTTGTTAGTG	CCAACCAAGG	GGTAAACAGGA	1740

ATGCTGTGT CTGCTTTTAC TGTATTCTC TCCAAAGCTT ACCCAGCAAT AGGAAGTCCC 1800
 ATACCATTTG ATAAAATTTT GTATAACAGG CAACAGCATT ATGACCCCAAG GACTGGAATC 1860
 TTTACTTGTG AGATACCAGG AATATACTAT TTTTCATACC ACGTGCATGT GAAAGGGACT 1920
 CATGTTTGGG TAGGCTGTGA TAAGAATGGC ACCCTCTGTA TGTACACCTA TGATGAATAC 1980
 ACCAAAGGCT ACCTGGATCA GGCTTCAGGG AGTGCCATCA TCGATCTCAC AGAAAATGAC 2040
 CAGGTGTGGC TCCAGCTTCC CAATGCCGAG TCAAATGGCC TATACTCCTC TGAGTATGTC 2100
 CACTCTCTCT TCTCAGGATT CCTAGTGGCT CCAATGTGAG TACACCCACC AGAGCTAATC 2160
 TAAATCTTGT GCTAGAAAAA GCATTCTCTA ACTCTACCCC ACCCTACAAA ATGCATATGG 2220
 AGGTAGGCTG AAAAGAATGT AATTTTATT TTCTGAAATA CAGATTGAG CTATCAGACC 2280
 AACAAACCTT CCCCCTGAAA AGTGAGCAGC AACGTAAAAA CGTATGTGAA GCCTCTCTTG 2340
 AATTTCTAGT TAGCAATCTT AAGGCTCTTT AAGGTTTCTT CCAATATTAA AAAATATCAC 2400
 CAAAGAGTC CTGCTATGTT AAAAACAAAC AACAAAAAAC AAAGCAACAA AAAAAAAAT 2460
 TAAAAAATA AACAGAAATA GAGCTCTAAG TTATGTGAAA TTGATTGGA GAACTCGGC 2520
 ATTTCTTTT TAAAAAGCC TGTTTCTAAC TATGAATATG AGAAGCTCTA GGAACATCC 2580
 AGGAGGTATC ATATAACTTT GTAGAACTTA AATACTTGAA TATTCAAATT TAAAGACAC 2640
 TGTATCCCTT AAAATATTTC TGATGGTGCA CTACTCTGAG GCCTGTATGG CCCCTTCAT 2700
 CAATATCTAT TCAATATATC AGGTGCATAT ATACTTGTTA AAGCTCTTAT ATAAAAAGC 2760
 CCCAAAATAT TGAAGTTTCA CTGAAATGCA AGGTGCTTTC ATCAATGAAC CTTTCAAAA 2820
 CTTTCTATG ATTGCAGAGA AGCTTTTAT ATACCCAGCA TAACTTGGA ACAGGTATCT 2880
 GACCTATTCT TATTTAGTTA ACACAAGTGT GATTAAATTG ATTTCTTTAA TTCCTTATTG 2940
 AATCTTATGT GATATTGATT TCTGGATTGA CAGAACATTA GCACATGTAC CTGTGCGCTC 3000
 CCATCAAGT GAAGTTATTA TTTACACTGA GGGTTTCAA ATTCTAGTAG AAGTGGAGAT 3060
 ATATTATTTA TTTATGCACT GTACTGTATT TTTATATTGC TGTTTAAAA TTTTAAGCTG 3120
 TGCTCACTT ATTAAGCAC AAAATGTTT ACCTACTCCT TATTACGAC ACAATAAAAT 3180
 AACATCAATA GATTTTAGG CTGAATTAAT TTGAAAGCAG CAATTGCTG TTCTCAACCA 3240
 TCTTTCAAG GCTTTTCAAT CGACACAATA AAATAACATC AATAG

Seq ID NO: 435 Protein sequence
 Protein Accession #: NP_000484.2

1 11 21 31 41 51
 MLPIPIPLLL VSLNLVHGVF YAERYQMPTG IKGFLPNTKT QFFIPYTIKS KGIIVRGEQG 60
 TPQPPPGAPG RHHPGSGPP GKPGYGSPLG QGEPGLPGPP GPSAVGKPGV PGLPGKPER 120
 GPYGPVKDVG PAGLPGRPRG PGPPGIPGPA GISVPGKPGQ QGPTGAPGPR GPPGKGPAP 180
 VPGMNGQKGE MGYGAPGRPG ERGLPGPQGP TGPSGPPGVG XRGENGVPQ PGIKGRDGF 240
 GEMGPIPPG PQGPPGERPG EGIGKFGAAG APGQPGIPGT KGLPGAPGIA GPPGPPGFGK 300
 PGLPGLKGER LPAGLPGGPG AKGEQGPAGL PGKPLGTGPP GNMGPQGPKG IPGSHGLFPG 360
 KGETGPAGPA GYPGAXGERG SPGSDGKPGY PGKPLDGPK GNPGLGPKG DPGVGGPPGL 420
 PGPVGPAGAK GMPGHNGEAG PRGAPGIPGT RSPGPPGIP GPPGSKGDPG SPGPPGPGI 480
 ATKGLNGPTG PPGPPGPRGH SGEPGLPGPP GPPGPPGQAV MPEGPIKAG RPSLSGTPLV 540
 SANQVGTGMP VSAFTVILSK AYPAIGTPIP FDKILYNRQ HYDPRGTGIFT CQIPGIYFYS 600
 YHVHVKGTHV WVGLYKNGTF VMYTYDEYTK GYLDQASGSA IIDLTENDQV WLQLPNAESN 660
 GLYSSEVHVS SFSGLVLPAM

Seq ID NO: 436 DNA sequence
 Nucleic Acid Accession #: XM_062811
 Coding sequence: 1..888

1 11 21 31 41 51
 ATGTGGGGCG CTGCGCGCTC GTCCGCTCTC TCATCCTGGA ACGCCGCTTC GCTCCTGCAG 60
 CTGCTGCTGG CTGCGCTGCT GCGCGCGGGG GCGAGGGCCA GCGGCGAGTA CTGCCACGGC 120
 TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 180
 GGCGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 240
 GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGCGGCTGG CGAGCCTGGC 300
 CGGCGGACCA AAGACGGCCC CGACGGCTCG GCAGTGCCCA TCTACGTGCC GTTCCTCATT 360
 GTTGGCTCCG TGTTTTCTGC CTTTATCATC TTGGGGTCCC TGTGTGCAGC CTGTTGCTGC 420
 AGATGTCTCC GGCTTAAGCA GGATCCCCAG CAGAGCCGAG CCCCAGGGGG TAACCGCTTG 480
 ATGGAGACCA TCCCATGAT CCCCAGTGCC AGCACTCCC GGGGGTCCGT CTCACGCCAG 540
 TCCAGCACAG CTGCCAGTTC CAGCTCCAGC GCCAATCAG GGGCCCGGGC GCCCCCAACA 600
 AGGTACAGAG CCACTGTGTT CTGCGCGGAA GGGACCATGA ACAACGTGTA TGTCAACATG 660
 CCCACGAATT TCTCTGTGCT GAACTGTGAG CAGGCCACCC AGATTGTGCC ACATCAAGGG 720
 CAGTATCTGC ATCCCCATA CGTGGGGTAC ACGGTGCAGC ACGACTCTGT GCCCATGACA 780
 GCTGTGCCAC CTTTCATGGA CGGCTGCAG CCGGCTACA GGCAGATTCA GTCCCCCTTC 840
 CCTCACACCA ACAGTGAACA GAAGATGTAC CCAGCGGTGA CTGTATAA

Seq ID NO: 437 Protein sequence
 Protein Accession #: XP_062811

1 11 21 31 41 51
 MWGARRSSVS SSWNAASLLQ LLLAALLAAG ARASGEYCHG WLDAQGVWRI GFQCPERFDG 60
 GDAITCCGSC ALRYCCSSAE ARLDQGGCDN DRQQGAGEPG RADKDGPDGS AVPIYVPFLI 120
 VGSVFVAFII LGSLVAACCC RCLRPKQDFQ QSRAPGGNRL METIPMIPSA STSRGSSSRQ 180
 SSTAASSSSS ANSGARAPPT RSQTNCLPE GTMNNVVNM PTNFSVLNCO QATQIVPHQG 240
 QYLHPPYVGY TVQHDSVPMT AVPPFMDGLQ PGYRQIQSPF PHTNSEQKMY PAVTV

Seq ID NO: 438 DNA sequence
 Nucleic Acid Accession #: NM_004004.1
 Coding sequence: 1..681

1 11 21 31 41 51
 ATGGATTGGG GCACGCTGCA GACGATCCTG GGGGGTGTGA ACAAACTCTC CACCAGCATT 60
 GGAAAGATCT GGCTCACCGT CCTCTTCATT TTTGCGATTA TGATCCTCGT TGTGGCTGCA 120
 AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTTGTCTGCA ACACCTGCA GCCAGGCTGC 180

AAGAACGTGT GCTACGATCA CTACTTCCCC ATCTCCACA TCCGGCTATG GGCCTGCGAG 240
 CTGATCTTCG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACGTGGCCTA CCGGAGACAT 300
 GAGAGAGAAG GGAAGTTCAT CAAGGGGGAG ATAAAGAGTG AATTTAAGGA CATCGAGGAG 360
 ATCAAAACCC AGAAGGTCOG CATCGAAGGC TCCCTGTGGT GGACCTACAC AAGCAGCATC 420
 TTCTTCCGGG TCATCTTCGA AGCCGCCCTC ATGTAGCTCT TCTATGTCA GTACGACGGC 480
 TTCTCCATGC AGCGGCTGGT GAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC 540
 TTTGTGTCCC GGGCCACGGA GAAGACTGTC TTCACAGTGT TCATGATTGC AGTGTCTGGA 600
 ATTTGCATCC TGCTGAATGT CACTGAATTG TGTATTTCG TAATTAGATA TTGTTCTGGG 660
 AAGTCAAAAA AGCCAGTTTA A

Seq ID NO: 439 Protein sequence
 Protein Accession #: NP_003995.1

1 11 21 31 41 51
 MDWGTQLTIL GGVNKHSTSI GKILVTLVFI PRIMILVVAA KEVWGDEQAD FVCNTLQPGC 60
 KNVCYDHYFP ISHIRLWALQ LIFVSSPALL VAMHVAYRRH EKRRKFIKGE IKSEPKDIEE 120
 IKTKVRIEIG SLWWTYTSIS FFRVPEAAP MYVIFYMYDG FSMQRLVKCN ANPCPNTVDC 180
 FVSRPTEKTV FTVFMIAVSG ICILLNVTEL CYLLIRYCSG KSKKPV

Seq ID NO: 440 DNA sequence
 Nucleic Acid Accession #: XM_061091.1
 Coding sequence: 1..2481

1 11 21 31 41 51
 ATGCCAAATA CTTACAGAAC AACCAGGATT GAAATTTGGC TTCTCCAAGA GCCGCCCGGG 60
 CACCGAGCGC TGGTGCCTCG TCTCCTTCCG GTGAGTCCCA GCCCGAGATT GGCTCTGGCG 120
 CCGGGTACC CGCCAGTGCC GGCTGCCGAT GACCCGATTCA CGCTCCCGAT GATTGGAGGT 180
 CAGATGCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTTA 240
 GTTGGGAAGC CTCCTTTTGA GGCACACGAA GTCCATGTAA GCAAGAAAC CATCGGGAAG 300
 ATTTACAGTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTCTGTGTA 360
 GATGGGTCTA ACAGCGTCGG GAAAGGGAGC TTTGAAAGGT CCAAGCACTT TGCCATCACA 420
 GTCTGTGACG GTCTGGACAT CAGCCCCGAG AGGGTCAGAG TGGGAGCATT CCAGTTCACT 480
 TCCACTCTCT ATCTGGAAAT CCCCTTGGAT TCATTTTCAA CCAACACGGA AGTGAAGGCA 540
 AGAATCAAGA GGATGGTTTT CAAAGGAGGG CGCACGGAGA CGGAACCTGC TCTGAAATAC 600
 CTCTGCACA GAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660
 GTCACTGATG GGAAGTCCCA GGGGATGTG GCACCTGCCAT CCAAGCAGCT GAAGGAARAG 720
 GGTGTCACTG TGTGTGCTGT GGGGTCAGG TTTCCAGAGT GGGAGGAGCT GCATGCACTG 780
 GCCAGCGGCG CTAGAGGAGC GCACGTGCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC 840
 GGCCTCTTCA GCACCTCAG CAGCTCGGCC ATCTGTCCA GCGCCACGCC AGCTGGGAGC 900
 CCGAGCTTG TCTTCATGGA GCGGTTAATG GGCATCTCTC TGATAGGCCC CTGTGACTCG 960
 CAGCCCTGCC AGAATGGAGG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTGCTCT 1020
 TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG 1080
 GTCGACCTCG TCTTCTGCTT GGACAGCTCT GCGGGCACCA CTCTGGACGG CTTCCTCGCG 1140
 GCCAAAGTCT TGGTGAAGCG GTTGTGTCGG GCGGTGCTGA GCGAGGACTC TCGGGCCCGA 1200
 GTGGGTGTGG CCACATACAG CAGGGAGCTG CTGGTGGCGG TGCTGTGGGG GGAGTACCAG 1260
 GATGTGCTCG ACCTGGCTCG GAGCCTCGAT GGCATTCCCT TCCGTGGTGG CCCCACCCTG 1320
 ACGGGCAGTG CCTTGCAGCA GCGGCGAGAG CGTGGCTTCG GGAGCGCCAC CAGGACAGGC 1380
 CAGGACCGGC CACGTAGAGT GGTGGTTTGG CTCACTGAGT CACACTCCGA GGATGAGGTT 1440
 GCGGGCCCGA CCGCTCACGC AAGGGCGCGA GAGCTGTCTC TGCTGGGTGT AGGCAGTGAG 1500
 GCGGTGCGGG CAGAGCTGGA GGAGATCACA GGCAGCCCAA AGCATGTGAT GGTCTACTCG 1560
 GATCCTCAGG ATCTGTTCAA CCAAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG 1620
 CGGCGAGGGT GCGCGACACA AGCCCTGGAC CTGCTCTTCA TGTGGACAC CTCTGCCTCA 1680
 GTAGGGCCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT 1740
 GAGGTGAACC CTGAGGTGAC ACAGGTGCGC CTGGTGGTGT ATGGCAGCCA GGTGCAGACT 1800
 GCCTTCGGGC TGGACACCAA ACCCACCGG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC 1860
 CCTTACCTAG GTGGGGTGGG CTCAGCCGCG ACCGCCCTGC TGACATCTTA TGACAAAGTG 1920
 ATGACCGTCC AGAGGGGTGC CCGGCTTGGT GTCCCAAAAG CTGTGGTGGT GCTCACAGGC 1980
 GGGAGAGGCG CAGAGGATGC AGCCGTTTCT GCCCAGAAGC TGAGGAACAA TGGCATCTCT 2040
 GTCTTGTGCG TGGGCGTGGG GCCTGTCTTA AGTGAGGGTC TGCGGAGGCT TGCAAGTCCC 2100
 CGGGATTCCC TGATCCACGT GGCAGCTTAC GCGACCTGCG GGTACCAACA GGACGTGCTC 2160
 ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG CCACTCAACC TCTGCAAAAC CAGCCCGTGC 2220
 ATGAATGAGG GCAGCTGCGT CCTGCAGAAAT GGGAGCTACC GCTGCAAGTG TCGGATGGC 2280
 TGGGAGGCGC CCCACTGCGA GAACCGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG 2340
 GGATGGATTG TTGAGACGCC CTGAGGCGAC ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT 2400
 ACCCTGCCCA GCAACTACAG AGAAGGCCCTG GGCACGTAAA TGGTGCCTAC CTTCTGGAAT 2460
 GTCGTGTCGC CAGGTCTCTA G

Seq ID NO: 441 Protein sequence
 Protein Accession #: XP_061091.1

1 11 21 31 41 51
 MPNTSGTTRI EIWLLEPPG HRLVAALLP VSPSPALALA PGYPPVPAAD DRFTLPMIGG 60
 QMHGEKVDLW SLGVLYEYFL VGKPPPEANE VHVSKETIGK ISAASKMMC SAAVDIMFLL 120
 DGSNSVKGGS FERSKHFAIT VCDGLDISFE RVRVGAQFQS STPHLEFPD SFSTQQEVKA 180
 RIKRMVFKGG RTETELALYK LLHRLPGGR NASVPQILII VTDGKSGQDV ALPSKQLKER 240
 GVTVPFVGVFR FPRWEELHAL ASEPRGQHVLA EQVEDATN GLFSTLSSSA ICSSATPAGS 300
 PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAFGGEAN CALKLSLECR 360
 VDLEFLDLSS AGTTLDGFLR AKVFVKRFVR AVLSEDSRAR VGVATYSREL LVAVFVGEYQ 420
 DVPLDVSLD GIPFRGGPTL TGSALRQAAE RGFSAATRTG QDRPRRVVL LTESHSEDEV 480
 AGPARHARAR ELLELLGVGSE AVRAELEBIT GSPKHMVVS DPQDLFNQIP ELQGLKCSRQ 540
 RFGCRTQALD LVFMLDTSAS VGPFNAQMQ SFVRSALQF EVNPDVTQVG LVVYGSQVQT 600
 AFGLDTKPTR AAMLRALISA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG 660
 GRGAEDAAVP AQRLLRNGIS VLVVGVGPVL SEGRLRLAGP RDSLIHVAAY ADLRYHQDVL 720

IEWLCEGEAKQ PVNLCRPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVSQ 780
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Seq ID NO: 442 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2424

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    TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC 120
    AGCAAAATGA TGTGGTGCTC GGCTGCAGTG GACATCATGT TTCTGTTAGA TGGGTCTAAC 180
    AGCGTCGGGA AAGGGAGCTT TGAAGAGTCC AAGCACTTTG CCATCACAGT CTGTGACGGT 240
    CTGGACATCA GCCCCGAGAG GGTTCAGAGT GGAGCATTCC AGTTTCAGTTC CACTCCTCAT 300
15  CTGGAATTCC CCTTGGATTG ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
    ATGGTTTTCA AAGGAGGGCG CACGGAGACG GAACTTGCTC TGAATACCTT TCTGCACAGA 420
    GGGTTGCGTG GAGGCAGAAA TGCTTCTGTG CCCCAGATCC TCATCATCGT CACTGATGGG 480
    AAGTCCACGG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTACTGTGT 540
    TTTGCTGTGG GGGTCAGATT TCCACAGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT 600
20  AGAGGCGCAG ACGTGTGTTT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC 660
    ACCCTGAGCA GTCTCGGCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720
    CCCTGTGAGC ACAGGACGCT GGAGATGATC CGGAGTTTCG CTGGCAATGC CCCATGCTGG 780
    AGAGGATCGC GGGGAGCCTT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
    AGAGTGTTCG TAACCCAGCC TGCCACCTGC TACAGGACCA CCTGCCAGG CCCCTGTGAC 900
25  TCGCAGCCCTT GCCAGAAATG AGGCACATGT GTTCCAGAAG GACTGGACGG CTACCAAGTGC 960
    CTCTGCCCCG TGGCCTTTGG AGGGGAGGCT AACTGTGCCC TGAAGCTGAG CCTGGAATGC 1020
    AGGGTCGACC TCCTCTTCTC GCTGGACAGC TCTGCGGGCA CCATCTGGA CGGCTTCCTG 1080
    CGGGCCAAAG TCTTCGTGAA GCGGTTTGTG CCGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140
    CGAGTGGGTG TGGCCAGATA CAGCAGGGAG CTGCTGGTGG CGGTGCTTGC GGGGGAGTAC 1200
30  CAGGATGTGC CTGACCTGTT CTGGAGCCTC GATGGCATTG CCTTCCGTGG TGGCCCCACC 1260
    CTGACGGGCA GTGCCCTTGG CAGGCGGCGA GAGCGTGGCT TCGGGAGCGC CACCAGGACA 1320
    GGCCAGGACC GGCACGATAG AGTGGTGGTT TTGCTCACTG AGTCACACTC CGAGGATGAG 1380
    GTTTCGGGGC CAGGCGCTCA CGCAAGGGCG CGAGAGCTGC TCCTGTCTGG TGTAGGCAGT 1440
    GAGGCGGTGC GGGCAGAGCT GGAGGAGATC ACAGGCAGCC CAAAGCATGT GATGGTCTAC 1500
35  TCGGATCCTC AGGATCTGTT CAACCAAAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG 1560
    CAGCGGCCAG GGTGCGGAGC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC 1620
    TCAGTAGGGC CCGAGAAATT TGCTCAGATG CAGAGCTTTC TGAGAAGCTG TGCCTCCAG 1680
    TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGCTGC TGTATGCGAG CCAGGTGCAG 1740
    ACTGCCTTGC GGCTGGACAC CAACCCACC CGGCTGCGA TGCTGCGGGC CATTAGCCAG 1800
40  GCCCCCTACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
    GTGATGACCG TCCAGAGGGG TGCCCGGCTT GGTGTCCCCA AAGCTGTGGT GGTGCTCA 1920
    GCGCGGAGAG GCGCAGAGGA TGCAGCCGTT CTGCCCCAGA AGCTGAGGAA CAATGGCATC 1980
    TCTGTCTTGG TCGTGGGCGT GGGGCCCTGT CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT 2040
    CCCCAGGATT CCGTATCCCA CGTGGCAGCT TACGCCGACC TGCGGTACCA CCAGGACGTG 2100
45  CTCATTGAGT GGCTGTGTGG AGAAGCCAAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCCG 2160
    TGCATGAATG AGGGCAGCTG GTCCTGTCAG AATGGGAGCT ACCGCTGCAA GTGTGCGGAT 2220
    GGCTGGGAGG GCCCCCCTG CGAGAACCCT GAGTGGAGCT CTGTCTCTGT ATGTGTGAGC 2280
    CAGGGATGGA TTCTTGAGAC GCCCCTGAGG CACATGGCTC CCGTGCAGGA GGGCAGCAGC 2340
    CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTCTCG 2400
50  AATGTCTGTG CCCCAGGTCC TTAG
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Seq ID NO: 443 Protein sequence
Protein Accession #: Eos sequence

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    MVFKGGRJET ELALKYLHRH GLPGGRNASV FQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
60  FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
    PCEHRTLEMT REFAGNAPCW RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCPGPCD 300
    SQPCQNGGTC VEBGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
    RAKVFVKRFP RAVLSDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420
    LTGSALRQAA ERGFGSATRT QDRPRRVVV LLTESHSEDE VAGPARHARA RELLLGVGS 480
65  EAVRAELEBI TGSPKHMVYV SDPQDLFNQI PELQGHLCNR QRPGRCTQAL DLVFMLDTS 540
    SVGPENFAQM QSFVRSCALQ FEVNPVDVTQ GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
    APYLGGVGSA GTALLHIYDK VMTVQRGARP GVFKAVVVLV GGRGAEDAAV PAQKLRRNGI 660
    SVLVVGVGVP LSEGLRRLAG PRDSLHVAA YADLRYHQDV LIEWLCEGAK QPVNLCRPS 720
    CMNEGSCVLQ NGSYRCKCRD WEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
70  RTPPSNYREG LGTEMVPTFW NVCAPGP
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Seq ID NO: 444 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 89..2356

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    GTCGCGCTGC TCCTTCGCTT ATATCAACAT GCCCCCTTTC CTGTGCTGGG AAGCCGCTCTG 120
    TGTTTTCCCTG TTTTCCAGAG TGCCCCCATC TCTCCCTCTC CAGGAAGTCC ATGTAAGCAA 180
80  AGAAACCATC GCGAAGATTT CAGCTGCCAG CAAAATGATG TGGTGCTCGG CTGCACTGGA 240
    CATCATGTTT CTGTTAGATG GGTCTAACAG CGTCGGGAAA GGGAGCTTTG AAAGGTCCAA 300
    GCACTTTGCC ATCAGAGTCT GTGACGCTCT GGACATCAGC CCGAGAGAGG TCAGAGTGGG 360
    AGCATTCAGT TTCAGTTCCA CTCCTCATCT GGAATTCCTT TTGATTTCAT TTTCACCCCA 420
85  ACAGGAAGTG AAGGCAAGAA TCAAGAGGAT GGTTTTCAAA GGAGGGCGCA CGGAGACGGA 480
    ACTTGCTCTG AAATACCTTC TGCACAGAGG GTTGCCTGGA GGCAGAAATG CTCTGTGACC 540
    CCAGATCCTC ATCATCGTCA CTGATGGGAA GTCCAGGGG GATGTGGCAC TGCCATCCAA 600
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5	GCAGCTGAAG	GAAAGGGGTG	TCACTGTGTT	TGCTGTGGGG	GTCAGGTTTC	CCAGGTGGGA	660
	GGAGCTGCAT	GCACTGGCCA	GCGAGCCTAG	AGGGCAGCAC	GTGCTGTGGG	CTGAGCAGGT	720
	GGAGGATGCC	ACCAACGGCC	TCTTCAGCAC	CCTCAGCAGC	TGCGCCATCT	GCTCCAGCGC	780
	CACGCCAGAC	TGACGGGTGG	AGGCTCACCC	CTGTGAGCAC	AGGACGCTGG	AGATGGTCCG	840
	GGAGTTCGCT	GGCAATGCCC	CATGCTGGAG	AGGATCGCGG	CGGACCCCTG	CGGTGCTGGC	900
	TGCACACTGT	CCCTTCTACA	GCTGGAAGAG	AGTGTTCCTA	ACCCACCCCTG	CCACCTGCTA	960
	CAGGACCACC	TGCCCAGGCC	CCTGTGACTC	GCAGCCCTGC	CAGAATGGAG	GCACATGTGT	1020
	TCAGAAAGGA	CTGGACGGCT	ACCAAGTGCT	CTGCCCGCTG	GCCTTTGGAG	GGGAGGCTAA	1080
10	CTGTGCCCTG	AAGCTTGAGC	TGGAATGCAG	GGTCGACCTC	CTCTTCCTGC	TGGACAGCTC	1140
	TGCGGGCACC	ACTCTGGACG	GCTTCCTGCG	GGCCAAAGTC	TTCGTGAAGC	GGTTTGTGCG	1200
	GGCCGTGCTG	AGCGAGGACT	CTCGGGCCCG	AGTGGGTGTG	GCCACATACA	GCAGGGAGCT	1260
	GCTGTGTGGC	GTGCTGTGGG	GGAGTACCA	GGATGTGCTC	GACCTGGTCT	GGAGCCTCGA	1320
	TGGCATTCCT	TCCGCTGGTG	GCCCCACCCT	GACGGGCAGT	GCCTTGGCGC	AGGCGGCAGA	1380
	GGCTGGCTTC	GGGAGCGCCA	CCAGGACAGG	CCAGGACCGG	CCAGGTAGAG	TGTTGGTTTT	1440
15	GCTCACTGAG	TCACACTCCG	AGGATGAGGT	TGCGGGCCCA	GCGCGTCACG	CAAGGGCGCG	1500
	AGAGCTGGCT	CTGCTGGGTG	TAGGCAGTGA	GGCCGTGCGG	GCAGAGCTGG	AGGAGATCAC	1560
	AGGCAGCCCA	AAGCATGTGA	TGCTCTACTC	GGATCCTCAG	GATCTGTTC	ACCAATATCC	1620
	TGAGCTGACG	GGGAAGCTGT	GCAGCCGGCA	GCGGCCAGGG	TGCGGACAC	AAGCCCTGGA	1680
	CCTGCTCTTC	AGTGTGGTGA	CCTCTGCCCT	AGTAGGGCCC	GAGAATTTTG	CTCAGATGCA	1740
20	GAGCTTTGTG	AGAAGCTGTG	CCCTCCAGTT	TGAGGTGAAC	CCTGACGTGA	CACAGGTCCG	1800
	CCTGTGTGGT	CTGCGGAGCT	AGGTGCAGAG	TGCTTCGGG	CTGGACACCA	AACCCACCCG	1860
	GGCTGCGATG	CTGCGGGCCA	TTAGCCAGGC	CCCTTACCTA	GGTGGGTGGG	GCTCAGCCCG	1920
	CACCCGCCCTG	CTGCACATCT	ATGACAAAGT	GATGACCGTC	CAGAGGGGTG	CCCAGCCTGG	1980
25	TGTCCCAAAA	GCTGTGGTGG	TGCTCACAGG	GCGGAGAGGC	GCAGAGGATG	CAGCCGTTTC	2040
	TGCCCCAAGG	CTGAGGAACA	ATGGCATCTC	TGCTTGTGGT	GTGGCGGTGG	GGCCTGTCTT	2100
	AAGTGAGGGT	CTGCGGAGCT	TTGCAGGTCC	CCGGGATTC	CTGATCCACG	TGGCAGCTTA	2160
	CGCCGACCTG	CGGTACCAAC	AGGACGTGCT	CATTGAGTGG	CTGTGTGGAG	AAGCCAAAGCA	2220
	GCCAGTCAAC	CTCTGCAAA	CCAGCCCGTG	CATGAATGAG	GCCAGCTGGC	TCCTGCAGAA	2280
30	TGGGAGCTAC	CGCTGCAAGT	GTGCGGATGG	CTGGGAGGGC	CCCCACTGCG	AGAACCGATT	2340
	CTTGAGACGC	CCCTGAGGCA	CATGGCTCCC	GTGCAGGAGG	GCAGCAGCCG	TACCCCTCCC	2400
	AGCAACTACA	GAGAAGGCCT	GGGCACTGAA	ATGGTGCCCTA	CCTTCTGGAA	TGCTGTGCGC	2460
	CCAGTCCCTT	AGAATGTCTG	CTTCCCGCCG	TGGCCAGGAC	CACATATTCTC	ACTGAGGGAG	2520
	GAGGATGTCC	CAACTGCAGC	CATGCTGCTT	AGAGACAAGA	AAGCAGCTGA	TGTCACCCAC	2580
35	AAACGATGTT	GTGAAAAAGT	TTTGATGTGT	AAGTAAATAC	CCACTTTCTG	TACCTGTCTG	2640
	GCCTTGTGTA	GGCTATGTCA	TCTGCCACCT	TTCCCTTGAG	GATAAACAGG	GGGTCTCTGA	2700
	GACTTAAATT	TAGCGGCCTG	ACGTTCCCTT	GCACACAATC	AATGCTCGCC	AGAATGTTGT	2760
	TGACACAGTA	ATGCCACGCA	GAGGCCTTTA	CTAGAGCATC	CTTTGGACGG		

Seq ID NO: 445 Protein sequence
Protein Accession #: Eos sequence

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	MPPFLLEAV	CVFLFSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMPLLDGSN	60
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	MVFKGGRTE	ELAKYLLHR	GLPGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKERVTV	180
	FAVGVRFPFW	EELHALASEP	RGQHVLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
	PCEHRTLENV	REFPAGNAPCW	RGRSRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCPPGCD	300
50	SQPCQNGGTC	VPEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVDLLFLVLS	SAGTTLDGFL	360
	RAKVVFVKRFV	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVFDLVWSL	DGIPFRGGPT	420
	LTGSALRQAA	ERGGFSATRT	GQDRPRRVVV	LLTESHSEDE	VAGPARHARA	RELLLLGVGS	480
	EAVRAELEBI	TGSPKHMVY	SDPQDLFNQI	PELQGLKCSR	QRPCRTQAL	DLVFMIDTSA	540
	SVGPENFAQM	QSFVRSALQ	FEVNPVDTQV	GLVVYGSQVQ	TAFLGLDKPT	RAAMLRASIQ	600
55	APYLGGVGS	GTALLHIYDK	VMTVQRGARP	GVPKAVVVLT	GGRGAEDAAY	PAQKLRNNGI	660
	SVLVVGVGPV	LSEGLRRLAG	PRDSLIHVAA	YADLRYHQDV	LIEWLCGEAK	QPVNLCCKPS	720
	CNNEGSCVLIQ	NGSYRCKRD	GWEGPHCENR	FLRRP			

Seq ID NO: 446 DNA sequence
Nucleic Acid Accession #: NM_031942.1
Coding sequence: 145..1260

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	CCGATCTGGG	CACCCGCCAC	CAGCATGGAC	GCTCGCCGCG	TGCCCGCAGAA	AGATCTCAGA	180
	GTAAAGAAGA	ACTTAAAGAA	ATTGAGATAT	GTGAAGTTGA	TTTCCATGGA	AACCTCGTCA	240
	TCCTCTGATG	ACAGTTGTGA	CAGCTTTGCT	TCTGATAATT	TTGCAAAAC	GAGGCTGCAG	300
70	TCACTTCGGG	AAGGCTGTAG	GACCCGCGAGC	CAGTGCAGGC	ACTCTGGACC	TCTCAGGGTG	360
	GCGATGAAGT	TTCCAGCGCG	GAGTACCAGG	GGAGCAACCA	ACAAAAAAGC	AGAGTCCCCG	420
	CAGCCCTCAG	AGAATTCTGT	GACTGATTCC	AACTCCGATT	CAGAAGATGA	AAGTGGAAATG	480
	AATTTTGTGG	AGAAAAGGGC	TTTAAATATA	AAGCAAAACA	AAGCAATGCT	TGCAAAACTC	540
	ATGCTCTGAAT	TAGAAAGCTT	CCCTGGCTCG	TTCCGTGGAA	GACATCCCCC	CCCAGGCTCC	600
75	GACTCACAA	CAAGGAGACC	GCGAAGGCGT	ACATTCGCCG	GTGTTGCTTC	CAGGAGAAAC	660
	CCTGAACGGA	GAGCTCGTCC	TCTTACCAGG	TCAAGGTCCC	GGATCCTCGG	GTCCCTTGAC	720
	GCTCTACCCA	TGGAGGAGGA	GGAGGAAGAG	GATAAGTACA	TGTTGGTGAG	AAAGAGGAAG	780
	ACCGTGGATG	GCTACATGAA	TGAAGATGAC	CTGCCACAGAA	GCCGTCGCTC	CAGATCATCC	840
	GTGACCCCTC	CGCATATAAT	TCGCCAGTGG	GAAGAAATTA	CAGAGGAGGA	GTTGGAGAAC	900
80	GTCTGCAGCA	ATTCTCAGAA	GAAGATATAT	AACCGTTTAC	TGGGCTCTAC	TTGTTCATCA	960
	TGCCGTGAGA	AGACTATTGA	TACCAAAACA	AACCTGCAGAA	ACCCAGACTG	CTGGGGCGTT	1020
	CGAGGCCAGT	TCTGTGGCCC	CTGCCCTTCA	AACCGTTATG	GTGAAGAGGT	CAGGGATGCT	1080
	CTGCTGGATC	CGAACTGGCA	TGCGCGCCT	TGTGAGGAA	TCTGCAACTG	CAGTTTCTGC	1140
	CGGCAGCGAG	ATGGACGGTG	TGCGACTGGG	GTCCCTGTGT	ATTAGCCAA	ATATCATGGC	1200
85	TTTGGGAATG	TGCTATGCTA	CTTGAAAAGC	CTGAACACAG	AATTTGAAAT	GCAAGCATAA	1260
	TATCTGAAA	ATTTGCTGCC	CTGCTTCTAC	TTCTCAAATC	TTTCTGTGAA	AAGTTTCCAA	1320
	TTTTTCACT	GAAACCTGAG	TTAAAATCT	TGATGATCAG	CCTGTTTCAT	AAGAACTCC	1380
	AATCAAGTTA	ATCTTAGCAG	ACATGTGTTT	CTGGAGCATC	ACAGAAGGTA	TATTGCTAGT	1440

TACACTTTGC CCTCTGCAG TTTCTTCTCT GCTCCCAACC CCCATCTCAT AGCATCCCCC 1500
 TCTATTTTCCA ATGCTCTCTT CCAACCGCTT AGTTTCTGAA TTTCTTTTAA ATTACAGTTT 1560
 TATGAAAGCA TATTTTATTT ACTTGGTGTT GAAATAGCCC TCATAAAACC TAAGCACTTG 1620
 5 GAAACACAAAT AATAGTATTA ACTAACTAGA TCTATTGAAT TTCAGAGAAG AGCCTTCTAA 1680
 CTTGTTTACA CAAAACCGAG TATGATTTAG CACTCATACT AGTTGAAATT TTTAATAGAA 1740
 TCAAGGCACA AAAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATGT 1800
 CTCTCAATCC CATGTATTGC GCTTATGTTA CAAGTTGTGG TCACAGTTGA GACTTAATTT 1860
 CTCCTAATTT CTTCGCCCCG AAGGCTAAGT GGTGCGTCCA GCTTACACGA TCATAATTCA 1920
 10 AAGGTTGGTG GGCAATGTAA TACTTAATTA AAATAATGAT GGAAGAGCTA TCTGGAGATT 1980
 ATGAGTAAGC TGATTGTAAT TTTAGTATA AAACCTTAGT ATAATTGTAG TTTGCAAGT 2040
 TTATTTTCACT TCACATGTAA GGTATTGCAA ATAAATTCCT GGACAATTTT GTATGGAAAC 2100
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 TATACAAAAG TTTATTTTAA TAATAAATG TTTGTTCTAA AAAAAAAAAA

Seq ID NO: 447 Protein sequence
 Protein Accession #: NP_114148.1

1 11 21 31 41 51
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 NIKQNKAMLA KLMSLESEFP GSFRGRHPLP GSDSQSRFR RRTFPGVASR RNPERRARPL 180
 TRSRSRILGS LDALPMEEBE EEDKYMILVRK RKTVDGYMNE DDLPRSRRSR SSVTLPHIIR 240
 30 PVSEITEEEL ENVCNSNREK IYNRSLGSTC HQCRQKTI DT KTNCRNPDWC GVRGQPCGFC 300
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 CTGAGCTCTG CGAGTATCAT CATTTGTGTT GTCCCTCATCA AGGTGATTC TGGATAAATAC 180
 TACTTCTCTC GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
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 45 GCAGTGGCAG TCCGCTCTC CAAGGACCAG TCCACACTGC AGGTGCTGGA CTGGGCCACA 360
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 AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
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 50 AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
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 CTCACGGCAG CCCACTGCTT CAGGAAACAT ACGATGTGT TCAACTGGAA GGTGCGGGCA 780
 GGCTCAGACA AACTGGGAGC CTTCCTCATCC CTGGCTGTGG CCAAGATCAT CATCATTTAA 840
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 55 ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
 GCCACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
 GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
 GCGTACCAGG GGGAAAGTCA CAGAGAAGAT ATGTGTGCAG GCATCCCGGA AGGGGGTGTG 1140
 GACACCTGCC AGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
 60 GTGGGATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
 AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

Seq ID NO: 449 Protein sequence
 Protein Accession #: NP_063947.1

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 70 GNWFSACFDN FTEALAEATC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
 GPCLSGSLVS LHCLACGKSL KTPRVVGEE ASVDSWPQV SIQYDKQHV GGSILDPHV 240
 LTAHCFRKH TDVFNWKVRA GSKLGSFPPS LAVAKIIIE FNPMPKND IALMKLQFPL 300
 TFSGTVRPIC LPFFDEELTP ATPLWIIGW FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
 AYQGEVTEKM MCAGIPEGV DTCQDSGGP LMYQSDQWHV VGIVSWGYC GGPSTPGVYT 420

Seq ID NO: 450 DNA sequence
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 85 GACCGGGGCA GAGCCTGGCG GAGCTACCGT GTACGGTTCC TCTGTGGGAA GCCTGTGAGG 180
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 AATGTACAGT CATGGAACCC TGGAGATACC CTGGTCATTG CCAGTACTGA TTACTCCATG 300
 TACCAGGCAG AAGAGTTCCA GGTGCTTCCC TGCAGATCCT GCGCCCCCAA CCAGGTCAA 360

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 CACGCAGAAA TGGCTCTAAG GGGACTCTGC TCCACGTGGG GCCAGGCGTG TGACTGACGC 3180
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 GATTGCTTCC TTTCTTTTAA AGACGACAGT CTTTGTGTG AGCACTGAAT TATTGAAAA 3300
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 GGAACCGTTT GAGCCTTATA GATCAATTTT ATTCAATTTT TTTAACTCAG CAAGTGAGAA 3420
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Seq ID NO: 455 Protein sequence
 Protein Accession #: NP_037414.2

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1 11 21 31 41 51
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 PADEDMWDET ELGLYKNEY VDARDTNMGA WFEAQVVRVT RKAPSRDEPC SSTSRPALBE 180
 DVIYHVKKYD YPENGVMQMN SRDVRARAT IIKWQDLEVG QVVMNLNYPD NPKERGFWYD 240
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 SKCHKRQDVN RLRCVCAHL CGGRQDPEKQ LMCDECDMAF HIYCLDPPLS SVPSDEWYC 360
 PRCRNDASEV VLGERLRES KKKAOMASAT SSSQRDWGKG MACVGRTEKEC TIVPSNHYGP 420
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 SGGRLDLSGNK RTAEQSCDQK LTNTRALAL NCFAPINDQE GAEAKDWRSG KPVVRVRNVK 540
 GGNKSKYAPB EGNRYDGYK VVKYWPEKKG SGFLVWRVLL RRDDDEPGPW TKEGKDRIKK 600
 LGLTMQYPEG YLEALANRER EKENSKEEES EQQEGGFASP RTGKGKWKRK SAGGGPSRAG 660
 SPRRTSKTKF VEPYSLTAQQ SSLIREDKSN AKLWNEVLAS LKDRPASGSP FQLFLSKVEE 720
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Seq ID NO: 456 DNA sequence
 Nucleic Acid Accession #: NM_001200.1
 Coding sequence: 325..1514

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1 11 21 31 41 51
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 TTTATGAAAT CATAAAACTT GCAACAGCCA ACTCGAAAT CCCCGTGACC AGACTTTTGG 900
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 TGCTGTATCA TCTGAACCTC ACTAATCATG CCATTGTTCA GACGTTGGTC AACTCTGTGA 1380
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Seq ID NO: 457 Protein sequence
 Protein Accession #: NP_001191.1

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5	MVAGTRCLLA	LLLPPVLLGG	AAGLVPELGR	RKPAAASSGR	PSSQPSDEVL	SEFELRLLSM	60
	PGLKQRPPTS	RDVAVPPYML	DLYRRHSGQP	GSPAPDHRLE	RAASRANTVR	SFHHEESLEE	120
	LPETSGKTRR	RFFFNLSISP	TEEFITSDEL	QVRFREMQDA	LGNNSSFHHR	INIYEIIPKA	180
	TANSKFPVTR	LLDT					

Seq ID NO: 458 DNA sequence
Nucleic Acid Accession #: NM_001999.2
Coding sequence: 1..8736

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	CAGCCGCGCG	CGCAACAGGT	TCGGTCCGCT	ACAGCAGGCT	CTGAAGGCGG	GTTTCTAGCG	180
	CCCGAGTATC	GCGAGGAGGG	TGCCGAGTGT	GCCAGCCGCG	TCCGCGGCGG	AGGACAGCAG	240
20	GACGTGCTCC	GAGGGCCCAA	CGTGTGCGGC	TCCAGATTCC	ACTCCTACTG	CTGCCCTGGA	300
	TGGAAGACAG	TCCCTGGAGG	AAACCAAGTGC	ATTGTCCCGA	TTTGTAGAAA	TAGTTGTGGA	360
	GATGGATTTC	GTTCCCGTCC	TAACATGTGT	ACTTGTTCCT	GTGGGCAAAAT	ATCATCAACC	420
	TGTGGATCAA	AATCAATTCA	GCAGTGCAGT	GTGAGATGCA	TGAATGGTGG	GACCTGTGCA	480
	GATGACCACT	GCCAGTGCCA	GAAAGGATAT	ATTGGAACCT	ATTGTGGACA	ACCTGTCTGT	540
25	GAAAAATGGAT	GTCAGAAATGG	TGGACGTTGC	ATCGCCCAAC	CGTGTGCTTG	TGTTTATGGG	600
	TTCACTGGTC	CACAGTGTGA	AAGAGATTAC	AGGACAGGCC	CGTGTTCAC	TCAGGTCAAC	660
	AAACAGATGT	GCCAGAGGCA	GCTGACAGGC	ATTGTCTGCA	CGAAGACTCT	GTGCTGTGCC	720
	ACCACTGGAG	GGGGGTGGGG	CCATCCCTGT	GAGATGTGTC	CAGCCCAAGC	TCAGCCCTGC	780
	CGACGGGGTT	TCATCCCAAA	CATCCGCACT	GGAGCTTGCC	AAGATGTGTA	TGAATGCCAG	840
30	GCTATCCGAG	GGATATGCCA	AGGAGGAAAC	TGTATCAATA	CAGTGGGCTC	TTTTGAATGC	900
	AGATGCCCTG	CTGTGTCAAA	ACAGAGTGAA	ACTACTCAGA	AATGTGAAGA	CATTGATGAG	960
35	TGCAGCATCA	TTCTCGGATA	ATGTGAAACT	GGTGAATGTT	CCAACACCGT	GGGAAGCTAT	1020
	TTTTGTGTTT	GTCACAGTGG	ATATGTAACC	TCAACAGATG	GCTCTCGATG	CATCGATCAG	1080
	AGAACAGGCA	TGTGTTTCTC	GGGCTGTGGT	AATGGCCGCT	GTGCACAAGA	GCTCCCGGGG	1140
	AGAATGACGA	AAATGCAGTG	CTGCTGTGAG	CCTGGCCGCT	GCTGGGGCAT	CGGAACCAT	1200
	CCTGAAGCCT	GTCCTGTGAG	AGGTTCTGAG	GAATATCGCA	GACTTTGCAT	GGATGGACTT	1260
40	CCAATGGGAG	GAATTCAGG	GAGTGTGTTT	TCCAGACCTG	GAGGCACTGT	GGGAAATGGC	1320
	TTTGCCCAAA	GTGGCAATGG	CAATGGCTAT	GGCCCAAGAG	GGACAGGCTT	CATCCCATC	1380
	CCTGGAGGCA	ATGCTTTTTC	TCTGTGGCTT	GGGGGAGCCG	GTGTGGGGGC	CGGGGACAG	1440
	GGACCTATCA	TCACTGAGCT	AACAATCTGT	AACAGACAA	TAGATATCTG	TAAGCATCAT	1500
45	GCTAACCTTT	GTTTAAATGG	ACGCTGTATA	CCAAGTGTCT	CAAGCTACCG	ATGTGAATGC	1560
	AACATGGGTT	ATAAGCAGGA	TGCAAAATGA	GATTGTATAG	ATGTTGATGA	ATGCACATCA	1620
	AATCCCTGCC	CTAATGGAGA	TTGTGTTAAC	ACACCTGGTT	CCTATTATTG	TAAATGTCTAT	1680
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50	AATGGGGTTC	TTTGTAAAAA	CGGTCCGATG	GTGAACCTAG	ATGGAAGTTT	CCAGTGCATT	1800
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	ACAACTACCA	ACATGTGTTT	GAATGGAATG	TGCATCAATG	AAGATGGCAG	CTTCAAGTGC	1920
	ATCTGCAAA	CAGGATTTGT	CTTGGCTCCA	AATGGGCGTT	ACTGTACTGA	TGTTGATGAA	1980
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	TGTGACTGTG	CCCCAGGGCT	GGCTGTGGGC	ATGGATGGAC	GTGTGTGTGT	TGATACTCAC	2100
55	ATGCGCAGTA	CCTGCTATGG	AGGAATCAAG	AAAGGAGTGT	GTGTGCGTCC	TTTCCCGGCT	2160
	GCAGTGACCA	AGTCCGAATG	CTGCTGTGCC	AATCCAGACT	ATGGTTTTGG	AGAACCCTGC	2220
	CAGCCATGCC	CTGCAAAAAA	TTCAAGTGA	TTCCAGCGCC	TTTGTAGTAG	TGGAGTAGGT	2280
	ATCACTGTGG	ATGGAAGAGA	TATCAATGAA	TGTGCTTTGG	ATCCTGATAT	ATGTGCCAAT	2340
	GGGATTGTGT	AAAACCTACG	TGTTAGTTAC	CGTTGTAATT	GCAACAGTGG	CTATGAACCA	2400
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	GATAACGGAT	TGTGCCGAAA	CACGCCAGGA	AGTTACAGCT	GTACGTGCCC	ACCAGGGTAT	2520
	GTGTTTCAGGA	CTGAGACAGA	GACCTGTGAA	GATATAAATG	AATGTGAAAG	CAACCCATGT	2580
	GTCAATGGGG	GTCAGAGAAA	CAACCTTGGA	TCTTTCAATT	GTGAATGTTT	GCCCCGCGCA	2640
	AAACTCAGCT	CCACAGGATT	GATCTGTATT	GACAGCCTGA	AGGGGACCTG	TTGGCTCAAC	2700
65	ATCCAGGACA	GCCTCTGTGA	TGTGAATATT	AATGGAGCCA	CTCTGAAATC	TGAATGCTGT	2760
	GCCACCCTCG	GAGCCGCTCG	GGGGAGCCCC	TGTGAGCGGT	GTGAAGTAGA	TACAGCTTGC	2820
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	TGCCCTGAAG	GCCTTACGTT	GGATGGGACT	GGCCGTGTAT	GTTTGGATAT	TCGATGGGAG	3000
70	CAGTGTACT	TGAAGTGGGA	TGAAGATGAA	TGCATCCACC	CCGTTCTCTG	AAAGTTCCGC	3060
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	GGGATGTTC	TTACTGGGCG	GCCATTTTAC	AAAGACATCA	ATGAATGCAA	AGCAATTCCT	3240
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75	AGTGGCTTGG	CTTAGACAT	GGAGGAAAGA	AACTGCACGG	ACATCGACGA	GTGCAGGATT	3360
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80	AATGAATGCT	CCCTGAGTGA	CAATCTCTGC	AGAAATGGAA	AATGTGTGAA	CATGATTGGA	3660
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	GATATTGATG	AATGTATGAT	AATGAACGGA	GGCTGTGACA	CCCAGTGCAC	AAATTACAG	3780
	GGAAGCTACG	AATGCAGCTG	CAGTGAAGGT	TATGCCCTGA	TGCCAGATGG	GAGATCGTGT	3840
	GCAGACATTG	ATGAATGTGA	AAACAATCCT	GATATCTGTG	ATGGCGGCCA	GTGTACCAAC	3900
85	ATTCTGGAG	AGTATCGCTG	CCTCTGCTAT	GATGGCTTCA	TGGCTTCCAT	GGACATGAAA	3960
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	GAGAACACAA	AGGGATCCCT	CATTTGCCAC	TGTCAGCTGG	GTTACTCAGT	GAAGAAGGGG	4080
	ACCACAGGAT	GTACAGATGT	GGATGAGTGT	GAAATGGTGT	CTCATAACTG	CGACATGCAT	4140
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	AATGCTCAGT	GTGTAATATC	CCCGGGCTCA	TACCGCTGTG	CCTGCTCCGA	AGGTTTCACT	4320
	GGTGTGGCT	TTACCTGCTC	AGATGTTGAT	GAGTGTGCAG	AAAACATAAA	CCTCTGTGAG	4380

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	GTCTCTGGAA	CATGTAATAA	CCTGCCTGGA	ATGTTTCATT	GCATCTGCGA	TGATGGTTAT	4560
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	AAGTTTGAGC	CTCGAGGAGA	TGGGAGTCTG	TCTTGCAACA	CCGAGATCGG	GGTGGGCGTC	4800
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	AACCCCATCA	CAATCATTTT	AGAAGACATT	GACGAATGCC	AGGAGTTACC	AGGTCTCTGC	4980
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	TGCTGCTGCA	CATATAAATG	GGCAAAAGCT	GGGAACAAC	CTTGTGAACC	ATGCCCACT	5340
	CCAGGAACAG	CTGACTTTAA	AACCATATGT	GGAAATATTC	CTGGAATCAC	CTTTGACATT	5400
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	GAAGATCCCA	ACATTTGTCT	TTTTGGTTCC	TGTACTAATA	CTCCAGGGGG	CTTCCAGTGC	6240
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50	TGCGAGCTTT	GCCCACTTCC	TGGAACCTGCC	CAGTACAAAA	AGATATGTCC	TCATGGCCCA	7320
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55	GTCTTGCAAG	AGGATGGAAA	GACATGCAAA	GACCTTGATG	AATGTCAAA	AAAGCAGCAT	7620
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60	CACAGGTGCC	AACACGGCTG	CCAGAACATC	CTGGGTGGCT	ACAGATGTGG	CTGCCCCCAA	7920
	GGCTACATCC	AGCACTACCA	GTGGAATCAG	TGTGTGCGAT	AGAATGAATG	CTCCAATCCC	7980
	AATGCCCTGTG	GCTCTGCTTC	CTGTACAAC	ACCCTGGGGA	GTTAACAAGT	CGCCTGCCCC	8040
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WO 02/086443

PCT/US02/12476

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	TTGGTTTGAA	AGCATAAGT	AAATATGATG	TCTGTCCCTG	GCAGTGTGGG	CAGAGTAGGA	240
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	GTAGACAGAA	TCCTTGGGAA	TACAGTAATT	GACATATATT	CTGTATTATT	ATGCTTGAAA	480
	AATCTCCTCC	ACTAACCACT	TTCCCTATAG	ATTGCCACAA	GCACATAATA	AGAAACAATA	540
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70	AAGGAAAGTA	GGTCCAGGAA	AATCTAGGAG	ATATTCTTCA	ACCAATCTAT	AAAGGCATTA	660
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75	TAGGAGAACT	ATTTAGGAAC	AGAAAAAAT	GCCTGAAATG	ATTTCTCATT	TGAACCTCAT	960
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	CCATAGATTG	GTCCCTCTGA	ACCCGGTTT	GTCTCAGCTT	GTTATCCTGT	TTTTTCTTCT	1140
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Protein Accession #: BAB21525.1

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CCTGCTGTCT TGACAGACCT TGAATATGTT AGGCTGGGGC ATTCTTTACA CCTACAAAAA 1320
GTTATTTTCC AGAGAATGTA GCTGTTTCCA GGGTTGCAAC TTGAATTAAG ACCAAACAGA 1380
35 ACATGAGAA ACACACACAC ACACACATAT ACACACACAC AACTTTCACA CATACACACC 1440
ACTCCACCA CCGTCATGAT GGAGGAATTA CGTTATACAT TCATATTTTG TATTGATTTT 1500
TGATTATGAA AATCAAAAAT TTTCACATT GATTATGAAA ATCTCCAAAC ATATGCACAA 1560
GCAGAGATCA TGGTATATAA AATCCCTTTG CAATCCACT CAGCCCTGAC AATCCATCCA 1620
CACACGCCCA GGCCTGTTTA TCTACACTGC TGCCCACTCC TCTCTCCAGC TCCCATGCT 1680
40 GTACCTGGAT CACTCTGAAG CAAATTCCGA GCATTACATC ATTTTGTCCA TAAATATTTC 1740
TAACATCCTT AATATACAA TCGGAATTCA AGCATCTCCC ATTTGCCCCA AATGTTTGG 1800
CTGTTTGTGT AATGGGTPV TTTGTATTAG GATTCAAGCA AGGCCCATAT ATTGCATTGA 1860
TTTGAATGCT CTGTAAGTCT CTTTCCATCT ACAGAGTTTA GCACATTGTA ACGTTGTCTG 1920
TTGAAATCCC GAGGTGTCTT TTGACATGGT TCTCTGAAGT TATCTTTCCT ATAAATGGT 1980
45 AGTTAGATCT GGAGGTCTGA TTTTGTGGCA AAAATACTTC CTAGGTGGTG CTGGTACTT 2040
CTTGTGTCAT CCGTGCAGGA GGCAGATAAT GCTGGTGCTT CTCTATTGGT AATGTTAAGA 2100
CTGCTGGGTG GGTGTGGAGT TCTTGGCTTT AATCATTCT TACAAAGTTC AGCATTTT

Seq ID NO: 467 Protein sequence
Protein Accession #: NP_001901.1

50 1 11 21 31 41 51
MKTLLLLLLV LLELGEAQGS LHRVPLRRHP SLKKKLRRS QLSEFWKSHN LDMIQFTESC 60
SMDQSAKEPL INYLDMEYFG TISIGSPPQN FTVIFDTGSS NLWVPSVYCT SPACKTHSRP 120
55 QPSQSSTYSQ PGQSFSLQYG TGSLSGIIGA DQVSVEGLTV VGGQFGEVST EPQQTFFVDAE 180
PDGILGLGYP SLAVGGVTPV FDNMAQNVL DLPMFVSVMY SNPEGGAGSE LIFGGYDHS 240
FSGSLNWVEV TKQAYWQIAL DNIQVGGTVM FCSEGCQAIV DTGTSITLTP SDKIKQLQNA 300
IGAAPVDGBY AVECANLNMV PDVFTINGV FYTLSPATYT LLDFVDMQMF CSSGFGGLDI 360
60 HPPAGPLWL GDVFIRQFYS VFDRGNRRVG LAPAVP

Seq ID NO: 468 DNA sequence
Nucleic Acid Accession #: NM_018058.1
Coding sequence: 319..1575

65 1 11 21 31 41 51
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70 TACACCGACA AGTTGTTCAA GTTCCGCAAT AACCGGTGGG AAGACATCCT GAGCGATGAG 180
GTCAACGTGG CCCGTGTGTG GGCAGCCTC TTGCGGGAC GCTCTGTGGC CTGTGTGGAC 240
AGAAAGGGCT CTGGACGCTA CTCTATCTAC ATTGCCAATT ACGCCTACGG TAATGTGGGC 300
CCTGATGCCC TCATTGAAAT GGACCCCTGAG GCCAGTGACC TCTCCCGGGG CATTCGTGGC 360
CTCAGAGATG TGGCTGCTGA GGCTGGGGTC AGCAAAATATA CAGGGGGCCG AGGCGTCAGC 420
75 GTGGGCCCCA TCCTCAGCAG CAGTGCCTCG GATATCTTCT GCGACAATGA GAATGGGCC 480
AACTTCTCTT TCCACAACCG GGGCGATGGC ACCTTGTGG ACGTGTGGGC CAGTGTCTGT 540
GTGGACGACC CCCACAGCA TGGGCGAGGT GTCCGCCCTG CTGACTTCAA CCGTGTATGG 600
AAAGTGGACA TCGTCTATGG CCACTGGAAT GGCCCCCACC GCCTCTATCT GCAAAATGAG 660
ACCATGGGTA AGGTCCGCTT CCGGGACATC GCCTCACCA AGTTCTCCAT GCCTCCCT 720
80 GTCCGACGGT TCATCACGCG CCACTTTGAC AATGACCAAG AGCTGGAGAT CTCTTCAAC 780
AACATTGCTC ACOCGAGCTC CTCAGCCAAC CGCTCTTCC GCGTCATCCG TAGAGAGCAC 840
GGAGACCCCT TCATCGAGGA GCTCAATCCC GGCAGCGCCT TGGAGCTGA GGGCCGGG 900
ACAGGGGGTG TGGTACCGA CTTGACGCGA GACGGGATGC TGGACCTCAT CTGTCTCCAT 960
GGAGAGTCCA TGGCTGATCC GCTGTCCGTC TTCCGGGGCA ATCAGGGCTT CAACACAC 1020
TGGCTGCGAG TGGTGCACG CACCCGGGTT GGGGCCCTTG CCAGGGGAGC TAAGTGTG 1080
85 CTCTACACCA AGAAGAGTGG GGCACCTG AGGATCATCG ACGGGGGGCT AGGCTACCTG 1140
TGTGAGATGG AGCCCGTGGC ACACCTTTGG CTGGGGAAGG ATGAAGCCAG CAGTGTGGAG 1200
GTGACGTGGC CAGATGGCAA GATGGTGAGC CGGAACGTGG CCAGCGGGGA GATGAAC 1260

GTGCTGGAGA TCCTCTACCC CCGGGATGAG GACACACTTC AGGACCCAGC CCCACTGGAG 1320
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 ACACCTATGG AAGGTACAGG TGCCCGACCA ACAAGAAGTG CAGTCGGGGC TACGAGCCCA 1440
 ACGAGGATGG CACAGCCTGC GTGGGGACTC ACCGGGGCCC CGCCCCACCA 1500
 CCCCCACCGC TGCTGCTGCC ACTGCCGCTG CTGCTGCCGC TGCTGGAGCT GCCACTGCTG 1560
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 CCAGCTGCTG AGCAGGGGTG GACATGAAC CAGCGGATGG AGTCCAGCAG GGGAGTGGGA 1680
 AAGTGGGCTT GTGCTGCTGC CTAGACAGTA GGGATGTAAA GGCTGGGGAG CTAGACCCTC 1740
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 CTGTGCTGGG CACATAGCTG TGATCACAGC AGACAGGGTC GCTGCCCTGA TGGCGCTTAC 1860
 ATTCCAGTGG GTCTAATGAC CATATCTTAG GACACAGATG TGCCCAAGGA GGTGGTGTCA 1920
 CTGCACAGGA AGTATGAGGA CTTTAGTGTC CTGAGTTCAA ATCCTGATTC AGGAACTCAC 1980
 AAAGCTATGT GACCTTACAG CAGTCACTTA ACTTGTAGC CATCCATTAT CGCATCTGCA 2040
 AAATGGGGAT TAAAGATAGA ATCTTGGGGT TAGTGTGGAG ATTAGATTAA ATGTATGTAA 2100
 GACACTTGGC ACAAACCTG GCACATAGTA AAGGCTCAAT AAAAACCAAGT GCCTCTCACT 2160
 GGGCTTTGTC AACACGTG

Seq ID NO: 469 Protein sequence
 Protein Accession #: NP_060528.1

1 11 21 31 41 51
 MDPEASDLR GILALRDVAA EAGVSKYTG RGVSVGPILS SSASDIFCDN ENGFNPLFHN 60
 RDGDTFVDA ASAGVDDPHQ HGRGVALADF NRDGKVDIVY GNWNGPHRLY LQMSTHGKVR 120
 RDIAAPKFS MPSPVTVIT ADFDNDQELE IFFNNIAYRS SSANRLPRVI RREHGDPLIE 180
 ELNPGDALBP EGRGTGGVVT DFDGDMGLDL ILSHGESMAQ PLVFRGNQG FNNNWLVRVP 240
 RTRVGAFARG AKVVLTKKS GAHLRIIDGG SGYLCMEFV AHFGLGKDEA SSVETWPDG 300
 KMSVRNVASG EMNSVLEILY PRDEDTLQDP APLETMPNAS SSHSCALETS PYVSTPMEAT 360
 GAGPTRSAVG ATSPTRMAQP AWGLSASHRA PAPPPPLLL PLPLLLPLLE LPLLHRSS

Seq ID NO: 470 DNA sequence
 Nucleic Acid Accession #: AJ279016
 Coding sequence: 1..1962

1 11 21 31 41 51
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 CAGCGGGCTG AACCATGTT CACTGCAGTC ACCAACTCAG TTCTGCGCTC TGACTATGAC 120
 AGTAATCCCA CCCAGCTCAA CTATGGTGTG GCAGTTACTG ATGTGGACCA TGATGGGGAC 180
 TTTGAGATCG TCGTGGCGGG GTACAAATGGA CCCAACCTGG TTCTGAAGTA TGACCGGGCC 240
 CAGAAGCGGC TGTGAAACAT CGCGGTGATG GAGCGCAGCT CACCTACTA CGCGCTGCGG 300
 GACCGGCAGG GGAACGCCAT CGGGGTCA CA CCTGCGACA TCGACGGGGA CGGCCGGGAG 360
 GAGATCTACT TCCCTAACAC CAATAATGCC TTCTCGGGGG TGGCCACGTA CACGACAAG 420
 TTGTTCAAGT TCCGCAATAA CCGGTGGGAA GACATCCTGA GCGATGAGGT CAACGTGGCC 480
 CGTGGTGTGG CCAGCCTCTT TGCCGGACGC TCTGTGGCCT GTGTGGACAG AAAGGGCTCT 540
 GGAGCTACT CTATCTCAT TGCCTCAATT GCTTACGGTA ATGTGGGGCC TGATGGCCCTC 600
 ATTGAATAGG ACCCTGAGGC CAGTGACCTC TCCCGGGGCA TTCTGGCGCT CAGAGATGTG 660
 GCTGCTGAGG CTGGGGTCAG CAATATACA GGGGGCGAG GCGTCAGCGT GGGCCCCATC 720
 CTCAGCAGCA GTGCCTCGGA TATCTTCTGC GACAATGAGA ATGGGCCTAA CTTCCTTTTC 780
 CACAACCGGG GCGATGGCAG CTTTGTGGAC GCTGCGGCCA GTGTCTGGTGT GGAACGACCC 840
 CACCAGCATG GCGAGGTGTG CGCCCTGGCT GACTTCAACC GTGATGGCAA AGTGGACATC 900
 GTCTATGGCA ACTGGAATGG CCCCCACCGC CTCTATCTGC AAATGAGCAC CCATGGGAAG 960
 GTCCGCTTCC GGGACATCGC CTCACCAAG TTCTCCATGC CCTCCCTGT CCGCACGGTC 1020
 ATCACGCGCG ACTTTGACAA TGACCAAGAG CTGGAGATCT TCTTCAACAA CATTCCTTAC 1080
 CGCAGCTCCT CAGCAACCGC CCTCTTCCGC GTCATCCGTA GAGAGCACCG AGACCCCTC 1140
 ATCGAGGAGC CAATCCCGG CGACGCTGAG GCGCGGGCAC AGGGGGTGTG 1200
 GTGACGAGCT TCGACGGAGA CGGGATGCTG GACCTCATCT TGTCCCATGG AGAGTCCATG 1260
 GCTCAGCCGC TGTCCGCTCT CCGGGGCAAT CAGGGCTTCA ACAACAAGT GCTGCGAGTG 1320
 GTGCCACGCA CCCGGTTTGG GGCCTTTGCC AGGGGAGCTA AGGTCGTGCT CTACACCAAG 1380
 AAGATGTTGG CCCACCTGAG GATCATCGAC GGGGGCTCAG GCTACCTGTG TGAGATGGAG 1440
 CCGGTGGCAC ACTTTGGCCT GGGGAAGGAT GAAGCCAGCA GTGTGGAGGT GACGTGGCCA 1500
 GATGGCAAGA TGGTGAAGCG GAACGTGGCC AGCGGGGAGA TGAACCTAGT GCTGGAGATC 1560
 CTCTACCCGC GGGATGAGGA CACACTTCAG GACCCAGCCC CACTGGAGTG TGGCCAAGGA 1620
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 GTGTGCCCTC GAGACAAGCC CGTATGTGTC AACACCTATG GAAGCTACAG GTGCCGAGC 1740
 AACAAAGAGT GCAGTCCGGG CTACGAGCCC AACGAGGATG GCACAGCTG CGTGGGGACT 1800
 CTCGGCCAGT CACCGGGCCC CCGCCCCACC ACCCCACCG CTGCTGCTGC CACTGCCGCT 1860
 GCTGCTGGCG CTGCTGGAGC TGCCACTGCT GCACCGGTCC TCGTAGATGG AGATCTCAAT 1920
 CTGGGGTCGG TGGTTAAGGA GAGCTGCGAG CCCAGCTGCT GAGCAGGGGT GGGACATGAA 1980
 CCAGCGGATG GAGTCCAGCA GGGGAGTGGG AAAGTGGGCT TGTGCTGCTG CTTAGACAGT 2040
 AGGGATGTAA AGGCTTGGGA GCTAGACCTT CCCCAGCCC ATCCATGCAC ATTACTTAGC 2100
 TAACAATTAG GGAGACTCGT AAGGCCAGGC CCTGTGCTGG GCACATAGCT GTGATCACAG 2160
 CAGACAGGGT CGCTGCCCTG ATGGCGCTTA CATTCCAGTG GGTCTAATGA CCATATCTTA 2220
 GGACACAGAT GTGCCAGGG AGGTGGTGTG ACTGCACAGG AAGTATGAGG ACTTTAGTGT 2280
 CCTGAGTTCA AATCCTGATT CAGGAACCTA CAAAGCTATG TGACCTTACA CCAGTCACTT 2340
 AACTTGTTAG CCATCCATTA TCGCATCTGC AAAATGGGGA TTAAGAAATG AATCTTGGGG 2400
 TTAGTGTGGA GATTAGATTA AATGTATGTA AGACACTTGG CACAAAACCT GGCACATAGT 2460
 AAAGGCTCAA TAAAACCAAG TGCCTCTCAC TGGGCTTTGT CAACACG

Seq ID NO: 471 Protein sequence
 Protein Accession #: CAC08451

1 11 21 31 41 51
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 FEIVVAGYNG PNLVLKYDRA QKRLVNIADV ERSSPYALR DRQNAIGVT ACDIDGDGRE 120
 EIFYFLNTNNA FSGVATYTDK LFKFRNNRWE DILSDEVNVA RGVASLPAGR SVACVDRKGS 180

GRYSIYIANY AYGNVGPDAL IEMDPEASDL SRGILALRDV AAEAGVSKYT GGRGVSVGPI 240
 LSSASDIFC DNENGNFLF HNRGDGTFVD AASAGVDDF HQHGRGVALA DFNDRGKVDI 300
 VYGNWNGPHR LYLQNSTHKG VRFRIASPK FSPSPVVRTV ITADFNDQDE LEIFFNNIAY 360
 RSSSANRLFR VTRRHGDPDL IEELNPGDAL EPEGRGTGGV VTDPDGDGML DLILSHGSEM 420
 5 AQLPLSVFRGN QGFNNNWLRV VPRTRFGAFA RGAKVVLTK KSGAHLRIID GSGGYLCME 480
 FVAHFGLGKD EASSVEVTFW DGMVSRNVA SGMNSVLEI LYPRDEDTLQ DPAPLECGQG 540
 FSQENGHCMT DNECIQFPF VCPDRKPVCV NTYGSYRCRT NKKCSRGYEP NEDGTACVGT 600
 LGQSPGPRPT TPTAAATAA AAAAAGAATA APVLVDGDLN LGSVVKESCE PSC

Seq ID NO: 472 DNA sequence
 Nucleic Acid Accession #: FGENESH
 Coding sequence: 1..4794

15 1 11 21 31 41 51
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 GTTCTGAATG ATGACCGGGC CCAGAAGCGG CTGGTGAACA TCGCGTCTGA TGAGCGCAGC 180
 20 TCACCTACT ACGCCCTGCG GGACCGGCAG GGAACGCCA TCGGGGTAC AGCCTGCGAC 240
 ATCGACGGGG ACGGCCGGGA GGAGATCTAC TTCTCAACA CCAATAATGC CTCTCGGGC 300
 CACAGCAGCT CAGCGCAGT CCCTTCTGGG CTCACAGAA ACAGGCCTGT GCTGAAGCCT 360
 CCACCTACAA CCCCTGCAGG CCTCTGGGT CTGCCTCCAC TCAGCGGAAG GGACTTTTCC 420
 TCCTCCCTGG GTCCAGGCTT TCCGGACAGC AGGCAGGGAG AGAGGGTGCC GGTCCCTGC 480
 25 TGTGCGGGTG GACTGAGACC TACCATGAA CCAGAACCAT TTCTCTGAG ACCCAATCA 540
 GGGGTGGCCA CGTACACCGA CAAGTTGTTC AAGTTCCGCA ATAACCGGTG GGAAGACATC 600
 CTGAGCGATG AGGTCAAGT GGCCCGTGGT GTGGCCAGCC TCTTTGCGG ACCTCTGTG 660
 GCTGTGTGG ACAGAAAGGG CTCTGGACGC TACTCTATCT ACATTGCCAA TTACGCTAC 720
 GGTAAATGGG GCCCTGATGC CCTCATTGAA ATGGACCTG AGGCCAGTGA CCTCTCCCG 780
 30 GGCATTCTGG GCTCAGAGA TGTGGCTGCT GAGGCTGGGG TCAGCAAATA TACAGAAAGC 840
 TTCTCCACCA CTGCTCTTCC AAGCATTGGT GAGATATCTG GCAGAACCGA GGAGCGGGAA 900
 GGAGGAGACC CAGAGCAGG AGATGAGGAG CACAGTGGGG ATGGAAGCAC CAGCCAACTG 960
 TGCCCGCTGG GCTGGAAGGA CGGCAGTTC AAGGAAGAAG CAGCAGCTTT GGTGGAGGAA 1020
 CAGAGGGAGG CTGGGGCAGC TGGCGTGCCC AGAGGACGTC TTCGAACAGC TCTGCAGACT 1080
 35 TCCAAAGAGC ATTTGGTGA CAAGAACCTA TTTGGCCGCT CATGTTACTA TCTGTCTGC 1140
 GCGCCTTCTC CAGCCCAACC TTTCCCTGCC CGCCAAGCCC CCCAACCTA CCCTGTAGCC 1200
 CCCTTGTCA CTCAGCTAAT GACACATGGA CGTCTGGCTG GAAACTAGC CCGGAGTGT 1260
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 40 CTGAGAAGCT GGGAGGAAG CAGGCAGAAG GGGCAGGCCA TGTCCAGATG TGCCTCAGG 1440
 GAGCTGGGAG GTCCCTGAGG CCAAGCCACA CAGCAGCTGC CTGTAGAGA GGTGTATGAC 1500
 CTGGGAGAAC TCTCCATTTT ACAAGAACA GACGGAGATC CAGGAGGAGG AAGGGACTCG 1560
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 45 CTCTCCCATC CTTGGTCCC CAACTTCCCC AGCTGCTTGA GGCCTCTTGA AGCCGGGACA 1740
 GTGCCGGGAG CTGCCCTGCC TGGGAATCCT GGGAACTGGG TTCTGGACAT GGCCAAGGCC 1800
 CTGGCGTGGA ACCATGATGA AAAAGAGGAG GGAAGATTTC ATGGAGACCA TGAGCCGAGA 1860
 TTTAGGCTCA GGAAGCAGC GGAAGCAGAA TTCCCCCAG GCTCTCTGA GAGCCCTCTG 1920
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 50 TCTGCCACTC ACTGTGGGTC GATGTCTTTT CTAGGGGGCC GAGGCGTCAG CGTGGGCCCC 2040
 ATCTCAGCA CGAGTGCTTC GGATATCTTC TCGACAATG AGAATGGGCC TAACCTCCTT 2100
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 GCCTTCATCG TTCACTCAA ATATCACCTC TGCAGAGATT TTCTCACTC CCTGTGCCAC 2220
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 55 TTCTTGAGCG AAGGCTTGGC CTCCAGTGCC CACCGGAGGA CACTCAGCCT CCAGGGTTCT 2400
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 60 GCCCTGGCTG ACTTCAACCG TGATGGCAAA GTGGACATCG TCTATGGCAA CTGGAATGGC 2640
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 TCACCCAAGT TCTCCATGCC CTCCCTGTCT CGCACGGTCA TCACCGCGGA CTTTGACAAT 2760
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 65 GGTCAAGGAG AAGGTTTAA AATCAGAAAG GGAGGGTTCC CAGGGCCAGG GGTCAAGGCC 2940
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 AAAGGGAAGG GAAATGTGGC CCAAGTGTG CCCAGAACCC AAGCGCCACA AGATACAAAG 3120
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 70 GTCCAATCAC TACCAGGAAA AGGGGCTACG GGTCCAATC ACTACCAGGA AAAGGGGCTA 3240
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 75 CCAGGAAAAG GGGTACAGG GTCCAATCAC TACCAGGAAA AGGGGCTACG GGGTCCAATC 3540
 ACTACCAGGA AAAGGGGCTA CGGGCTCCAA TCACTACCAG GAAAAGGGGC TACGGGGTCC 3600
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 GTCCAATCAC TACCAGGAAA AGGGGCTACG GGTCCAATC ACTACCAGGA AAAGGGGCTA 3720
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 80 GCTATGGGAT CCAATCACTA CCAGGAAAAG GGGCTACGGG GTCCAATCAC TACCAGGAAA 3840
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 85 AACACCAACT GGCTGCGAGT GGTGCCACGC ACCCGGTTTG GGGCCTTTGC CAGGGGAGCT 4140
 AAGGTGCTGC TCTACACCAA GAAGAGTGGG GCCCACTGGA GGATCATCGA CCGGGGCTCA 4200
 GGCTACCTGT GTGAGATGGA GCCCGTGGCA CACTTTGGCC TGGGAAGGA TGAAGCCAGC 4260
 AGTGTGGAGG TGACGTGGCC AGATGGCAAG ATGGTGAGCC GGAAGCTGGC CAGCGGGGAG 4320

WO 02/086443

PCT/US02/12476

ATGAACCTCAG TGCTGGAGAT CCTCTACCCC CGGGATGAGG ACACACTTCA GGACCCAGCC 4380
CCACTGGAGT GTGGCCAAAGG ATTCTCCCAAG CAGGAAAATG GCCATTGCAT GGACACCAAT 4440
GAATGCATCC AGTTCCCATT CGTGTGCCCT CGAGACAAGC CCGTATGTGT CAACACCTAT 4500
5 GGAAGCTACA GGTGCCCGAC CAACAAGAA GTCAGTCGGG GCTACGAGCC CAACGAGGAT 4560
GGCACAGCCT GCGTGGGTAC TGAGCTAGGC TCTAGGCATA CAATGACGTG GAAACCAAGG 4620
CCCAAAAAGG AGCTGCAACT TTCCCAAGGC ATCTGCACCC CCGTCTGGTC CTTTTTCCTG 4680
CCGGGTTCGC GGCTGCTCCT CAAAAGAGCT CAGCTCCAGG CTGCTCCAG CACCCTTCTC 4740
CAGAAAGCTC CAGGTATTCC AGAAGCCCAA GTGTATGAAC AAGATCAGGA ATAA

Seq ID NO: 473 Protein sequence
Protein Accession #: FGENESH predicted

1 11 21 31 41 51
15 MACPGGLPAR CSGWMGLGGP SGSSPASPPH SSSRYNGPNL VLKYDRAQKR LVNIAVDERS 60
SPYYALRDQ GNAIGVTACD IDGDGREEIY FLNTNNAFSG HSSSAQVPSG LHRNRPVLKP 120
PPTTAPAGLLG LPPLSGRDFS SSGQASPDPS RQGERVPVPC CRGGLRPTHPE PEPFLLRPKS 180
GVATYTDKLF KFRNNRWEDI LSDEVNVARG VASLFAGRSV ACVDRKGSGR YSIYIANYAY 240
20 GNVGPDALIE MDPEASDLR GILALRDVAA EAGVSKYTEG FSHTASPSIG EISGRTEERE 300
GGDPEADEE HSGDGSTSQL CRLGWKDGQF KEEAAALVEE QREAGAAGVP RGRVRTALQT 360
SRKSLADKNL PGPPCYYSVC APSPAHPFPA RQAPQHYPVA PLVTQLMTHG RLAGKLARSV 420
PHFRAPGMDP KCKGRHAEFG LMAEALGAWP ALSTTVVPGG LRSWEESRQK GQAMSRCALR 480
ELGGPWSQAT QHLPALEYD LGEPPILOQT DGDPGRRRDS PKVTQECHLV ATPALGGLE 540
25 GPCRVAKREI GRETGAUGRP LSHPLVPNFP SCLRLPEAGT VPGAALPGNP GNVVLDMAKA 600
LAWNQMEKEE GKINGDHEPR FRLRKAREAE FPPGSSEEP LQPPSGLRGS PVLQVGLGLA 660
SATHCGMSF LGGPGVSVGP ILSSASDIF CNENGPNFL FHNRGDGTFF DAAASAERRL 720
AFIVHLKYHL CRDPFHSLLCH LAETGPSSSC CPWHARLLQA PHCHHGLSMS FTRTGSRFYS 780
30 FLTQGLASA HRLRLSLQGS QGAPPCLLAR APCVLGSLIP TAYYIVLWSA IPESLMTHSY 840
LSSERVNVGV DDPHQHGRGV ALADFNDRGK VDIVYGNWNG PHRLYLQMS T HGKVRFRDIA 900
SPKFSMPSPV RTVITADFDN DQELIIPFNN IAYRSSANR LFRCSILARG SSSLTAGGRN 960
GGQEGRLIRR GGPPGPGGQA KVNTPGLMKK QKGRKDEDA RGCNAGQSL AKEPASAIAG 1020
KGKGNVAQSV PRTQAPQDTK PHYHKKGLQG PITTRKRGYV VQSLPGKQAT GSNHYQEKGL 1080
RGPITTRKRK YGVQSLPQKG ATGSNHQYQEK GLQGPITTRK RGYGLQSLPK KGATGSNHYY 1140
35 RKGLRAPITR RKRGVGVQSL PGKATGSNH YQEKGLRGP TTRKRGYGLQ SLPGKATGS 1200
NHQYQEKGLQ PITTRKRGYR VQSLPQKQAT GSNHYQEKGL RGPITTRKRK YGLQSLPGKE 1260
AMGSNHQYQEK GLRAPITTRK RGYGVQSLPQ KGATGSNVIR REHGDPLIEE LNPDALEPE 1320
GRGTGVVVD FDDGMLDLI LSHGESMAQP LSVFRGNQGF NNNWLRVVR TRFGAFARGA 1380
KVVLYTKKSG HRLRLSLQGS GYLCEMEFVA HFLGLKDEAS SVEVTWPDGK MVSRRNVASG 1440
40 MNSVLEILYP RDEDTLQDPA PLECCQGFSG QENGHCMOTN ECIQPPFVCP RDKPVCVNTY 1500
GSYRCRTNKK CSRGYEPNED GTACVGTGLG SRHTMTWKPR PKKELQLSQG ICTPVNSPFL 1560
PGCRLLLKRA QLQAPSTLL QKAPGIPBAQ VYEQDQE

Seq ID NO: 474 DNA sequence
Nucleic Acid Accession #: NM_003661.1
Coding sequence: 1..1152

1 11 21 31 41 51
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GCTGCTGGCA CCATGGACCC AGAGAGCAGT ATCTTTATTG AGGATGCCAT TAAGTATTTT 180
AAGGAAAAAG TGAGCACACA GAATCTGCTA CTCTGCTGTA CTGATAATGA GGCCCTGGAAC 240
GGATTCTGGG CTGCTGCTGA ACTGCCCAGG AATGAGGCAG ATGAGCTCCG TAAAGCTCTG 300
55 GACAACTTGG CAAGACAAAT GATCATGAAA GACAAAAACT GGCACGATAA AGGCCAGCAG 360
TACAGAAACT GGTTCCTGAA AGAGTTTCTT CGGTGAAAAA GTGAGCTTGA GGATAACATA 420
AGAAGGCTCC GTGCCCTTGC AGATGGGGTT CAGAAGGTCC ACAAGGCAC CACCATCGCC 480
AATGTGGTGT CTGGCTCTCT CAGCATTTCC TCTGGCATCC TGACCCTCGT CGGCATGGGT 540
CTGGCACCTT TCACAGAGGG AGGCAGCCTT GTACTCTTGG AACCTGGGAT GGAGTTGGGA 600
60 ATCAGAGCCC CTTTGACCGG GATTACCAGC AGTACCATGG ACTACGGAAG GAAGTGGTGG 660
ACACAAGCCG AAGCCACAGA CTTGGTCATC AAAAGCCTTG ACAAAATTGA GGAGGTGAGG 720
GAGTTTTTGG GTGAGAACAT ATCCAACCTT CTTTCCTTAG CTGGCAATAC TTACCAACTC 780
ACACGAGGCA TTGGGAAGGA CATCCGTGCC CTCAGACGAG CCAGAGCCAA TCTTCAGTCA 840
GTACCGCATG CCTCAGCTC ACGCCCCCGG GTCACGTAGC CAATCTCAGC TGAAGCGGT 900
65 GAACAGGTGG AGAGGGTTAA TGAACCCAGC ATCCTGGAAG TAGACAGAGG AGTCAAGCTC 960
ACGGATGTGG CCCCTGTAA GCTTCTTCTT GTGCTGGATG TAGTCTACCT CGTGTACGAA 1020
TCAAAGCACT TACATGAGGG GGCAAGTCA GAGACAGCTG AGGAGCTGAA GAAGGTGGCT 1080
CAGGAGCTGG AGAGGAAGCT AAACATTCTC AACAATAATT ATAAGATTCT GCAGGCGGAC 1140
CAAGAACTGT GA

Seq ID NO: 475 Protein sequence
Protein Accession #: NP_003652.1

1 11 21 31 41 51
75 MSALFLGVGV RAEEAGARVO QNVPSGTDGT DPQSKPLGDW AAGTMDPES IFIEDAIKYF 60
KEKVSTQNL LLLTDNEAWN GFVAAELPR NEADELRKAL DNLARQIMK DKQWHDKGQ 120
YRNWFLKEFP RLKSELEDNI RRLRALADGV QKVHKGTTIA NVVSGSLIS SGILTIVMG 180
LAPFTEGSL VLEPGMELG ITAALTGITS STMDYGKKWW TQAQAHDLVI KSLDKLKEVR 240
80 EPLGENISNF LSLAGNTYQL TRGIGKDIRA LRRARANLQS VPHASASRPR VTEPIAESG 300
EQVERVNEPS ILEMSRGVKL TDVAPVSFFL VLDVVYLVEY SKHLHEGAKS ETAEELKKVA 360
QELEEKLNL NNNYKILQAD QEL

Seq ID NO: 476 DNA sequence
Nucleic Acid Accession #: NM_014452.1
Coding sequence: 1..1968

1 11 21 31 41 51

	1	11	21	31	41	51	
	ATGGGGACCT	CTCCGAGCAG	CAGCACCGCC	CTCGCCTCCT	CGAGCCGCAT	CGCCCGCCGA	60
	GCCACAGCCA	CGATGATGCG	GGGCTCCCTT	CTCCTGCTTG	GATTCTCTAG	CACCACCACA	120
5	GCTCAGCCAG	AACAGAAGGC	CTCGAATCTC	ATTGGCACAT	ACCGCCATGT	TGACCGTGCC	180
	ACCGGCCAGG	TGCTAACCTG	TGACAAGTGT	CCAGCAGGAA	CCTATGTCTC	TGAGCATTGT	240
	ACCAACACAA	GCTGCGCGGT	CTGCAGCAGT	TGCCCTGTGG	GGACCTTTAC	CAGGCATGAG	300
	AATGGCATAG	AGAAATGCCA	TGACTGTAGT	CAGCCATGCC	CATGGCCAA	GATTGAGAAA	360
	TTACCTTGTG	CTGCCTTGAC	TGACCGAGAA	TGCACTTGCC	CACCTGGCAT	GTTCCAGTCT	420
10	AACGCTACCT	GTGCCCCCA	TACGGTGTGT	CCTGTGGGTT	GGGGTGTGCG	GAAGAAAGGG	480
	ACAGAGACTG	AGGATGTGCG	GTGTAAGCAG	TGTGCTCGGG	GTACCTTCTC	AGATGTGCTT	540
	TCTAGTGTGA	TGAAATGCAA	AGCATACACA	GACTGTCTGA	GTCAGAACTT	GGTGGTGATC	600
	AAGCCGGGGA	CCAAGGAGAC	AGACAACGTC	TGTGGCACAC	TCCCGTCCCT	CTCCAGCTCC	660
	ACCTCACCTT	CCCCTGGCAC	AGCCATCTTT	CCACGCCCTG	AGCACATGGA	AACCCATGAA	720
15	GTCCCTTCTT	CCACTTATGT	TCCCAAAGGC	ATGAATCAA	CAGAATCCAA	CTCTCTTGCC	780
	TCTGTTAGAC	CAAAAGTACT	GAGTAGCATC	CAGGAAGGGA	CAGTCCCTGA	CAACACAAGC	840
	TCAGCAAGGG	GAAAGTGAAG	CGTGAACAAG	ACCCTCCCAA	ACCTTCAGGT	AGTCAACCAC	900
	CAGCAAGGCC	CCCACACAGC	ACACATCTGT	AAGCTGCTGC	CGTCCATGGA	GGCCACTGGG	960
	GGCGAGAAGT	CCAGCAAGCC	CATCAAGGGC	CCCAAGAGGG	GACATCTTAG	ACAGAACCTA	1020
20	CACAAGCATT	TTGACATCAA	TGAGCAITTG	CCCTGGATGA	TTGTGCTTTT	CCTGCTGCTG	1080
	GTGCTTGTGG	TGATTTGTGT	GTGCAGTATC	CGGAAAGGCT	CGAGGACTCT	GAAAAAGGGG	1140
	CCCGCGCAGG	ATCCCACTGC	CATTGTGGAA	AAGGCAGGGC	TGAAGAAATC	CATGACTCCA	1200
	ACCCAGAACC	GGGAGAAATG	GATCTACTAC	TGCAATGGCC	ATGGTATCGA	TATCCTGAAG	1260
	CTTGTAGACG	CCCAAGTGGG	AAGCAGTGG	AAAGATATCT	ATCAGTTTCT	TTGCAATGCC	1320
25	AGTGAGAGGG	AGGTGTGCTG	TTTCTCCAAT	GGGTACACAG	CCGACCACGA	GCGGGCTTAC	1380
	CGAGCTCTGC	AGCACTGGAC	CATCCGGGGC	CCCGAGGCCA	GCCTCGCCCA	GCTAATTAGC	1440
	GCCTCTGCGC	AGCACCGGAG	AAACGATGTT	GTGGAGAAGA	TTCGTGGGCT	GATGGAGAGC	1500
	ACCACCCAGC	TGGAACCTGA	CAAACTAGCT	CTCCCGATGA	GCCCCAGCCC	GCTTAGCCCC	1560
	AGCCCCATCC	CCAGCCGCAA	CGCGAACTT	GAGAATTCCG	CTCTCCTGAC	GGTGGAGCCT	1620
30	TCCCCACAGG	ACAAGAACAA	GGGCTTCTTC	GTGGATGAGT	CGGAGCCCTT	TCTCCGCTGT	1680
	GACTCTACAT	CCAGCGGCTG	CTCCGCGCTG	AGCAGGAACG	GTTCCTTTAT	TACCAAGAA	1740
	AAGAAGGACA	CAGTGTGTGC	CGAGGTACGC	CTGGACCCCT	GTGACTTGCA	GCCTATCTTT	1800
	GATGACATGC	TCCACTTTCT	AAATCCTGAG	GAGCTGCGGG	TGATGGAAGA	GATTCCCCAG	1860
	GCTGAGGACA	AACTAGACCG	GCTATTCGAA	ATTATTGGAG	TCAAGAGCCA	GGAGCCAGC	1920
35	CAGACCTTCC	TGGACTCTGT	TTATAGCCAT	CTTCTGACC	TGCTGTAG		

Seq ID NO: 477 Protein sequence
Protein Accession #: NP_055267.1

	1	11	21	31	41	51	
40	MGTSPPSSSTA	LASCSRIARR	ATATMIAGSL	LLGLPLSTTT	AQPEQKASNL	IGTYRHVDRA	60
	TGQVLTCDCK	PAGTVVSEHC	TNTSLRVCS	CPVGTPTRE	NGIEKCHDCS	QPCPWPMEIK	120
	LPCAALTDRE	CTCPGMPQS	NATCAPHTVC	PVWGVRKKG	TETEDVRKAC	CARGTFSDVP	180
45	SSVMCKKAYT	DCLSNLVVI	KPGTKETDNV	CGTLPSFSSS	TSPSPGTATP	PRPEHMETHE	240
	VPSSTYVPKG	MNSTESNNSA	SVRPKVLSSI	QEGTVPDNTS	SARGKEDVNK	TLPLNLQVNH	300
	QQPHHRHLL	KLLPMEATG	GEKSSTPIKG	PKRGHPRQNL	HKHFDINEHL	PWMIVLFLLL	360
	LVVIVVVCIS	RKSSRTLKKG	PRQDPSAIVE	KAGLKKSMTP	TQNREKWIYY	CNGHGIDILK	420
	LVAQVGSQW	KDIYQFLCNA	SEREVAAFSN	GYTADHERAY	AALQHWIRG	PEASLAQLIS	480
50	ALRQHRRNDV	VSKIRGLMED	TTQLETDKLA	LPMSPLSP	SPIPSNKL	ENSALLTVEP	540
	SPQDKNKGF	VDESEPLLRC	DSTSSGSSAL	SRNGSPITKE	KIDTVLRQVR	LDPCDLQPIF	600
	DMMLHFLNPE	ELRVLEBIPQ	AEDKLDRLFE	IIGVKSQEAS	QTLDSVYSH	LPDLL	

Seq ID NO: 478 DNA sequence
Nucleic Acid Accession #: XM_044533
Coding sequence: 238..2751

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60	GCTCTGCCCA	AGCCGAGGCT	GCGGGGCGGG	CGCCGGCGGG	AGGACTGCGG	TGCCCGCGGG	60
	AGGGGCTGAG	TTTGCCAGGG	CCCACTTGAC	CTGTTTCC	ACCTCCCGCC	CCCCAGGTCC	120
	GGAGGCGGGG	GCCCCCGGGG	CGACTCGGGG	GCGGACCGCG	GGGCGGAGCT	GCCGCCCGTG	180
	AGTCCGCGCG	AGCCACCTGA	GCCCGAGCCG	CGGGACACCG	TGCTCTCTGC	TCTCCGAATG	240
	CTGCGCACCG	CGATGGGCGT	GAGGAGCTGG	CTGCGCGCCC	CATGGGGCGC	GCTGCGCGCT	300
65	CGGCCACCGC	TGCTGCTGCT	CCTGCTGCTG	CTGCTCCTGC	TGCAGCCGCC	GCCTCCGACC	360
	TGGGCGCTCA	GCCCCCGGAT	CAGCCTGCCT	CTGGGCTCTG	AAGAGCGGCC	ATTCTCAGA	420
	TTGGAAGCTG	AACACATCTC	CAACTACACA	GCCCTTCTGC	TGAGCAGGGA	TGGCAGGACC	480
	CTGTACGTGG	GTGCTCGAGA	GGCCCTCTTT	GCACTCAGTA	GCAACCTCAG	CTTCTTGCCA	540
	GGCGGGGAGT	ACCAGGAGCT	GCTTTGGGGT	GCAGACGCG	AGAAGAAACA	GCAGTGACAG	600
70	TTCAAGGGCA	AGGACCCACA	GCGCGACTGT	CAAAACTACA	TCAAGATCCT	CCTGCCGCTC	660
	AGCGGCAGTG	ACCTGTTTAC	CTGTGGCACA	GCAGCCTTCA	GCCCCATGTG	TACCTACATC	720
	AACATGGAGA	ACTTACCCCT	GCGAAGGGAC	GAGAAGGGGA	ATGTCCTCCT	GGAAGATGGC	780
	AAGGGCCGTT	GTCCCTTCGA	CCCGAATTTT	AAGTCCACTG	CCCTGGTGGT	TGATGGCGAG	840
	CTCTACACTG	GAACAGTCAG	CAGCTTCCAA	GGGAATGACC	CGGCCATCTC	GCGGAGCCAA	900
	AGCCTTCGCC	CCACCAAGAC	CGAGAGCTCC	CTCAACTGGC	TGCAAGACCC	AGCTTTTGTG	960
75	GCCTCAGCCT	ACATTCTCTG	GAGCCTGGGC	AGCTTGCAAG	GCGATGATGA	CAAGATCTAC	1020
	TTTTTCTTCA	GCGAGACTGG	CCAGGAATTT	GAGTTCTTTG	AGAACACCAT	TGTGTCCCGC	1080
	ATTGCCCGCA	TCTGCAAGGG	CGATGAGGGT	GGAGAGCGGG	TGCTACAGCA	GCGCTGGACC	1140
	TCCTTCTTCA	AGGCCCAAGT	GCTGTGCTCA	CGGCCGACG	ATGGCTTCCC	CTCAACGTG	1200
	GTGACAGGAT	TCTTCAAGCT	GAGCCCCAGC	CCCCAGGACT	GGCGTGACAC	CCTTTTCTAT	1260
80	GGGGTCTTCA	TCTTCCAGCT	GCACAGGGGA	ACTACAGAAG	GCTCTGCGGT	CTGTGCTTTC	1320
	ACAATGAAGG	ATGTGCAGAG	AGTCTTCAGC	GGCCTCTACA	AGGAGGTGAA	CCGTGAGACA	1380
	CAGCAGTGGT	ACACCGTGAC	CCACCCGGTG	CCCACACCCC	GGCCTGGAGC	GTGCATCACC	1440
	AACAGTGGCC	GGGAAAGGAA	GATCAACTCA	TCCCTGCAGC	TCCAGAGCCG	CGTGCTGAAC	1500
	TTCTTCAAGG	ACCACCTTCT	GATGGAGCGG	CAGGTCGAG	GCGCGCTGCT	GCTGCTGCAG	1560
85	CCCAGGCTC	GACTACACGC	CGTGGCTGTA	CACCGCTGCC	CTGGCCTGTC	CCACACCTCA	1620
	GATGTCTCTT	TCCTGGGCAC	TGGTGACGGC	CGGCTCCACA	AGGCAGTGAG	CGTGGGCCCC	1680
	CGGGTGACCA	TCATTGAGGA	GCTGCAGATC	TTCTCATCGG	GACAGCCCGT	GCAGAATCTG	1740

CTCCTGGACA CCCACAGGGG GCTGCTGTAT GCGGCTCACC ACTCGGGCGT AGTCCAGGTT 1800
 CCCATGGCCA ACTGCAGCCT GTACAGGAGC TGTGGGGACT GCCTCCTCGC CCGGGACCCC 1860
 TACTGTGCTT GGAGCGGCTC CAGCTGCAAG CACGTACAGCC TCTACCAGCC TCAGCTGGCC 1920
 ACCAGGCGGT GGATCCAGGA CATCGAGGGA GCCAGCGCCA AGGACCTTTG CAGCGCGTCT 1980
 TCGGTGTGTG CCCCGTCTTT TGTACCAACA GGGGAGAAGC CATGTGAGCA AGTCCAGTTC 2040
 CAGCCCAACA CAGTGAACAC TTTGGCCTGC CCGCTCCTCT CCAACCTGGC GACCCGACTC 2100
 TGGCTACGCA ACGGGGCCCC CGTCAATGCC TCGGCCTCCT GCCACGTGCT ACCCACTGGG 2160
 GACCTGCTGC TGGTGGGCAC CCAACAGCTG GGGGAGTTCC AGTGCTGGTC ACTAGAGGAG 2220
 GGCTTCCAGC AGCTGCTAGC CAGCTACTGC CCAGAGGTGG TGGAGGACGG GGTGGCAGAC 2280
 CAAACAGATG AGGGTGGCAG TGTACCCGTC ATTATCAGCA CATCGCTGTG GAGTGCACCA 2340
 GCTGGTGGCA AGGCCAGCTG GGGTGCAGAC AGGTCTACT GGAAGGAGTT CCTGGTGATG 2400
 TGCACGCTCT TGTGCTGGC CGTGTGCTC CCAATTTTAT TCTGTCTCTA CCGGCACCGG 2460
 AACAGCATGA AAGTCTTCTT GAAGCAGGGG GAATGTGCCA GCGTGCACCC CAAGACCTGC 2520
 CCTGTGGTGC TGCCCTCTGA GACCCGCCCA CTCACCGGCC TAGGGCCCCC TAGCACCCCG 2580
 CTCGATCACC GAGGGTACCA GTCCCTGTCA GACAGCCCCC CGGGGTCCCG AGTCTTCACT 2640
 GAGTCAGAGA AGAGGCCACT CAGCATCCAA GACAGCTTCG TGGAGGTATC CCCAGTGTGC 2700
 CCCCAGCCCC GGGTCCGCTT TGGCTCGGAG ATCCGTGACT CTGTGGTGTG AGAGCTGACT 2760
 TCAGAGGAC GCTGCCCTGG CTTCAGGGGC TGTGAATGCT CGGAGAGGGT CAACTGGACC 2820
 TCCCTCCGCG TCTGCTCTTC GTGGAACACG ACCGTGGTGC CCGGCCCTTG GGAGCCTTGG 2880
 GGCCAGCTGG CCTGTGCTC TCCAGTCAAG TAGCGAAGCT CCTACCACCC AGACACCCAA 2940
 ACAGCCGTGG CCCCAGAGGT CCTGGCCAAA TATGGGGGCC TGCCCTAGTT GGTGGAACAG 3000
 TGCTCCTTAT GTAACTGAG CCCCCTTTT AAAAAACAAT TCCAATGTG AAATAAGAT 3060
 GAGAGGGAAG AGATAGCATG GCATGCAGCA CACACGGCTG CTCAGTTTCA TGGCCTCCCA 3120
 GGGGTGCTGG GGGTCTCTTC AAAGTGGTTG TCTGAGACAG AGTTGGAAC CCTCACCAAC 3180
 TGGCTCTTTC ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCCTGTCTC ACTGCAGATT 3240
 CAGGACCAGC TTGGCTGCGT TGCGTTCTGC CTTGCCAGT AGCCGAGGAT GTAGTTGTTG 3300
 CTGCCGTGCT CCAACACCT CAGGACCAG AGGCTAGGT TGGCACTGCG GCCCTACCA 3360
 GGTCTCTGGC TCGACCCAA CTCTGGAGC TTTCAGCCT GTATCAGGCT GTGSCCACC 3420
 GAGAGGACAG CGCAGCTCA GGAGAGATT CTGACAAATG TACGCCCTTC CTCAGAAAT 3480
 CAGGGAAGAG ACTGTGCGCT GCCTTCTTCC GTTGTGTGCT GAGAACCCGT GTGCCCCCTC 3540
 CCACCATATC CACCTCTGCT CCATCTTTGA ACTCAAACAC GAGGAACATA CTGACCCCTG 3600
 GTCTCTCTCC CAGTCCCCAG TTCACCTTCC ATCCCTCACC TTCTTCCACT CTAAGGGATA 3660
 TCAACACTGC CCAGCACAGG GGCCTGAAT TTATGTGGTT TTTATACATT TTTTAATAAG 3720
 ATGCACITTA TGTCTTTTT TAATAAAGTC TGAAGAATTA CTGTTT

Seq ID NO: 479 Protein sequence
 Protein Accession #: XP_044533.3

1 11 21 31 41 51
 MLRTAMGLRS WLAAPWGALE PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL 60
 RFEAEHISNY TALLSRDRGR TLYVGAREAL FALSSNLSFL PGGEYQELLW GADAEEKQOC 120
 SFKKGDPQRD CQNYIKILLP LSGSHLFTCG TAAPSPMCTY INMENFTLAR DEKGNVLLED 180
 GKRCRPFDPN FKSTALVVDG ELYTGTVSSF QGNDDPAISRS QSLRPTKTES SLNWLQDPAP 240
 VASAYIPESL GSLQDDDKI YFFSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW 300
 TSFLKQQLLC SRPDDGFPEF VLQDVFTLSP SPQDWRDTLP YGVFTSQNHR GTTEGSAVCV 360
 FTMKDVQRVP SGLYKEVNRE TQQNYVTTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL 420
 NPLKDHFLMD GQVSRMLLL QFQARYQORVA VHRVPLGHHT YDVLFLGTGD GRLHKAHSV 480
 PRVHIEELQ IPSSGPQVQN LLLDTHRGLL YAASHSGVVV VPMANCSLYR SCGDCLLARD 540
 PYCAWSGSSC KHSVLYQPL ATRPNIQDIE GASAKDLCSA SSVVSFSPVP TGEKPCQEVQ 600
 FQNTVNTLA CPLLSNLTGR LMLRNGAPVN ASASCHVLPD GDLLLVGTQQ LGFQCWSLE 660
 EGPQQLVASV CREVEDGVA DQTEGGSVV VIISTSRVSA PAGGKASWGA DRSYWKFLV 720
 MCTLFVLAVL LPVLFLLYRH RNSMKVFLKQ GECAVHPKT CPVVLPPETR PLNLGPPST 780
 PLDRHGYQSL SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV

Seq ID NO: 480 DNA sequence
 Nucleic Acid Accession #: NM_004217.1
 Coding sequence: 58..1092

1 11 21 31 41 51
 GGCCGGGAGA GTAGCAGTGC CTGGACCCC AGCTCTCCTC CCCCTTTCTC TCTAAGGATG 60
 GCCCAGAAGG AGAATCCTTA CCGCTGGCCC TACGGCCGAC AGACGGCTCC ATCTGGCCTG 120
 AGCACCCCTGC CCCAGCGAGT CCTCCGAAA GAGCCTGTCA CCCCATCTGC ACTTGTCTCT 180
 ATGAGCCGCT CCAATGTCCA GCCCACAGCT GCCCCTGGCC AGAAGGTGAT GGAGAATAGC 240
 AGTGGGACAC CGGACATCTT AACCGCGCAC TTCACAAATG ATGACTTTGA GATTGGGCGT 300
 CCTCTGGGCA AAGGCAAGTT TGGAAACGTG TACTTGGCTC GGGAGAAGAA AAGCCATTTC 360
 ATCGTGGCCG TCAAGTCTCT TTCAAGTCC CAGATAGAGA AGGAGGCGCT GGAGCATCAG 420
 CTGCGCAGAG AGATCGAAAT CCAGGCCAC CTGCACCATC CCAACATCCT GCGTCTCTAC 480
 AACTATTTTT ATGACCGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGGAG 540
 CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTTGACGAGC AGCGAACAGC CACGATCATG 600
 GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATTCA CAGAGACATA 660
 AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTGGGCTGG 720
 TCTGTGCATG CGCCCTCCCT GAGGAGGAAG ACAATGTGTG GCACCTGGA CTACCTGCCC 780
 CCAAGAGATG TTGAGGGGCG CATGCACAA GAGAAGGTGG ATCTGTGGTG CATTTGGAGTG 840
 CTTTGTCTAT AGCTGCTGGT GGGGAACCCA CCGTTTGAGA GTGCATCACA CAACGAGACC 900
 TATCGCCGCA TCGTCAAGGT GGACCTAAAG TTCCCGCTT CTGTGCCCCAC GGGAGCCGAG 960
 GACCTCATCT CCAAACTGCT CAGGCATAAC CCGTCGGAAC GGCTGCCCTT GGGCCAGGTC 1020
 TCAGCCACCC CTGGGTCCG GGCCTACTCT CGGAGGGTGC TGCCCTCCCT TGCCCTTCAA 1080
 TCTGTGCGCT GATGGTCCCT GTCATTCACT CCGGTGCGTG TGTTTGTATG TCTGTGTATG 1140
 TATAGGGGAA AGAAGGATC CTAACCTGT TTTTCTACCT CCTCCTTTGT 1200
 TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 481 Protein sequence
 Protein Accession #: NP_004208

1 11 21 31 41 51

MAQKENSYPW	PYGRQTAPSG	LSTLPQRVLR	KEPVTSPALV	LMSRSNVQPT	AAPGQKVMEN	60
SSGTFDILTR	HFTIDDFEIG	RPLGKQKFGN	VYLAREKKSH	FIVALKVLFP	SQIEKEGVEH	120
QLRREIEIQA	HLHHPNLLRL	YNYFYDRRRR	YLILEYAPRG	ELYKELQKSC	TFDEQRTATI	180
MEELADALMY	CHGKVKIHRD	IKPENLLGL	KGELKIADFG	WSVHAPSLRR	KTMCGLDYL	240
PPEMIEGRMH	NEKVDLCIG	VLCYELLVGN	PPFESASHNE	TYRRIVKVDL	KFPASVPTGA	300
QDLISKLLRH	NPSERLFLAQ	VSAHPWVRAN	SRRLPPSAL	QSV		

Seq ID NO: 482 DNA sequence
Nucleic Acid Accession #: AK055663
Coding sequence: 38..1423

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AAAACCCACAA	AGATCCCTTTT	TTGGCAAGTT	GTTACGGGAA	TTTAGACTTG	TAGCAGCTGA	120
CCGAAGGTCC	TGGAAGATAC	TGCTCTTTGG	TGTAATAAAC	TTGATATGTA	CTGGCTTCCT	180
GCTTATGTGG	TGCAGTTCTA	CTAATAGTAT	AGCTTTAACT	GCCTATACCT	ACCTGACCAT	240
TTTTGATCTT	TTTAGTTTAA	TGACATGTTT	AATAAGTTAC	TGGGTAAACAT	TGAGGAAACC	300
TAGCCCTGTC	TATTCATTGG	GGTTTGAAAG	ATTAGAAATC	CTGGCTGTAT	TTGCCCTCCAC	360
AGTCTTGGCA	CAGTGGGGAG	CTCTCTTTAT	ATTAAAGAA	AGTGCAGAAC	GCTTTTGGGA	420
ACAGCCCGAG	ATACACACGG	GAAGATTATT	AGTTGGTACT	TTTGTGGCTC	TTTGTTCCAA	480
CCTGTTCACG	ATGCTTCTTA	TTCGGAATAA	ACCTTTTGCT	TATGTCTCAG	AAGCTGCTAG	540
TACGAGCTGG	CTTCAAGAGC	ATGTTGCAGA	TCTTAGTCGA	AGCTTGTGTG	GAATTATTCC	600
GGGACTTAGC	AGTATCTTCC	TTCCCGAAT	GAATCCATTT	GTTTTGATTG	ATCTTGCTGG	660
AGCATTAGCT	CTTTGTGTTA	CATATATGCT	CATTGAAATT	AATAATTATT	TTGCCGTAGA	720
CACCTGCTCT	GCTATAGCTA	TTGCCCTGAT	GACATTGGGC	ACTATGTATC	CCATGAGTGT	780
GTACAGTGGG	AAAGTCTTAC	TCCAGACAAC	ACCACCCCAT	GTTATTGGTC	AGTTGGACAA	840
ACTCATCAGA	GAGGTATCTA	CCTTAGATGG	AGTTTGAAGA	GTCCGAAATG	AACATTTTTC	900
GACCCTAGGT	TTTGGCTCAT	TGGCTGGATC	AGTGCATGTA	AGAATTCCAG	GAGATGCCAA	960
TGAACAAATG	GTTCTTGCTC	ATGTGACCAA	CAGGCTGTAC	ACTCTAGTGT	CTACTCTAAC	1020
TGTTCAAATT	TTCAAGGATG	ACTGGATTAG	GCCTGCGCTT	TTGTCTGGGC	CTGTTGCAGC	1080
CAATGTCCTA	AACTTTTCAG	ATCATCACGT	AATCCCAATG	CCTCTTTTAA	AGGGTACTGA	1140
TGATTGAAC	CCAGTTACAT	CAACTCCAGC	TAAACCTAGT	AGTCCACCTC	CAGAATTTTC	1200
ATTTAAACAT	CCTGGGAAAA	ATGTGAACCC	AGTTATTCTT	CTAAACACAC	AAACAAGGCC	1260
TTATGGTTTT	GTTCTTCAAT	ATGGACACAC	ACCTTACAGC	AGCATGCTTA	ATCAAGGACT	1320
TGGAGTTCCA	GGAATTGGAG	CAACTCAAGG	ATTGAGGACT	GGTTTTACAA	ATATACCAAG	1380
TAGATATGGA	ACTAATAATA	GAATTGGACA	ACCAAGACCA	TGATAGACTC	TAACITATTT	1440
TTATAAGGAA	TATTGATCTC	TTGGCTTCCA	ATTTATTTAG	TAATCCAACT	TTGCATTGAC	1500
TGTTTAATCA	TTTACTCTAA	ATGTTAGATA	ATAGTAGTCT	TGTTCACTAT	TCATGAAACC	1560
TATGAAACTA	TTTCTTCTTA	AAATGTATTT	GTGACAGTGA	AATCCTCGTA	AATGTTAAAG	1620
GCTTTAAATA	GGCTTCTCTT	AGAAATGTG	TTTCTTTAAA	TTTGGAATTT	GGTATCTTTG	1680
GTTTTGTAGT	TGACTGTCAGT	GTGATGTGAC	CTTACCTTTA	TAAGAGCCAC	TTGATGGAGT	1740
AGATCTGTCA	CATTACTAAG	ATACGATATT	TCTTTTCTTT	TCCGAGACGG	AGTCTTGCTC	1800
TGCCACTGTG	CCCGGCCAAT	ACATTATTAT	TAACTTAAGG	CTGTACTTTA	TTAAGGCTTC	1860
CTTAGTTTTT	GTTTGTGTTT	GTGTTTGGAG	ATGGAGTCTC	ACTCTGTCCG	CCAGGCTGGA	1920
ATGCACTGGC	ATGATCTCAG	CTCACTGCAA	CCTCTGCTCT	CTGAGTTCAA	ATGATTCTCC	1980
TGCCCTCAGC	TCCGAGTAG	CTGGGATTAC	AGGCACCTGC	CACCACGCCC	AGCTAATTTT	2040
TGTATTTTAA	GTAAAGACGG	GGGATTTTCA	CATGTTGGCC	AGGCTGGTCT	TGAACCTCTG	2100
ACCTCATGAT	CCACCCACCT	TAGCCTCCCA	AAGTGCTGGG	ATTAGGTGTG	AGCCACCGCA	2160
CCTGGCCGAT	ATTTCTTTTA	ATGAAATTTA	TAAATATGCT	TCTTGAATAA	TACACATTTT	2220
GGGAAAGGGA	AAAATGCTG	TTCAAAAAGT	AAAGGTCTCT	TTTATAGCTT	TTCCAAACTT	2280
AATTGCTAAA	TTTTCTTTTG	AGGTTCTCCT	GAATTATGTC	TTACAAACTA	AAAGCAAAAA	2340
TTTTTAGCAG	AAATTTTGA	ATACATTCTA	TCTAGCACAA	TTTGAATTTT	TAATTATCAA	2400
GATTTTGTGT	AAAGTTTCTC	TCCTTTAAAA	ATTTTAGTAC	ATTTGTAAT		

Seq ID NO: 483 Protein sequence
Protein Accession #: BAB70980.1

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MGTIHLFRKP	QRSFFGKLLR	EPRLVAADRR	SWKILLFVGI	NLICTGFLLM	WCSSTNSIAL	60
TAYTYLTIFD	LFSMLTCLIS	YWVTLRKPSP	VYSFGFERLE	VLAVFASTVL	AQLGALFILK	120
ESAERPLEQP	BIHTGRLLVG	TFVALCFNL	TMLSRNKPF	AYVSEAASTS	WLQEHVADLS	180
RSLCGIIPGL	SSIFLPRMNP	FVLIDLAGAF	ALCITYMLIE	INNYFAVDTA	SAIAIALMTF	240
GTMPMSVYS	GKVLQITPP	HVIGQLDKLI	REVSTLDGVL	EVNRNEFWTL	GFGSLAGSVH	300
VRIRRDANEQ	MVLAHVNTNL	YTLVSTLTQ	IFKDDWIRPA	LLSGPVAANV	LNFSDDHVIP	360
MELLKGTDDL	NPVTSTPAKP	SSPPPEFSFN	TPGKNVNPVI	LLNTQTRPYG	FGLNHGHTFY	420
SSMLNQGLGV	PGIGATQGLR	TGFTNIPSR	GTNNRIGQPR	P		

Seq ID NO: 484 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..900

1	11	21	31	41	51	
ATGCCGCCGC	GGGAGCTGAG	CGAGGCCGAG	CGGCCCCGCG	TCCGGGCCCC	GACCCCTCCC	60
CGCGGGCGGC	GTAGCGCGCC	CCAGAGCTG	GGCATCAAGT	GCGTGTGGT	GGGCGACGGC	120
GCCGTGGGCA	AGAGCAGCT	CATCGTCAGC	TACACCTGCA	ATGGGTACCC	CGCGCGCTAC	180
CGGCCCACTG	CGCTGGAGCT	CTTCTCTGGT	ACGTACGTTT	AATCGCCCGT	CGCGCGCGGT	240
GGCTGCGGCG	GGGCTGTGCA	CCGGGGAGCT	GGGGCGGGCG	TCTCGGCGGG	AGGGCGCAGA	300
GGACCCCGGG	GAGGAGACTG	GAGCAGGCC	CGAGGTGGCG	CTGCTGCGGC	CCAGGACGCT	360
CTTCTTAATC	CAGCTCTTCC	CCGCCCGCGC	CCTGCACTGC	AAGTCTGGT	GGATGGAGCT	420
CCGGTGCAGA	TTAGCTCTG	GGACACAGCG	GGACAGGAGG	ATTTGACCG	ACTTCGTTCC	480
CTTTGCTACC	CGGATACCGA	TGTCTTCTCG	GCGTGCTTCA	GCGTGGTGCA	GCCAGCTCG	540
TTTCAAAACA	TCACAGAGAA	ATGGCTGCCC	GAGATCCGCA	CGCACAAACC	CCAGGCGCCT	600
GTGCTGCTGG	TGGGCACCCA	GGCGACCTG	AGGGACGATG	TCAACGTACT	AATTCAGCTG	660

GACCGGGGG GCGGGGAGG CCGGTGCCCC CAACCCAGG CTGAGGGTCT GGCCGAGAA 720
 ATCCGAGCCT GCTGCTACCT TGAGTGCTCA GCCTTGACGC AGAAGAACTT GAAGGAAQDA 780
 TTTGACTCGG CTATTCTCAG TGCCATTGAG CACAAAGCCC GGCTGGAGAA GAAACTGAAT 840
 GCCAAAGGTG TCGGACCCCT CTCCGCTGC CGCTGGAAGA AGTTCTTCTG CTTCGTTTGA

Seq ID NO: 485 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
 RPTALDTFSG TYVQSPVRPR GCGGAVHRGA GAGVSAGRRR GPRGSDWSRP RGGAGAAQDA 120
 LPNSGSPRPA FAVQVLVDGA PVRIELWDTA GQEDFDRLRS LCYPDTDVFL ACPFVVQPSS 180
 FQNITEKWL P EIRTHNPQAP VLLVGTQADL RDDVNVLIQL DQGGREGVPV QPQAQGLAEK 240
 IRACCYLECS ALTQKNLEK FDSAILSABE HKARLEKKLN AKGVRTLSRC RWKKFFCFV

Seq ID NO: 486 DNA sequence
 Nucleic Acid Accession #: XM_063832.2
 Coding sequence: 1..711

1 11 21 31 41 51
 ATGCCGCGGC GGGAGCTGAG CGAGGCGGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
 CCGCGGCGGC GTAGCGCGCC CCCAGAGCTG GGCATCAAAGT GCGTGCTGGT GGGCGACGGC 120
 GCCGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
 CGGCCCACTG CGCTGGACAC CTCTCTGTGT CAAGTCTCTG TGGATGGAGC TCCGGTGGCG 240
 ATTGAGCTCT GGGACACAGC GGGACAGGAG GATTTTGACC GACTTCGTTC CCTTTGCTAC 300
 CCGGATACCG ATGTCTTCTT GCGGTGCTTC AGCGTGGTGC AGCCCAAGCTC CTTTCAAAAC 360
 ATCAGAGAGA AATGGCTGCG CCAGATCCGC ACGCACAAAC CCCAGGCGCC TGTGCTGCTG 420
 GTGGGCAACC AGGCCGACCT GAGGGACGAT GTCAACGTAC TAATTGAGCT GGACCGAGGG 480
 GGCCGGGAGG GCGCCGTGCC CCAACCCAG GCTCAGGGTC TGGCCGAGAA GATCCGAGG 540
 TGCTGCTACC TTGAGTGCTC AGCCTTGACG CAGAAGAACT TGAAGGAAGT ATTTGACTCG 600
 GCTATTCTCA GTGCCATTGA GCACAAAGCC CGGCTGGAGA AGAAACTGAA TGCCAAAGGT 660
 GTGGCGACCC TCTCCGCTG CCGCTGGAAG AAGTCTTCT GCTTCGTTTG A

Seq ID NO: 487 Protein sequence
 Protein Accession #: XP_063832.1

1 11 21 31 41 51
 MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
 RPTALDTFSV QVLVDGAPVR IELWDTAGQE DFDRLSLCY PTDVFLACP SVVQPSFQFN 120
 ITEKWLPEIR THNPQAPVLL VGTQADLRDD VNVLIQLDQG GREGPVPQPO AQGLAEKIRA 180
 CCYLECSALT QKNLEKVFDS AILSAIEHKA RLEKKLNAGK VRTLSRCRWK KFFCFV

Seq ID NO: 488 DNA sequence
 Nucleic Acid Accession #: NM_014398.1
 Coding sequence: 64..1314

1 11 21 31 41 51
 GGCACCGATT CCGGGCCTGC CCGGACTTCG CCGCACGCTG CAGAACCTCG CCCAGCGCCC 60
 ACCATGCCCC GGCAGCTCAG CGCGGCGGCC GCGCTCTTGG CGTCCCTGGC CGTAATTTTG 120
 CACGATGGCA GTCAAATGAG AGCAAAAGCA TTTCCAGAAA CCAGAGATTA TTCTCAACCT 180
 ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACGAGC TAAGCAAGCA 240
 CCTCACCAAA CTTTAGCAGC AGGATTCATG GATGGTCATA TCACCTTTCA AACACGCGGC 300
 ACAGTAAAAA TTCCAACAAC TACCCAGCA ACTACAAAAA AACTGCAAC CACCAGCCCA 360
 ATTACTACA CCGTGTGTAC AACCCAGGCC ACACCCAACA ACTCACACAG AGCTCTCCA 420
 GTTACTGAAG TTACAGTCGG CCCTAGCTTA GCCCCTTATT CACTGCCACC CACCATCACC 480
 CCACGAGCTC ATACAGCTGG AACCACTTCA TCAACCGTCA GCCACACAAC TGGGAACACC 540
 ACTCAACCCA GTAACAGAGC CACCCCTTCA GCAACTTTAT CGATAGCACT GCACAAAAGC 600
 ACAACCGGTC AGAAGCCTGA TCAACCCACC CATGCCCGAG GAACAACGGC AGCTGCCACC 660
 AATACCAACC GCACAGCTGC ACCTGCCTCC ACGGTTCTCG GGCCCAACCT TGCACCTCAG 720
 CCATCGTCAG TCAAGACTGG AATTTATCAG GTTCTAAACG GAAGCAGACT CTGTATAAAA 780
 GCAGAGATGG GGATACAGCT GATTGTTCAA GACAAGGAGT CGGTTTTTTC ACCTCGGAGA 840
 TACTTCAACA TCGACCCCAA CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CCGAAAATCC 900
 AACCTTCTGT TGAATTTTCA GGGCGGATT TGAATCTCA CATTACCAA GGATGAAGAA 960
 TCATATTATA TCAGTGAAGT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC 1020
 CAAGGAATCA AACATGCGGT GGTGATGTTT CAGACAGCAG TCGGCAATTC CTTCAGTGC 1080
 GTGAGTGAAC AGAGCCTCCA GTTGTGAGCC CACCTGCAGG TGAACAACAC CGATGTCCAA 1140
 CTTCAAGCCT TTGATTTTGA AGATGACCAC TTTGGAAATG TGGATGAGTG CTCGTCTGAC 1200
 TACACAATTG TGCTTCTGT GATTGGGGCC ATCGTGGTGT GTCTCTGCCT TATGGGTATG 1260
 GGTGTCTATA AAATCGCCT AAGGTGTCAA TCATCTGGAT ACCAGAGAAT CTAATTGTTG 1320
 CCGGGGGGGA ATGAAATATA TGGAAATTAG AGAACTCTTT CATCCCTTCC AGGATGGATG 1380
 TTGGGAAATT CCGTCAGAGT GTGGGTCTTT CAAACAATGT AAACCAACAT CTTCTATTCA 1440
 AATGAAGTGA GTCATGTGTG ATTTAAGTTC AGGCAGCACA TCAATTCTTA AATACTTTT 1500
 GTTTATTTTA TGAAGATAT AGTGAGCTGT TTAATTTCTA GTTTCCTTTA GAATATTTTA 1560
 GCCACTCAAA GTCAATCAATT GAGATATGTT GAATTAACAT AATATATGTA AAGTAGAATA 1620
 AGCCTTCAAA TTATAAACCA AGGTCATATT GTAACATAA CTACTGTGTG TGCATTGAAG 1680
 ATTTTATTTT ACCCTTGATC TTAACAAGC CTTTGTCTTG TTATCAATG GACTTTCAGT 1740
 GCTTTTACTA TCTGTGTTTT ATGGTTTCAT GTAACATACA TATTCCTGGT GTAGCACTTA 1800
 ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTGGAGAC GAGATTTTCC TCTGTTCACC 1860
 CAGGCTGGAG TACAGTGGCA CGATCTCGGC TTATGGCAAC CTCGCGCTCC CGGGTTCAG 1920
 TGATTTCTCT GCTTCAGCTT CCGAGTAGC TGGGATTACA GGCACACACT ACCACGCTG 1980
 GCTAATTTT GTATTTTAT TATAGACGGG TTTCAACATG TTGGCCAGAC TGGTCTTGAA 2040
 CTCTTGACCT CAGGTGATCC ACCCACTCA GCCTCCCAA GTGCTGGGAT TACAGGCATG 2100
 AGCCATTGCG CCGGCTCTTA AATGTTTTT TTAATCATCA AAAGAACAA CATATCTCAG 2160

GTTGTCTAAG TGTTTTATG TAAACCAAC AAAAAGAACA AATCAGCTTA TATTTTAT 2220
 CTTGATGACT CCGTCTCCAG AATGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA 2280
 CTAACAATA AGCAAGAGAC AATAAATG GCCCTTAATT ATTAACAAAG TGCCAGAGTC 2340
 TAGGCTAAGC ACTTTATCTA TATCTCATTT CATCTCACA ACTTATAAGT GAATGAGTAA 2400
 ACTGAGACTT AAGGGAACCT AATCACTTAA ATGTCACCTG GCTAACTGAT GGCAGAGCCA 2460
 GAGCTTGAAT TCATGTTGGT CTGACATCAA GGTCTTTGGT CTTCTCCCTA CACCAAGTTA 2520
 CCTACAAGAA CAATGACACC ACACCTGCCC TGAAGGCTCA CACCTCATAC CAGCATACGC 2580
 TCACCTTACA GGGAAATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG 2640
 AGCTTTGCGA ATAACAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC 2700
 TGAGGGGCTT TGTAAACAT TAGTCAGTTG CTCATTTTAA TGGGATTGCT TAGCTGGGCT 2760
 GTAAAGATGA AGGCATCAAA TAAACTCAAA GTATTTTAA ATTTTITTTGA TAATAGAGAA 2820
 ACTTCGTAA CCAACTGTTT TTTCTGAGT GTATAGCCCC ATCTTGTGGT AACTTGCTGC 2880
 TTCTGCATT CATATCCATA TTTCTATTTG TTCATTTAT TCTGTAGAGC AGCCTGCCAA 2940
 GAATTTTATT TCTGCTGTTT TTTTGTCTGC TAAAGAAAGG AACTAAGTCA GGATGTTAAC 3000
 AGAAAAGTCC ACATAACCTT AGAATTCTTA GTCAAGGAAT AATTCAAGTC AGCCTAGAGA 3060
 CCATGTTGAC TTTCCTCATG TTTTCTCTTA TGACTCAGTA AGTTGGCAAG GTCCTGACTT 3120
 TAGTCTTAAT AAACATTGA ATTGTAGTAA AGGTTTTTGC AATAAAAACT TACTTTGG

Seq ID NO: 489 Protein sequence
 Protein Accession #: NP_055213.1

1 11 21 31 41 51
 MPRQLSAAAA LFASLAVILH DGSQMRKAF PETRDYSQPT AAATVQDIKK PVQPAKQAP 60
 HQTLAARFMD GHITFQTAAT VKIPTTTTAT TKNTATTSPI TYTLVTTQAT PNNSTAPPV 120
 TEVTVPFSLA PYSLPPTITP PAHTAGTSSS TVSHTTGNTT QPSNQTTLPA TLSIALHKST 180
 TGQKPDQPTH APGTTAAAHN TTRTAAPAST VPGPTLAPQP SSVKTIYQV LNSRLCLKA 240
 EMGIQLIVQD KESVFPSPRY FNIDPNATQA SGNGCTRKSN LLLNFQGGFV NLFTKDEES 300
 YYISEVGAYL TVSDPETVVO GIKHAVVMFQ TAVGHSFKCV SEQSLQLSAH LQVKTVDVQL 360
 QAFDFEDDHF GNVDECSSDY TIVLPVIGAI VVGLCLMGMG VYKIRLRCQS SGYQRI

Seq ID NO: 490 DNA sequence
 Nucleic Acid Accession #: NM_005409.3
 Coding sequence: 94..378

1 11 21 31 41 51
 TTCCTTTCAT GTTCAGCAIT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60
 CAACAGCACC AGCAGCAACA GCACAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
 TTGGCTGTGA TATGTGTGTC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACCC 180
 TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 ATAATGTACC CAAATTAACA CTGTGACAAA ATAGAAGTGA TTATTACCTT GAAAGAAAAA 300
 AAAGGACAAC GATGCCATAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT 360
 GAAAGAAAGA ATTTTAAAAA ATATCAAAAC ATATGAAGTC CTGGAAGAGG GCATCTGAAA 420
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAACTG 480
 AGACTTTTCT ATGGTTTGTG GACTTTCAAC TTTGTACAG TTATGTGAAG GATGAAAGGT 540
 GGGTGAAGAG ACCAAAAACA GAAATACAGT CTTCTGAAT GAATGACAAT CAGAAATCCA 600
 CTGCCAAAGG GATGCCAGCA ATTAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
 GGTACCATC GAGATTACA AAGTCTTTC ACGTCTTAC TTGTGTATT ATACATTCAT 720
 GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
 GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
 CATCTATGTG TCGTAAAGCA TFCCTCAAC ATTTTTCAT CCAAAATACAC ACTTCTTTCC 960
 CCAATATCA TGTAGCACAT CAATATGTAG GAAACATTC TTATGCATCA TTTGGTTTGT 1020
 TTTATAACCA ATTCATTAAA TGTAAATCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
 TGGGACTACT GCACAGATGC ACATATTTCA TAACCAAAAT AGCAGCACCG GTCTTAATTT 1140
 GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
 TGTACTTTTT GTTTTGAATC GTTTGTATTA ATGATAGCAA TATCTTGGAC ACATTGTAAA 1260
 TACAAATGT TTTTGTCTAC CAAAGAAAAA TGTGTAAAAA TAAGCAAAATG TATACCTAGC 1320
 AATCACTTTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
 TTGTTTATGC CTATATACTG TAAATTTTAG GTATACTCAA GACTAGTTTA AAGAAATCAA 1440
 GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTCTTTT TTAACAAAAA AAA

Seq ID NO: 491 Protein sequence
 Protein Accession #: NP_005400.1

1 11 21 31 41 51
 MSVKGMAIAL AVILCATVVO GPFMPKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60
 EVIITLKENK GQRCLNPKSK QARLIHKVE RKNF

Seq ID NO: 492 DNA sequence
 Nucleic Acid Accession #: NM_000577.1
 Coding sequence: 41..520

1 11 21 31 41 51
 GGCACGAGGG GAAGACCTCC TGTCTATCA GGCCCTCCCC ATGGCTTTAG AGACGATCTG 60
 CCGACCTCTT GGGAGAAAAA CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAAACA 120
 GAAGACCTTC TATCTAGGGA ACAACCAACT AGTTGCCGGA TACTTGCAAG GACCAAAATGT 180
 CAATTTAGAA GAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
 CCATGGAGGG AAGATGTGCC TGTCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
 GGAGGCAGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCCTT 360
 CATCCGCTCA GCAGTGGGCC CCACCAACAG TTTTGTAGTCT GCGCGCTGCC CCGTTTGGTT 420
 CCTCTGCACA GACGATGAGG CTGACGACCT ACCAATATGC CTGACGAAAG 480
 CGTCATGCTC ACCAAATTCT ACTTCCAGGA GGACGAGTAG TACTGCCACG GCCTGCCTGT 540
 TCCCATTTCT GCATGGCAAG GACTGCAGGG ACTGCCAGTC CCCCTGCCCC AGGGCTCCCC 600

GCTATGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACAACAA 660
 CCTGGTCACA GGACTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCCAGAATG 720
 GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCTTGCA CAAAGCCCTT CCATGTGCGC 780
 TCTGCATTCA GGATCAAAAC CCGACCACCT GCCCAACCTG CTCTCTCTTT GCCACTGCCT 840
 CTTCCCTCCCT CATTCACCAT TCCCATGCCC TGGATCCATC AGGCCACTTG ATGACCCCCA 900
 ACCAAGTGGC TCCACACACC TGTTTTACAA AAAAGAAAAA ACCAGTCCAT GAGGGAGGTT 960
 TTTAAGGGTT TGTGGAATAT GAAAATTAGG ATTTCATGAT TTTTCTTTT CAGTCCCGT 1020
 GAAGGAGAGC CCTTCATTG GAGATTATGT TCTTTCGGG AGAGGCTGAG GACTTAAAT 1080
 ATTCTGCTAT TGTGAAATG ATGGTGAAAG TAAGTGGTAG CTTTCCCTT CTTTCTCTC 1140
 TTTTCTGTG ATGTCCCAAC TTGTAATAAT TAAAGTTAT GGTACTATGT TAGCCCCATA 1200
 ATTTTTTTTT TCCTTTTAAA ACACTTCCAT AATCTGGACT CCTCTGTCCA GGCAGTCTG 1260
 CCCAGCTCC AAGCTCCATC TCCACTCCAG ATTTTITACA GCTGCTGCA GTACTTTACC 1320
 TCCTATCAGA AGTTTCTCAG CTCCCAAGGC TCTGAGCAA TGTGGCTCCT GGGGGTTCTT 1380
 TCTTCTCTG CTGAAGGAAT AAATTGCTCC TTGACATTGT AGAGCTTCTG GCACCTGGAG 1440
 ACTTGTATGA AAGATGGCTG TGCCTCTGCC TGTCTCCCC ACCAGGCTGG GAGCTCTGCA 1500
 GAGCAGGAAA CATTGCTCGT ATATGTCTCA GGTCCCTGCA GGGCCAAGCA CCTAGCCTCG 1560
 CTCTTGCGAG GTACTCAGCG AATGAATGCT GTATATGTTG GGTGCAAGT TCCCTACTTC 1620
 CTGTGACTTC AGCTCTGTTT TACAATAAAA TCTTGAATAA GCCTAAAAA AAAAAAAA 1680
 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAA

Seq ID NO: 493 Protein sequence
 Protein Accession #: NP_000568.1

1 11 21 31 41 51
 MALETICRPS GRKSSKMQAF RIWDVNQKTF YLRNNQLVAG YLQGPVNLE EKIDVVPPIEP 60
 HALEFLGIHGG KMCLSCVKSG DETRLQLEAV NITDLSENRK QDKRFAPIRS DSGPTTGFES 120
 AACPGWFLCT AMEADQPVSL TMPDEGVMV TKPYFQEDE

Seq ID NO: 494 DNA sequence
 Nucleic Acid Accession #: NM_002081.1
 Coding sequence: 222..1898

1 11 21 31 41 51
 GGCTGCCCGA GCGAGCGTTC GGACCTCGCA CCCCGCGCGC CCCGCGCGCC CGCGCGCGCC 60
 GGCTTTTGTG GTCTCGGCTT CCTCGGCGCG CGCGCGCTCT GGACCGCGAG CCGCGCGCGC 120
 CGGAGACCTTG GCTCTGCCCT TCGCGGCGCG GAACTGCGCA GGACCGCGCC AGGATCCGAG 180
 AGAGGCGCGG GCGGGTGGCC GGGGCGCGCG CCGGCCCGCG CATGGAGCTC CGGCGCGGAG 240
 GCTGGTGGCT GCTATGTGCG GCCGCGCGCG TGGTGGCTG CGCCCGCGGG GACCCGCGCA 300
 GCAAGAGCGG GAGCTGCGCG GAGGTCCGCG AGATCTACGG AGCCAAGGGC TTCAGCCTGA 360
 GCGACGTGCC CAGGCGGAG ATCTCGGGTG AGCACCTGCG GATCTGTCCC CAGGGCTACA 420
 CCTGCTGCAC CAGCGAGATG GAGGAGAAC TGGCCAACCG CAGCCATGCC GAGCTGGAGA 480
 CCGGCTCCG GGACAGCAGC CGGTCCTGCG AGGCCATGCT TGGCACCAG CTGCGCAGCT 540
 TCGATGACCA TTTCACAGAC CTGCTGAACG ACTCGGAGCG GACGCTCGAG GCCACCTTCC 600
 CCGCGCGCTT CCGAGAGCTG TACACGCGAG ACGCGAGGGC CTTCCGGGAC CTGTACTCAG 660
 AGCTGCGCCT GTACTACGCG GGTGCCAAC TGCACTTGGG GAGAGCGCTG GCCGAGTTCT 720
 GGGCGCGCCT GCTCGAGCGC CTCTCAAGC AGCTGCAACC CAGCTGCTG CTGCTGATG 780
 ACTACCTGGA CTGCTGGGCG AAGCAGGCGG AGGCGCTGCG GCCCTTCGGG GAGGCCCGGA 840
 GAGAGCTGCG CTTGCGGGCG ACCCGTGCTT TCGTGGCTGC TCGCTCCTTT GTGCGAGGCG 900
 TGGCGGTGGC CAGCGACGTG GTCCGGAAG TGGCTCAGGT CCCCCTGGGC CCGGAGTGCT 960
 CGAGAGCTGT CATGAAGCTG GTCTACTGTG CTCACTGCCT GGGAGTCCCC GGGCGCAGGC 1020
 CCTGCCCTGA CTATTGCCGA AATGTGCTCA AGGGCTGCCT TGCCAACAG GCCGACCTGC 1080
 ACGCGAGTG GAGGAACCTC CTGGACTCCA TGGTGTCTAT CACCGACAAG TTCTGGGGTA 1140
 CATCGGCTGT GGAGAGTGTC ATCGGCGAGG TGCACACGTG GCTGGCGGAG GCCATCAACG 1200
 CCCTCCAGGA CAACAGGGAC ACGCTCACGG CCAAGGTCAT CAGGGCTGCG GGGAAACCCA 1260
 AGGTCAACCC CAGGGCCCTT GGGCTGAGG AGAAGCGCGG CCGGGCGAAG CTGGCCCCCG 1320
 GGGAGAGGCC CACTTACAGC ACGCTGGAGA AGCTGGTCTC TGAAGCCAAG GCCCAGCTCC 1380
 GCGACGTCCA GGACTTCTGG ATCAGCCTCC CAGGGACACT GTGCACTGAG AAGATGGCCC 1440
 TGAGCACTGC CAGTGATGAC CGCTGCTGGA ACGGGATGGC CAGAGGCGCG TACCTCCCCG 1500
 AGGTCTATGG TGACGGCTG GCCAACCAGA TCAACAACCC CAGAGTGAGG GTGGACATCA 1560
 CCAAGCCGGA CATGACCATC CGGCAGCAGA TCAATGCAGT GAAGATCATG ACCAACCAGC 1620
 TGGCGAGCGC CTACAACGCG AACGACGTGG ACTTCCAGGA CGCCAGTGAC GACGGCAGCG 1680
 GCTCGGCGAG CGGTGATGCG TGTCTGATG ACCTCTCGCG CCGGAAGGTC AGCAGGAAGA 1740
 GCTCCAGCTC CCGGACGCCC TTGACCCATG CCTTCCAGG CTTGTCAAG CAGGAAGGAC 1800
 AGAAGACCTC GGCTGCCAGC TGCCCCCAGC CCGGACCTT CCTCTGCC CTCTCTCTCT 1860
 TCCTGGCCCT TACAGTAGCC AGGCCCGGCT GCGGTAAT GCCCCAAGGC CCCAGGGACA 1920
 GAGGCCAAGG ACTGACTTTG CCAAAAAATC AACACAGACG ATATTTAATT CACTCAGCC 1980
 TGGAGAGGCC TGGGTGGGA CAGGGAGGGC CGGCGGCTCT GAGCAGGGGC AGGCGCAGAG 2040
 GTCCAGCCCC CAGGCTGCG CTGCGCTGCC TTTCTGCTT TTAATTTTGT ATGAGGTCTT 2100
 CAGGTCACTG GGGAGCCAGT GTGCCAAAA GCCATGTATT TCAGGGACCT CAGGGGCACC 2160
 TCGGCTGCTC TAGCCCTCCC CCCAGCTCCC TGACCCGCG CAGAAGCAGC CCTTCGAGGC 2220
 CTACAGAGGA GGCCTCAAAG CAACCCGCTG GAGCCCAAG CAGGCTGTG CCTTCCCTCC 2280
 CGCTCTCTCC CACTGGGACT CCCAGCAGAG CCCACCAAGC AGCCCTGGCC CACCCCCAG 2340
 CCTCCAGAGA AGCCCCGAC GGGCTGTCTG GGTGTCCGCC ATCCAGGGTC TGGCAGAGCC 2400
 TCTGAGATGA TGCATGATG CCTCCCTTCA GCGCAGGCTG CAGAGCCCG CCCACCTCC 2460
 CTGCGCCCTT GAGGGTCCCC AGOBTCTGCA GGGTGAAGCC TGAGACAGCA CCACTGTCTGA 2520
 GGAATCTGAG AGGTGCTCTT CCACAGACCC TGCACTGAGG GGCCTCCAT GCGCAGATGA 2580
 GGGGCACTG ACCCACTGCG GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAAGGCCAG 2640
 GGAGGACCG TGGCTCTGCG CAATGTGGGC TGCCCCCTCG ACACAGGGCT CACAGGGCAG 2700
 GCCTTGCTGG GGTCCAGGGC TGTGGAGGA CCCCGAGGGC TGAGGAGCAG CCAGGACCCG 2760
 CAGTCTCCCA TCCTCACCCA GATCAGGAAC CAGGGCTCTC CTGTTCACGG TGACACAGGT 2820
 CAGGGCTCAG AGTGACCTTC GGCTGTACCC TGCTCACAGG GATGCTGGTG GCTGGTGA 2880
 CCCGCACTG CACACGGGAA TGCCTAGGTC CCTTCCGAG CAGCCAGCT GCACTGCAGG 2940
 GCACGGGGAG CTGGATGATT AAGGGCTTTT CCRAACATGC ATCCATTAC TGACACTTCC 3000
 TGTCTTGTG CATGGAGAGC TGTTCGCTCC TCCAGATGG CTTCCGAGGC CCGCAGGGCC 3060
 CACTTGGAGC CCTGGTGACC TCCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCCAGGC 3120

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PCT/US02/12476

CTGGACGGGC CCTCCTTCCC TCCTGTGCCC CAGCTGCCAG GTGGCCCTGG GGAGGGGTGG 3180
TGTGGTGTGT GGAAGGGGTC CTGCAGGGGG AGGAGGACTT GGAGGGTCTG GGGGCAGCTG 3240
TCCTGAACCG ACTGACCCCTG AGGAGGCCGC TTAGTGCTGC TTTGCTTTTC ATCACCGTCC 3300
CGCACAGTGG ACGGAGGTCC CCGGTTGCTG GTCAAGTCCC CATGGCTTGT TCTCTGGAAC 3360
CTGACTTTAG ATGTTTTTGG ATCAGGAGCC CCCAACACAG GCAAGTCCAC CCCATAATAA 3420
CCCTGCCAGT GCCAGGGTGG GCTGGGACT CTGGCACAGT GATGCCGGGC GCCAGGACAG 3480
CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGCGCT CAGACCCAC CCTACGCTCA 3540
TCTCTGGAAG GGGCAGCCCT GAGTGGTCAC TGGTCAGGGC AGTGGCCAAG CCTGCTGTGT 3600
CCTTCTCCA CAAGGTCCCC CCACGCTCA GTGTCAGCGG GTGACGTGTG TTCTTTTGTAG 3660
TCCTTGTATG AATAAAGGC TGGAAACCTA AA

Seq ID NO: 495 Protein sequence
Protein Accession #: NP_002072.1

1 11 21 31 41 51
MELRARGMWL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSQVQ QAEISGEHLR 60
ICPQGYTCCT SEMENLANR SHALETALR DSSRVLQAML ATQLRSFDDH FQHLNDSEK 120
TLQATPPGAP GELYTONARA FRDLYSELRL YVRGANLHLE BTLAEFWARL LERLFKQLHP 180
QLLLPDDYLD CLGKQAEALR PFGEAPRELRL LRATRAFVAA RSPVQGLGVA SDVVRKVAQV 240
PLGPECSRVA MKLVYCAHCL GVPGARPCPD YCRNVKGLCL ANQADLDAEW RNLLDSMVL 300
TDKFWGTSGV ESVGSGVHTW LAEAINALQD NRDTLTAKVI QCGGNPKVNP QGPGPEEKRR 360
RGKLAPRERP PSGTLEKLVS EAKAQLRDVQ DFWSLPGTL CSEKMLSTA SDDRCWNGMA 420
RGRYLPVVMG DGLANQINNP EVEVDITKPD MTRIQQIMQL KIMTNRLRSA YNGNDVDFQD 480
ASDDGSGSGS

Seq ID NO: 496 DNA sequence
Nucleic Acid Accession #: NM_001650.2
Coding sequence: 40.1011

1 11 21 31 41 51
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AGGCGGTGGG GTAAGTGTGG ACCTTTGTGT ACCAGAGAGA ACATCATGGT GGCTTTCAAA 120
GGGGTCTGGA CTCAGCTTT CTGGAAGCA GTCAAGCGG AATTCTGGC CATGCTTATT 180
TTTGTCTCC TCAGCTGGG ATCCACCATC AACTGGGGT GAACAGAAA GCCTTTACCG 240
GTGACATGG TCTCATCTC CCTTGTCTT GGAATCAGCA TTGCAACCAT GGTGCGATGC 300
TTTGGCCATA TCAGCGGTGG CCACATCAAC CCTGCAGTGA CTGTGGCCAT GGTGTGCACC 360
AGGAAGATCA GCATCGCCAA GTCTGTCTTC TACATCGCAG CCCAGTGCCT GGGGGCCATC 420
ATTGGAGCAG GAATCCTCTA TCTGGTCACA CCTCCAGTG TGGTGGGAGG CTTGGGAGTC 480
ACCATGGTTC ATGGAATCT TACCGCTGGT CATGGTCTCC TGGTTGAGTT GATAATCACA 540
TTTCAATTGG TGTCTACTAT CTCTGCCAGC TGTGATTTCA AACGAGCTGA TGTCACCTGGC 600
TCAATAGCTT TAGCAATTGG ATTTCTGTT GCAATTGGAC ATTTATTGC AATCAATTAT 660
ACTGGTGCCA GCATGAATCC CGCCGATCC TTTGGACCTG CAGTATCAT GGGAAATTTG 720
GAAAACCATT GGATATATTG GGTGGGCC ATCATAGGAG CTGTCTCTGC TGGTGGCCTT 780
TATGAGTATG TCTCTGTGCC AGATGTTGAA TTCAAACGTC GTTTTAAAGA AGCCTTCAGC 840
AAAGCTGCCC AGCAACAAA AGGAAGCTAC ATGGAGGTGG AGGACAACAG GAGTCAGGTA 900
GAGACGGATG ACCTGATTCT AAAACCTGGA GTGGTGCATG TGATTGACGT TGACCGGGGA 960
GAGGAGAAAG AGGGGAAAGA CCAATCTGGA GAGGTATTGT CTTCAATATG ACTAGAAGAT 1020
CGCACTGAAA CAGACACAAG CTCCTTAGAA CTGTCTCTAG ATTTCTCTCC ACCCATTAAG 1080
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GTCTAAACAA TAAATATTTC ATAATTACA AAGGAGGAAC GGAAGAAACC TATTGTGAAT 1200
TCCAAATCTA AAAAAGAAA TATTTTAAAG ATGTTCTTAA GCAATATAT ACCTATTTTA 1260
TCTAGTTACC TTTCATTAA AACCATTAT AACCCTGTGT CAAGATTGG TTAAGCTCTG 1320
CCTGACAGAA CTCAAAGACA CGTCTATCAG CTTATTCTCT CTCTACTGGA ATATTGGTAT 1380
AGTCAATTCT TATTGAATA TTTATTCTAT TAAACTGAGT TTAACAATGG C

Seq ID NO: 497 Protein sequence
Protein Accession #: NP_001641.1

1 11 21 31 41 51
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GTEKPLPVDV VLISLCFGLS IATMVQCFGH ISGGHINPAV TVAMVCTRKI SIAKSVFYIA 120
AQCLGAIIGA GILYLVTPPS VVGGLVITMV HGNLTAGHGL LVELIITFQL VFTIFASCD 180
KRTDVTGSIA LAIGFSVAIG HLPAINYGA SMNPARSFGP AVIMGNWENH WIYWVGPIIG 240
AVLAGGLYEV VPCPDVEPKR RFKEAFSKAA QQTGKSYMEV EDNRSQVETD DLILKPGVVH 300
VIDVDRGEEK KGKQSGEVL SSV

Seq ID NO: 498 DNA sequence
Nucleic Acid Accession #: AB020684.1
Coding sequence: 1..1744

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GACGGTTACC AGAGGAGAAG GACTCAGTCC TATTGAAGC TGTGAAGGAT TGGGAGATCC 180
TGCTTGCTTT TATGTGCTG TAATTTTAT TTTAAATGGA CTAATGATGG CATTATTCTT 240
CATATATGCG ACATATTTAA GTGGCAGCCG ATTAGGAGGC CTGGTTACAG TGTGTGCTT 300
CTTTTTCAT CATGAGAGT GTACCCGTGT AATGTGGACA CCACCTCTCC GTGAAAGCTT 360
CTCATATCCA TTTCTTGTTC TCCAGATGTT GCTAGTGACT CATATTCTCA GGGCTACAAA 420
ACTTTATAGA GGAAGCTTGA TTGCACTCTG CATTTCCAAT GTATTTTCA TGCTTCTTG 480
GCAGTTTGCT CAGTTTGATC TTCTTACTCA GATTGCATCA TTATTGTCAG TATATGTTGT 540
CGGGTACATT GATATATGTA AATTACGGA GATCATTAT ATACACATGA TTTCTCTTGC 600
ACTTTGTTTT GTTTTGATGT TTGGGAACCT AATGTTATTA ACTTCTTATT ATGCTTCTTC 660
TTTGGTAATT ATTTGGGGTA TTTGGCAAT GAAACCACAT TTCCTGAAAA TAAATGTATC 720

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TGAACCTAGT TTATGGGTTA TTCAAGGATG TTTTGGTTA TTTGGAAGTG TCATACTTAA 780
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 AGGTTTCAGCA AATCTGCAAA CCCAGTGGAA TATTGTAGGG GAGTTCAGCA ATTTGCCCCA 1320
 AGAAGAACTT ATAGAATGGA TCAAAATATG TACTAAACCA GATGCACTGT TTGCGGGTGC 1380
 CATGCCACAG ATGGCAAGTG TTAAGCTCTC TGCACCTCGG CCCATTGTGA ATCATCCACA 1440
 TTATGAAGAC GCAGGCTTGA GAGCCAGAAC AAAAATAGTA TACTCAATGT ATAGTCGGAA 1500
 AGCAGCCGAA GAAGTGAAGC GAGAACTGAT AAAGTTAAAG GTGAACATTG ACATTCTAGA 1560
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 AACGTTTTAT TTGTTCAATT TGAATGTCAT TCTAATTATA AAAATGACTT ACACCTTTAT 1920
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 TACTTGACTT TAATATTGTG GCTAAAGTGA GCAAGCTAC CTGTATAAAG AAAACACAGT 2040
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 ACAGTAGACT GGGCAGACAT GGAGTGTGTT CTATATAAAA CTATCTGTTT GTTTTACTTC 2280
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 GTGTCTCTTT GTCTCTCTCT CTCTCTCTCT CTCTCTCTCT CTCTCTCTCT TTTTCTGTCA 2460
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 TCGCAGCCCA AGCATGTGG AGCATCCACA CCTTGTATGG CAATGCAGAT TGGTAGCAGG 4080
 TTCCATAGGC GTACAAAACG GTATTAAAGC TCAGTGTGTT GCATATTGTT AGCATTACA 4140
 AATATTTTGG CTTTAGTAGT AGGAAGGTAA GGATGGGCAA AGAAGCGATC AAAATAGCTA 4200
 TTGCTACAAC ATTTTCGAAA ACAAGTTGG GGCTGTATTT CTTTAAAAAG ATAAGCCTCT 4260
 AAAAAATGCTT GGCAAAAAAA ATATAGTGTT AAAATAGGCC AGTGATATTA ATGAGAAAAT 4320
 GAAAGTATGT ATCAGGAATA AAGTGATATT GCATAGGAGT ATGTATTTT TATGAATTTT 4380
 ATGCCAGTTG TTTACATGTA CTATATATGT TAAATTAATA AAAATCATGA GAAATG

Seq ID NO: 499 Protein sequence
 Protein Accession #: BAA74900.1

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1 11 21 31 41 51
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 PLVINTLKRP NLYPEVILAS WYRIYTKIMD LIQIQTKICW TVTRGEGLSP IESCEGLGDP 60
 ACFYVAVIFI LNGLMMALFF IYGTYLSGSR LGQLVTVLCP PFNHGECTRV MWTPLRESF 120
 SYFFVLVQLM LVTHILRATK LYRGLIALC ISNVFFMLPW QFAQFVLLTQ IASLPAVVV 180
 GYIDICKLRK IYIHMISLA LCPVLMFGNS MLLTSYIASS LVIIWGLAM KPHFLKINVS 240
 ELSLWVIQGC FWLPGTVILK YLTSKIFGIA DDAHIGNLLT SKFPSYKDFD TLLYTCAEF 300
 DFMEKETPLR YTKTLLLPV LVVFVAIVRK IISDMWGLA KQTHVRKHQ FDHGLVYHA 360
 LQLLAYTALG ILIMRLKFL TPHMCMVASL ICSRQLFGWL FCKVHPGAIV FAILAAMSIQ 420
 GSANLQTOWN IVGEFSNLPO EELIEWIKYS TKPDAVPAGA MPTMASVKLS ALRPIVNHFH 480
 YEDAGLRART KIVYSMSYRK AAEVVKRELI KLVNYYILE ESWCVRRSKP GCSMPEINDV 540
 EDPANAGTFP LCNLLVKDSK PHFTTVFQNS VYKVLVVKE

Seq ID NO: 500 DNA sequence
 Nucleic Acid Accession #: NM_001276.1
 Coding sequence: 127..1278

85

1 11 21 31 41 51
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5 GGCAGAAATGG GTGTGAAGGC GTCTCAAACA GGCTTTGTGG TCCTGGTGCT GCTCCAGTGC 180
 TGCTCTGCAT ACAAACTGGT CTGCTACTAC ACCAGCTGGT CCCAGTACCG GGAAGGCGAT 240
 GGGAGCTGCT TCCCAGATGC CCTTGACCGC TTCCTCTGTA CCCACATCAT CTACAGCTTT 300
 10 GCCAATATAA GCAACGATCA CATCGACACC TGGGAGTGA ATGATGTGAC GCTCTACGGC 360
 ATGCTCAACA CACTCAAGAA CAGGAACCCC AACCTGAAGA CTCTCTGTGC TGTGCGGAGGA 420
 TGGAACTTTG GGTCTCAAAG ATTTTCCAAG ATAGCCTCCA ACACCCAGAG TCGCCGGGACT 480
 TTCATCAAGT CAGTACCGCC ATTCCTGCGC ACCCATGGCT TTGATGGGCT GGACCTTGCC 540
 TGGCTCTACC CTGGACGGAG AGACAAACAG CATTTTACCA CCCTAATCAA GGAAATGAAG 600
 GCGGAATTTA TAAAGGAAGC CCAGCCAGGG AAAAAGCAGC TCCTGCTCAG CGCAGCACTG 660
 TCTGCGGGGA AGGTCAACAT TGACAGCAGC TATGACATTG CCAAGATATC CCAACACCTG 720
 GATTTTCATTA GCATCATGAC CTACGATTTT CATGGAGCCT GCGTGGGAC CACAGGCCAT 780
 CACAGTCCCC TGTTCGGAGG TCAGGAGGAT GCAAGTCTCT ACAGATTGAG CAACACTGAC 840
 TATGCTGTGG GGTACATGTT GAGGCTGGGG GCTCTGCCA GTAAGCTGGT GATGGGCATC 900
 15 CCCACCTTGG GGAGGAGCTT CACTCTGGCT TCTTCTGAGA CTGGTGTGG AGCCCCAATC 960
 TCAGGACCGG GAATTCAGG CCGGTTCAAC AAGGAGGAGG GGACCTTTC CTACTATGAG 1020
 ATCTGTGACT TCCTCCGGG AGCCACAGTC CATAGAACC TCGGCCAGCA GGTCCCTAT 1080
 GCCACCAAGG GCAACGAGTG GGTAGGATAC GACGACCAGG AAAGCGTCAA AAGCAAGGTG 1140
 CAGTACCTGA AGGATAGGCA GCTGGCAGGC GCCATGGTAT GGGCCCTGGA CCTGGATGAC 1200
 20 TTCCAGGGCT CTTCTGCGG CCAGGATCTG CGCTTCCCTC TCACCAATGC CATCAAGGAT 1260
 GCACTCGCTG CAACGTAGCC CTCTGTCTG CACACAGCAC GGGGCGCAAG GATGCCCCGT 1320
 CCCCTCTGG TCCTCCGGG AGCCGAGCCT GATCACCTGC CCTGCTGAGT CCCAGGCTGA 1380
 GCCTCAGTCT CCCTCCCTTG GGGCCTATGC AGAGGTCCAC AACACACAGA TTTGAGCTCA 1440
 GGCCTGGTGG CAGAGAGGT AGGGATGGGG CTGTGGGGAT AGTGAGGCAT CGCAATGTAA 1500
 25 GACTCGGGAT TAGTACACAC TTGTGTGATG TTAATGGAAA TGTTTACAGA TCCCAAGGCC 1560
 TGGCAAGGGA ATTTCTCAA CTCCTGCCCC CCTAGCCCTC CTTATCAAAG GACACCATTT 1620
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 TACCCCTGTC AAAGCCAGCT TGAACCTTC ACTTAGGAAC GTAATCGTGT CCCCTATCCT 1740
 ACTTCCCTTT CCTAATTCCA CAGCTGCTCA ATAAAGTACA AGAGTTTAACT AGTGTGTTGG 1800
 30 CGCTTTGCTT TGGTCTATCT TTGAGCGCCC ACTAGACCCA CTGGACTCAC CTCGCCCATC 1860
 TCTTCTGGGT TCCTCTCTCT GAGCCTTGGG ACCCCTGAGC TTGCAGAGAT GAAGGCCGCC 1920
 ATGTT

Seq ID NO: 501 Protein sequence
 Protein Accession #: NP_001267.1

35 1 11 21 31 41 51
 MGVKASQTGF VVLVLLQCCS AYKLVCYVTS WSQYREGDGS CFPDLDRLPL CTHIIYSPAN 60
 40 ISNDHIDTWE WNDVILYGLM NTLKRNPNL KTLISVGGWN FGSQRFKSKIA SNTQSRRTPI 120
 KSVPPFLRTH GFDGLDLAWL YPGRRDKQHF TLIKEMKAE FIKEAQPGKK QLLLSAALSA 180
 GKVTIDSSVD IAKISHLDF ISIMTYDFHG AWRGTTGHHS PLFRGQEDAS PDRFSNTDYA 240
 VGMYLRLGAP ASKLVMIPT FGRSFTLASS ETGVGAPISG PGIPGRFTKE AGTLAYYEIC 300
 45 DFLRGATVHR TLGQQVPYAT KGNQWVGYDD QESVSKSVQY LKDRQLAGAM VWALDLDLDFQ 360
 GSFCGQDLRF PLTNAIKDAL AAT

Seq ID NO: 502 DNA sequence
 Nucleic Acid Accession #: NM_006474.1
 Coding sequence: 181..669

50 1 11 21 31 41 51
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 55 TTCCCCCAGC TCAGAATCTT GCTGCTCGGC CCCAGGAGA GCAACAACTC AACGGGAACG 180
 ATGTGGAAGG TGTCAGCTCT GCTCTTCGTT TTGGGAAGCG CGTCGCTCTG GGTCTGGCA 240
 GAAGGAGCCA GCAACAGGCA GCACAGGAT GACACTGAGA CTACAGGTTT GGAAGGCGGC 300
 GTTGCCATGC CAGGTGCCGA AGATGATGTG GTGACTCCAG GAACCAAGCA AGACCGCTAT 360
 AAGTCTGGCT TGACCACTCT GGTGGCAACA AGTGTCAACA GTGTAACAGG CATTGCTATC 420
 60 GAGGATCTGC CACTTCAGA AAGCACAGTC CACGCGCAAG AACAAAGTCC AAGCGCCACA 480
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 GTTGAGAAAG ATGGTTGTG AACAGTGACC CTGGTTGGAA TCATAGTTGG GGTCTTACTA 600
 GGCATCGGTT TCATGTGTGG AATCATCGTT GTGGTTATGC GAAAAATGTC GGAAGGATAC 660
 TCGCCCTAAA GAGCTCAAGG GTTACGCCCT GCTTGCCAAC GTGCTTTAAA AAAAGACCGT 720
 65 TTCTGACTCT GTGGCCCTGT CCCTGAGCTC GTGGGAGAGG GATGACCTG GGAACATTG 780
 CGGGCCCATC CAGATTCAC AGTGACTTTC CGTTTGCCAAT ATTAACCGAG GAAAGACCTT 840
 TCACAGATT TGGTTCTTAA ACTTT

Seq ID NO: 503 Protein sequence
 Protein Accession #: NP_006465.1

70 1 11 21 31 41 51
 MWKVSALLFV LGSASLWVLA EGASTGQPED DTETTGLEGG VAMPGAEDDV VTPGTSEDY 60
 75 KSGLTTLVAT SVNSVTGIRI EDLPTSESTV HAQEQSPSAT ASNVATSHST EKVDGDTQTT 120
 VEKDLSTVTV LVGIIVGVLL AIGFIGGIIV VVMRKMSGRY SP

Seq ID NO: 504 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 62..895

80 1 11 21 31 41 51
 CACTGCTCTG AGAATTTGTG AGCAGCCCTT AACAGGCTGT TACTTCACTA CAACTGACGA 60
 85 TATGATCATC TTAATTTACT TATTTCTCTT GCTATGGGAA GACACTCAAG GATGGGGATT 120
 CAGGATGGTA ATTTTTCATA ATCCATATG GCTTGAACGA GCAGCCGGTG TGTACCACAG 180
 AGAAGCACGG TCTGGCAAT ACAAGCTCAC CTACGCAGAA GCTAAGGCGG TGTGTGAATT 240
 TGAAGCGCGC CATCTCGCAA CTTACAAGCA GCTAGAGGCA GCCAGAAAAA TTGGATTICA 300

	TGTCGTGCT	GCTGGATGGA	TGGCTAAGGG	CAGAGTTGGA	TACCCCATTG	TGAAGCCAGG	360
	GCCCAACTGT	GGATTTGGAA	AACTGGCAT	TATTGATTAT	GGAATCCGTC	TCAATAGGAG	420
	TGAAAGATGG	GATGCCTATT	GCTACAACCC	ACACGCAAG	GAGTGTGGTG	GCGTCTTTAC	480
5	AGATCCAAAG	CAAAATTTTA	AATCTCCAGG	CTTCCCAAT	GAGTACGAAG	ATAACCAAAAT	540
	CTGCTACTGG	CACATTAGAC	TCAAGTATGG	TCAGCGTATT	CACCTGAGTT	TTTAGATT	600
	TGACCTTGAA	GATGACCCAG	GTTGCTTGGC	TGATTATGTT	GAAATATATG	ACAGTTACGA	660
	TGATGTCCAT	GGCTTTGTGG	GAAGATACTG	TGGAGATGAG	CTTCCAGATG	ACATCATCAG	720
	TACAGGAAAT	GTCATGACCT	TGAAGTTTCT	AAGTGATGCT	TCAGTGACAG	CTGGAGGTTT	780
10	CCAAATCAAA	TATGTTGCAA	TGGATCCTGT	ATCCAAATCC	AGTCAAGGAA	AAAATACAAAG	840
	TACTACTTCT	ACTGGAAATA	AAAACCTTTT	AGCTGGAAGA	TTTAGCCACT	TATAAAAAAA	900
	AAAAAAAGGA	TGATCAAAAC	ACACAGTGT	TATGTTGGAA	TCTTTTGGAA	CTCCTTTGAT	960
	CTCACTGTTA	TTATTAACAT	TTATTTATTA	TTTTTCTAAA	TGTGAAAGCA	ATACATAAAT	1020
	TAGGGAAT	TGGAAATAT	AGGAACTTT	AAACGAGAAA	ATGAAACCTC	TCATAATCCC	1080
	ACTGCATAGA	AATAACAAAG	GTTAAACATT	TCATATTTT	TTCITTCAGT	CATTTTCTA	1140
15	TTTGTGGTAT	ATGATATAT	GTACCTATAT	GTATTGTCAT	TGAAATTTT	GGAATCCTGC	1200
	TCATGTACA	GTTTGTATAT	ATACCTTTTA	AATCTTGAAC	TTTATAAACA	TTTTCTGAAA	1260
	TCATTGATTA	TTCTACAAAA	ACATGATTTT	AAACAGCTGT	AAAATATCT	ATGATATGAA	1320
	TGTTTATGC	ATTATTTAAG	CCTGCTCTTA	TTGTTGGAAT	TTGAGGTCAT	TTTCATAAAT	1380
20	ATTGTTGCAA	TAAATATCCT	TGAACACACA	AAAAAAA	AA		

Seq ID NO: 505 Protein sequence
Protein Accession #: Eos sequence

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25							
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	EGGHLATYKQ	LEAARKIGFH	VCAAGWMKAG	RVGYPIVKPG	PNCXFGKTGI	IDYGI RLNRS	120
	ERWDAYCYNP	HAKECGGVFT	DPKQIFKSPG	FPNEYEDNQI	CYWHIRLKYG	QRIHLSFLDF	180
30	DLEDDPGCLA	DYVEIYDSYD	DVHGFVGRYC	GDELDDIIS	TGNVMTLKFL	SDASVTAGGF	240
	QIKYVAMDFV	SKSSQGNKTS	TTSTGNKNFL	AGRFSHL			

Seq ID NO: 506 DNA sequence
Nucleic Acid Accession #: NM_007115.1
Coding sequence: 69..902

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35							
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	CTGACGATAT	GATCATCTTA	ATTACTTAT	TTCTCTTGCT	ATGGGAAGAC	ACTCAAGGAT	120
40	GGGGATTCAA	GGATGGAATT	TTTCATAACT	CCATATGGCT	TGAACGAGCA	GCCGGTGTGT	180
	ACCCACAGAGA	AGCACGGTCT	GGCAAAATACA	AGCTCACCTA	CGCAGAAAGT	AAGGCGGTGT	240
	GTGAATTTGA	AGGGCGCCAT	CTCGCAACTT	ACAAGCAGCT	AGAGGCAGCC	AGAAAAATTG	300
	GATTTTCATGT	CTGTGCTGCT	GGATGGATGG	CTAAGGCGAG	AGTTGGATAC	CCCATTGTGA	360
	AGCCAGGGCC	CAACTGATGA	TTTGGAAAAA	CTGGCATTAT	TGATTATGGA	ATCCGCTCTCA	420
45	ATAGGAGTAC	AAGATGGGAT	GCCTATTGCT	ACAACCCACA	CGCAAAAGAG	TGTGGTGGCG	480
	TCCTTACAGA	TCCAAGCGGA	ATTTTAAAT	CTCCAGGCTT	CCCAAAAGAG	TACGAAGATA	540
	ACCAATCTCG	CTACTGGCAC	ATTAGACTCA	AGTATGGTCA	GCCTATTAC	CTGAGTTTTT	600
	TAGATTTTGA	CCTTGAAGAT	GACCCAGGTT	GCTTGGCTGA	TTATGTTGAA	ATATATGACA	660
50	GTTACGATGA	TGTCCATGGC	TTTGTGGGAA	GATACTGTGG	AGATGAGCTT	CCAGATGACA	720
	TCATCAGTAC	AGGAAATGTC	ATTGACCTTGA	AGTTTCTAAG	TGATGCTTCA	GTGACAGCTG	780
	GAGGTTTCCA	AATCAAAAT	GTTGCAATGG	ATCCTGTATC	CAAAATCCAGT	CAAGGAAAAA	840
	ATACAGTAC	TACTTCTACT	GGAATAAAAA	ACTTTTATAGC	TGGAAGATTT	AGCCACTTAT	900
	AAAAAAATAA	AAGATGATC	AAAAACACACA	GTGTTTATGT	TGGAATCTTT	TGGAACCTCCT	960
55	TTGATCTCAC	TGTTATTATT	AACATTATT	TATTATTTT	CTAAATGTGA	AAGAAATACA	1020
	TAAATTAGGG	AAAATTTGGA	AATATAGGAA	ACTTTAAAGC	AGAAAAATGAA	ACCTCTCATA	1080
	ATCCCACTAG	ATAGAAATGA	CAAGCGTTAA	CATTTCCTA	TTTTTTCTT	TCAGTCATT	1140
	TTGTATTGTT	GGTATATGTA	TATATGTACC	TATATGTATT	TGCATTTGAA	ATTTTGAAT	1200
	CCTGCTCTAT	GTCAGTTT	GTATTACT	TTTAAATCT	TGAACCTTAT	GAACATTTTC	1260
60	TGAAATCATT	GATTATTTCTA	CAAAAACATG	ATTTTAAACA	GCTGTAAAT	ATTCTATGAT	1320
	ATGAATGTTT	TATGATTAT	TTAAGCCTGT	CTCTATTGTT	GGAATTTTCA	GTCAATTTTCA	1380
	TAAATATTGT	TGCAATAAAT	ATCCTTCGGA	ATTC			

Seq ID NO: 507 Protein sequence
Protein Accession #: NP_009046.1

	1	11	21	31	41	51	
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	EGGHLATYKQ	LEAARKIGFH	VCAAGWMKAG	RVGYPIVKPG	PNXXFGKTGI	IDYGI RLNRS	120
70	ERWDAYCYNP	HAKECGGVFT	DPKRIKSPG	FPNEYEDNQI	CYWHIRLKYG	QRIHLSFLDF	180
	DLEDDPGCLA	DYVEIYDSYD	DVHGFVGRYC	GDELDDIIS	TGNVMTLKFL	SDASVTAGGF	240
	QIKYVAMDFV	SKSSQGNKTS	TTSTGNKNFL	AGRFSHL			

Seq ID NO: 508 DNA sequence
Nucleic Acid Accession #: NM_001044.1
Coding sequence: 129..1991

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	GTGTGCCAT	TAGTAAGAGC	AAATGCTCCG	TGGGACTCAT	GTCTTCCGTG	GTGGCCCCGG	180
	CTAAGGAGCC	CAATGCGGTG	GGCCGGAAGG	AGGTGGAGCT	CATCCTTGTG	AAGGAGCAGA	240
85	ACGAGTGCA	GCTCACGAGC	TCCACCTCTA	CCAACCCGCG	CGAGAGCCCC	GTGGAGGCCG	300
	AGGATCGGGA	GACCTGGGGC	AAGAAGATCG	ACTTTCCTCT	GTCGCTCATT	GGCTTTGCTG	360
	TGGACCTGGC	CAACGTCTGG	CGGTTCCCT	ACCTGTGCTA	CAAAAATGGT	GGCGGTGCCT	420

5	TCCCTGGTCCC	CTACCTGGTC	TTTCATGGTCA	TTGCTGGGAT	GCCACTTTTC	TACATGGAGC	480
	TGGCCCTCGG	CCAGTTCAAC	AGGGAAGGGG	CCGCTGGTGT	CTGGAAGATC	TGCCCCATAC	540
	TGAAAGGTGT	GGGCTTCACG	GTTCATCTCA	TCTCACTGTA	TGTGGGCTTC	TTCTACAACG	600
	TCATCATCGC	CTGGGCGCTG	CACATCTCTT	TCTCCTCCTT	CACCACGGAG	CTCCCTGGGA	660
	TCCACTGCAA	CAACTCTCTG	AACAGCCCCA	ACTGCTCGGA	TGCCCATCCT	GGTGACTCCA	720
	GTGGAGACAG	CTCGGCGCTC	AACGACACTT	TTGGGACCAC	ACCTGCTGCC	GAGTACTTTG	780
	AACGTGGCGT	GCTGCACCTC	CACCAGAGCC	ATGGCATCGA	CGACCTGGGG	CCTCCGCGGT	840
	GGCAGCTCAC	AGCCTGCTG	GTGCTGGTCA	TCGTGCTGCT	CTACTTCAGC	CTCTGGAAGG	900
10	GGGTGAAGAC	CTCAGGGAAG	GTGGTATGGA	TCACAGCCAC	CATGCCATAC	GTGGTCTCTA	960
	CTGCCCTGCT	CCTGCGTGGG	GTCAACCTCC	CTGGAGCCAT	AGACGGCATC	AGAGCATACC	1020
	TGAGCGTTGA	CTTCTACCGG	CTCTGCGAGG	CGTCTGTTTG	GATTGACGCG	GCCACCCAGG	1080
	TGTGCTTCTC	CCTGGGCGTG	GGGTTCGGGG	TGCTGATCGC	CTTCTCCAGC	TACAACAAGT	1140
	TCACCAACAA	CTGCTACAGG	GACGCGATTG	TCACCACCTC	CATCAACTCC	CTGACGAGCT	1200
15	TCTCCTCCGG	CTTGGTCTTC	TTCTCCTTCC	TGGGGTACAT	GGCACAAGAG	CACAGTGTGC	1260
	CCATCGGGGA	CGTGCCCAAG	GTGGGGCCAG	GGCTGATCTT	CATCATCTAC	CCGGAAGCCA	1320
	TGGCCACGGT	CCCTCTGTCC	TACGCTGGGG	CCGTGGTCTT	CTTCATCATG	CTGCTCACCC	1380
	TGGGTATCGA	CAGCGCCATG	GGTGGTATGG	AGTCAGTGAT	CACCGGGCTC	ATCGATGAGT	1440
	TCAGCTGCTG	GCACAGACAC	CGTGAGCTCT	TCACGCTCTT	CATCGTCTCT	GCGACCTTCC	1500
20	TCCTGTCCCT	GTTCGTGCTC	ACCAACGGTG	GCATCTACGT	CTTCACGCTC	CTGGACCTTC	1560
	TTGCAGCCGG	CACGTCCATC	CTCTTTGGAG	TGCTCATCGA	AGCCATCGGA	GTGGCTTGGT	1620
	TTCTATGGTG	TAGGCTGGTT	AGCGACGACA	TCCAGCAGAT	GACCGGGCAG	CGGCCAGGCT	1680
	TGTACTGGCG	GCTGTGCTGG	AAGCTGGTCA	GCCCTGCTT	TCTCCTGTTT	TGTTGCTGGG	1740
	TCAGCATTGT	GACCTTCAGA	CCCCCCCCACT	ACGGAGCCTA	CATCTTCCCC	GACTGGGCCA	1800
25	ACGCGCTGGG	CTGGGTCTATC	GCCACATCCT	CCATGGCCAT	GGTGCCCATC	TATGCGGCTC	1860
	ACAAGTTCCT	CAGCTCGCTC	GGGTCTCTTC	GAGAGAAACT	GGCTACGCCC	ATTGCAACCG	1920
	AGAAGGACCG	TGAGCTGGTG	GACAGAGGGG	AGGTGCGCCA	GTTACGCTCT	CGCCACTGGT	1980
	TCAGGTGTGA	GAGGAGCAG	AGACGAAGAC	CCCAGGAAGT	CATCCTGCAA	TGGGAGAGAC	2040
	ACGAACAAAC	CAAGGAAATC	TAAGTTTCGA	GAGAAAGGAG	GGCAACTTCT	ACTCTTCAAC	2100
30	CTCTACTGAA	AACACAAACA	ACAAAGCAGA	AGACTCTCT	CTTCTGACTG	TTTACACCTT	2160
	TCCGTGCCCG	GAGGCAACCT	CGCGTGTCT	TGTGTGTCTG	TAATAACGAG	GTAGATCTGT	2220
	GCAGCGAGCG	CCACCCGTTT	GTGTCTCTCT	CAGGGCAGAA	AAACGCTCTA	CTTCATGCTG	2280
	TCGTGTGAG	GCTCCTCTCC	TCCCTGCTCC	CTGCTCCCGG	CTCTGAGGCT	GCCCCAGGGG	2340
	CACGTGTGTT	TCAGGCGGGG	ATCACGATCC	TTGTAGACGC	ACCTGCTGAG	AATCCCGCTG	2400
35	CTCACAGTAG	CTTCTAGTAC	CATTACTTTT	GCCCATATTA	AAAAGCCAAG	TGCTCTGCTT	2460
	GGTTTAGCTG	TGCAGAAAGT	GAAATGGAGG	AAACCAACAA	TTCATGCAAA	GTCTTTTCCC	2520
	GATGCGTGGC	TCCGAGTGGA	GGCGTAAAT	TGAGCGTTCA	GTTGACACAT	TGCACACACA	2580
	GTCTGTTTCA	AGGCATTGGA	GGATGGGGGT	CCTGGTATGT	CTCACCAAGA	AATTCTGTTT	2640
	ATGTTCTTGC	AGCAGAGAGA	AATAAACTC	CTTGAAACCA	GCTCAGGCTA	CTGCCACTCA	2700
40	GGCAGCCTGT	GGGTCTTGT	GGGTAGGGA	ACGGCTGAG	AGGAGCGTGT	CCTATCCCCG	2760
	GACGATGCA	GGGCCCCCAG	AGGAGCGTGT	CCTATCCCCG	GACGATGCA	GGGCCCCCAG	2820
	AGGAGCATGT	CTATCCCTCG	GACGATGCA	GGGCCCCCAG	AGGAGCGTGT	ACTACCCAC	2880
	AACGATGCA	GGGCCCCCAG	AGGAGCGTGT	ACTACCCAC	GACGATGCA	GGGCCCCCAG	2940
	TGGAGCGTGT	ACTACCCAC	GACGATGCA	GGGCCCCCAG	AGGAGCGTGT	CCTATCCCCG	3000
45	GACCGGACGC	ATGCGGGGCC	CCCACAGGAG	CGTGTACTAC	CCCAGGACGC	ATGCGGGGCC	3060
	CCCACAGGAG	CGTGTACTAC	CCCAGGATGC	ATGCGGGGCC	CCCACAGGAG	CGTGTACTAC	3120
	CCCAGGACGC	ATGCGGGGCC	CCCAGGATGC	CAGCCTGCAG	ACCAACACTC	TGCTTGGCCT	3180
	TGAGCGTGA	CCTCCAGGAA	GGGACCCAC	TGGAATTTTA	TTTCTCTCAG	GTGCGTGCCA	3240
	CATCAATAAC	AACAGTTTAA	ATGTTTTCGA	ATGGCTTTT	AAAATCATAT	TTACTGTGA	3300
50	ATCAAAACAA	ATTCAAGAA	GCAGTATCCG	CGAGCCTGCT	TGCTGATATT	GCAGTTTGTG	3360
	TTTACAGAA	TAATTAGCAA	TACTGAGTGA	AGGATGTTGG	CCAAAGCTG	CTTTCATAGG	3420
	CACACTGCCC	TCTGCCACTG	ACAGGAAAGT	GGATGCCATA	GTTTGAATTC	ATGCTTCAAG	3480
	TGCGTGGGCG	TGCTTACGTT	CTGCCCCAGG	GCAGGGGCGG	TGCAGGGCCA	GTGCTGGCTG	3540
	TCCCTGCA	GTGAGCTGG	GCTCCAGGGA	CTGGAGTGT	ATGCTCGGTG	GGAGCCGCTG	3600
55	GCCTGTGAAC	TGCCAGGCG	CTGCAGTTAG	CACAGAGGAT	GGCTTCCCCA	TTGCCTTCTG	3660
	GGGAGGGACA	CAGAGGACGG	CTTCCCCATC	GCCTTCTGGC	CGCTGCAGTC	AGCACAGAGA	3720
	GCCTTCTCCC	CATTGCTTTC	TGGGAGGGGA	CACAGAGGAC	AGTTTCCCCA	TGCTTCTG	3780
	GTGTGTAAG	ACAGCACAGA	GAGCGGCTTC	CCCATCGCCT	TCTGGGGAGG	GGCTCCGTGT	3840
60	VTFRPFGYGA	YIFPDWANAL	GWVIATSSMA	MVPIYAAKYF	CSLFGSFRFK	LAYAIAPKED	3900
	TAAGCACAAT	AAAAGACATC	CACAATGGAA	AAAAAAAAG	GAATTC		

Seq ID NO: 509 Protein sequence
Protein Accession #: NP_001035.1

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	ETWKKIDFL	LSVIGFAVDL	ANVWRFPYLC	YKNGGAFILV	PYLLFMVIAG	MPLFFYMELAL	120
	GQFNREGAAG	VWKICPILKG	VGFTVILISL	YVGFYFNVII	AWALHYLFSS	FTTELFWIHC	180
70	NNSWNPNCS	DAHPSDSSGD	SSGLNDTFGT	TPAAEYFERG	VHLHQSHGI	DDLGPFRWQL	240
	TACLVLVIVL	LYFSLWKGVK	TSGLVWNITA	TMPIYVLTAL	LLRGVTLPGA	IDGIRAYLSV	300
	DFYRLCEASV	WIDAATQVCF	SLGVGPGVLI	AFSSYNKFTN	NCYRDAIVTT	SINSLTSFSS	360
	GFVVSFLGY	MAQKHSVPIG	DVAKDGPGLI	FIIYPEAIAT	LPLSSAAVAV	PFIMLLTLGI	420
	DSAMGMESV	ITGLIDEFQL	LHRHRELFTL	FIVLATFLLS	LFCVTNGGIV	VFTLLDHFAA	480
75	GTSLFEGVLI	EAIGVAWFYQ	VGQFSDDIQQ	MTGQRPSLYW	RLCNKLVSPC	FLLFVVVVS	540
	VTFRPFGYGA	YIFPDWANAL	GWVIATSSMA	MVPIYAAKYF	CSLFGSFRFK	LAYAIAPKED	600
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Seq ID NO: 510 DNA sequence
Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

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	CTGTCACTGC	TGCTTCTGAT	GCCTGTCCAT	CCCCAGAGGT	TGCCCCGGAT	GCAGGAGGAT	180
	TCCCCCTTGG	GAGGAGGCTC	TTCTGGGGAA	GATGACCCAC	TGGCGGAGGA	GGATCTGCCC	240

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 TCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCTCA AGAACCCAG 420
 AATAATGCCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC 480
 CGGCCCTGCG CCCGGGTGTC CCCAGCCTGC GCGGGCGGCT TCCAGTCCCC GGTGGATATC 540
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 CCTCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT 720
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Seq ID NO: 511 Protein sequence
 Protein Accession #: NP_001207.1

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 DPQEPQNNAH RKEGDDQSH WRYGGDPFPW RVSPACAGRF QSPVDIRPQL AAFPCPALRPL 180
 ELLGFQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGRBY RALQLHLHWG AAGRPGSEHT 240
 VEGHRFPAEI HVVHLSTAFR RVDEALGRPG GLAVLAFLF EGPEENSAYE QLSRLLEEIA 300
 EEGSETQVPG LDISALLPSD FSRYPQYEGS LTPPPCAQGV IWTVFNTQVM LSAKQLHTLS 360
 DTLWGPDSR LQLNFRATQP LNRVIEASF PAGVDSPPRA AEPVQLNSCL AAGDILALVF 420
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Seq ID NO: 513 Protein sequence
Protein Accession #: Eos sequence

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CTTGGCTCCA TGGGTTCCGT GGTCAAGTCC GAGGCCAGCT CCAGCCCCCT TGTGGTTACC 780
TCTTCTCTCC ACTCCAGGGC GCCCTGCCAG GCCGGGGACC TCCGGGACAT GATCAGCATG 840
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Seq ID NO: 515 Protein sequence
Protein Accession #: CAA83435

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5 Seq ID NO: 516 DNA sequence
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 15 AGCTGAGGAA ACAGGAGAAG TTCATGAAGA GGAGCTTGTG GCAAGAAAGG AACCTTCTAC 300
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 20 GCTGTATGAG AATAAACCCA GAAGACCTTA CATACTCAA AGAGATTCTT ACTATTACTG 540
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25 Seq ID NO: 517 Protein sequence
 Protein Accession #: AAB50564

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35 Seq ID NO: 518 DNA sequence
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	GCATCTGTGG	AACCTCTTAC	CCAACCACAA	GCCCTGGGAC	CAGGTATGGC	AGGCCGCACT	1920
	CAGGGAGGCT	GGGGCTGCC	GCCATCGGCC	TGCTGCTCCT	TGGTCTCCTG	CTGCTGCTGT	1980
	TGGCCCCCT	TCTGCTGTTG	ACCTGTGACT	GTGGGGCAGG	TTCTACTGGG	GGAGTGACAG	2040
5	GTGGTTTAT	CCAGTTTCT	GATGGCTCAG	AAGGAACAA	TCATCAGTGG	GGAAATGAAG	2100
	GAGCCCATCC	TGAAGACAAG	GAAATCACAA	ATATTTGTGT	GCCTCCTGTA	ACAGCCAAATG	2160
	GAGCCGATT	CATGGAAAGT	TCTGAAGTTT	GTACAAATAC	GTATGCCAGA	GGCACAGCGG	2220
	TGGAAGGCAC	TTCAGGAATG	GAAATGACCA	CTAAGCTTGG	AGCAGCCACT	GAATCTGGAG	2280
	GTGCTGCAGG	CTTTGCAACA	GGGACAGTGT	CAGGAGCTGC	TTCAGGATTC	GGAGCAGCCA	2340
10	CTGGAGTTGG	CATCTGTTCC	TCAGGGCAGT	CTGGAACCAT	GAGAACCAAG	CATTCCACTG	2400
	GAGGAACCAA	TAAGGACTAC	GCTGATGGGG	CGATAAGCAT	GAATTTTCTG	GACTCCTACT	2460
	TTTCTCAGAA	AGCATTTGCC	TGTGCGGAGG	AAGACGATGG	CCAGGAAGCA	AATGACTGCT	2520
	TGTTGATCTA	TGATAATGAA	GGCGCAGATG	CCACTGGTTC	TCCTGTGGGC	TCCGTGGGTT	2580
	GTTCAGTTT	TATTGCTGAT	GACCTGGATG	ACAGCTTCTT	GGACTCACTT	GGACCCAAAT	2640
15	TTAAAAAAT	TGCAGAGATA	AGCCTTGGTG	TTGATGGTGA	AGGCAAGAA	GTTCAGCCAC	2700
	CCTCTAAAGA	CAGCGGTTAT	GGGATTGAAT	CCTGTGGCCA	TCCCATAGAA	GTCCAGCAGA	2760
	CAGGATTGTT	TAAGTCCGAG	AGTTTGTGAG	GAGTCAAGG	AGCTTCTGCT	TTGTCCGCTT	2820
	CTGGGTCTGT	CCAGCCAGCT	GTTTCCATCC	CTGACCCTCT	GCAGCATGGT	AACTATTTAG	2880
	TAACGGAGAC	TTACTCGGCT	TCTGGTTCCT	TCGTGCAACC	TTCCTGCTGA	GGCTTTGATC	2940
20	CACCTTCTAC	CAAAAATGTG	ATAGTGACAG	AAAGGGTGAT	CTGTCCCTAT	TCCAGTGTTC	3000
	CTGGCAACCT	AGCTGGCCCA	ACGCAGCTAC	GAGGGTCACA	TACTATGTCT	TGTACAGAGG	3060
	ATCCTTGCTG	CCGTGCTGAG	TGACCAAGAT	GAGCTGGAAT	ACCACACTGA	CCAAATCTGG	3120
	ATCTTTGGAC	TAAAGTATTC	AAAATAGCAT	AGCAAAGCTC	ACTGTATTGG	GCTAATAATT	3180
	TGGCACTTAT	TAGCTTCTCT	CATAAACTGA	TCACGATTAT	AAATTAATG	TTTGGGTTCA	3240
25	TACCCCAAAA	CAAAATATGT	GTCACTCCTA	ATTCTCAAGT	ACTATTCAAA	TTGTAGTAAA	3300
	TCTTAAAGTT	TTTCAAAACC	CTAAAATCAT	ATTCGC			

Seq ID NO: 523 Protein sequence
Protein Accession #: NP_001935.1

30	1	11	21	31	41	51	
	MMGLFPRTTG	ALAIFVVVIL	VHGELEIETK	GQYDEEEMTM	QQAQRKQKRE	WVKFAKPCRE	60
	GEDNSKRNPI	AKITSYQAT	QKITYRISGV	GIDQPPFGIP	VVDKNTGDLN	ITAIVDREET	120
	PSPLITCRAL	NAQGLDVEKP	LILTVKILDI	NDNPPVFSQQ	IFMGEIEENS	ASNSLVMILN	180
35	ATDADEPNHL	NSKIAFKIVS	QEPAGTGMFL	LSRNTGEVRT	LTNSLDRRQA	SSYRLVVSGA	240
	DKDGEGLSTQ	CECNIKVKDV	NDNPFMPFRDS	QYSARIBENI	LSSLELLRPQV	TDLDEEYTDN	300
	WLAVYFETSG	NEGNWFETQT	DPRTNEGILK	VVKALDYEQ	QSVKLISIAVK	NKAEFHQSVI	360
	SRYRVQSTPV	TIQVINVREG	IAPRPASKTF	TVQKGISSKK	LVDYILGTQY	AIDEDTNKAA	420
40	SNVKYVMGRN	DGGYLMIDSK	TAEIKFVKNM	NRDSTFIVNK	TITAEVLAI	EYTGKTSTGT	480
	VYVRVPDFND	NCPTAVLEKD	AVCSSSPSVV	VSARTLNNRY	TGPTYFALED	QPVKLPVAVS	540
	ITTLNATSL	LRAQGIPEFG	VYHISLVLT	SQNNRCMPR	SLTLEVQCQD	NRGICGTSYP	600
	TTSPGTRYGR	PHSGRLGPAA	IGLLLLGLLL	LLLAPLLLLT	CDGAGSTGG	VTGGFIPVPD	660
	GSSGTIHQWG	IEGAHPEDKE	ITNICVPPVT	ANGADFMESS	EVCTNTYARG	TAVEGTSGME	720
45	MTTKLGAATE	SGGAAGFATG	TVSGAASGFG	AATGVGICSS	GQSGTMRTRH	STGGTNKDYA	780
	DGAISMNPLD	SYFSQKAFAC	AEEDDQGEAN	DCLLIYDNEG	ADATGSPVGS	VGCCSPFIADD	840
	LDDSFLLDSL	PKFKLLAEIS	LGVDEGEGKEV	QPPSKDSGYG	IESCGHPFIEV	QQTGFVKCQT	900
	LSGSQASAL	SASGSVQPAV	SIPDPLQHGN	YLVETETYSAS	GSLVQPSSTAG	FDPLLTQNV	960
	VERTVICPIS	SVPGNLAGPT	QLRGSHTMLC	TEDPCSRLI			

Seq ID NO: 524 DNA sequence
Nucleic Acid Accession #: XM_058069.2
Coding sequence: 1..1413

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	AGCTCTACAA	GCCTGGAAAA	AAATAATGTG	CTATTTGGTG	AAAGATACTT	AGAAAAATTT	120
	TATGGCCTTG	AGATAAACAA	ACTTCCAGTG	ACAAAAATGA	AATATAGTGG	AAACTTAAATG	180
60	AAGGAAAAAA	TCCAAGAAAT	GCAGCACTTC	TTGGGTCTGA	AAGTGACCGG	GCAACTGGAC	240
	ACATCTACCC	TGGAGATGAT	GCACGCACCT	CGATGTGGAG	TCCCCGATGT	CCATCATTTT	300
	AGGGAAATGC	CAGGGGGGCC	CGTATGGAGG	AAACATTATA	TCACTACAG	AATCAATAAT	360
	TACACACCTG	ACATGAACCG	TGAGGATGTT	GACTACGCAA	TCCGGAAAGC	TTTCCAAGTA	420
	TGGAGTAATG	TTACCCCCTT	GAAATTCAGC	AAGATTAACA	CAGGCATGGC	TGACATTTTG	480
65	GTGGTTTTTG	CCCGTGGAGC	TCATGGAGAC	TTCCATGCTT	TTGATGGCAA	AGGTGGAATC	540
	CTAGCCCATG	CTTTTGGACC	TGGATCTGGC	ATTGGAGGGG	ATGCACATT	CGATGAGGAC	600
	GAATTCGGA	CTACACATT	AGGAGGCACA	AACTTGTTC	TCACTGCTGT	TCACGAGATT	660
	GGCCATTCTT	TAGGCTCTGG	CCATTCTAGT	GATCCAAAGG	CCGTAAATGT	CCCCACCTAC	720
	AAATATGTTG	ACATCAACAC	ATTTGCGCTC	TCTGCTGATG	ACATACGTGG	CATTCACTCC	780
70	CTGTATGGAG	ACCCAAAAGA	GAACCAACGC	TTGCCAAATC	CTGACAAATC	AGAACCAAGT	840
	CTCTGTGACC	CCAATTGTAG	TTTTGATGCT	GTCACTACCG	TGGGAAATAA	GATCTTTTTC	900
	TTCAAAGACA	GGTTCTTCTG	GCTGAAGGTT	TCTGAGAGAC	CAAAGACCAG	TGTTAATTTA	960
	ATTTCTTCTT	TATGGCCAAC	CTTGCCATCT	GGCATTGAAG	CTGCTTATGA	AATTGAAGCC	1020
	AGAAATCAAG	TTTTTCTTTT	TAAAGATGAC	AAATACTGGT	TAATTAGCAA	TTTAAGACCA	1080
75	GAGCCAAATT	ATCCCAAGAG	CATACATTCT	TTTGGTTTTT	CTAACTTTGT	GAATAAAATT	1140
	GATGCAGCTG	TTTTTAACCC	ACGTTTTTAT	AGGACCTACT	TCTTTGTAGA	TAACCAAGTAT	1200
	TGGAGGTATG	ATGAAAGGAG	ACAGATGATG	GACCTGCTGT	ATCCCAAACT	GATTACCAAG	1260
	AACTTCCAAG	GAATCGGGCC	TAAAAATGAT	GCAGTCTTCT	ACTCTAAAAA	CAAACTACTAC	1320
80	TATTTCTTCC	AAGGATCTAA	CCAATTGAA	TATGACTTCC	TACTCCAAAG	TATCACCAAA	1380
	ACACTGAAAA	GCAATAGCTG	GTTTGGTTGT	TGA			

Seq ID NO: 525 Protein sequence
Protein Accession #: P39900

85	1	11	21	31	41	51	
	MKPLILLILL	ATASGALPLN	SSTSLEKNNV	LFGERYLEKF	YGLEINKLEPV	TKMKYSGNLM	60
	KEKIQEMQHF	LGLKVVGQLD	TSTLEMMHAP	RCGVDPVHHF	REMPGGPVWR	KHYITYRINN	120

YTPDMNREDEV DYAIRKAFQV WSNVTPKXFS KINTGMADIL VVFARGAGHD FHAFDGGKGI 180
 LAHAFGPGSG IGGDAHFDED EFWTTHSGGT NLFLTAVHEI GHSLGLGHSS DPKAVMFPTY 240
 KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFP 300
 FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAEIEA RNQVFLFKDD KYWLISNLRP 360
 EPNYPKSIHS FGFPNFKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK 420
 NFQGIQPKID AVFYKKNKY YFFQGSNQFE YDFLLQRITK TLKSNWFGC

Seq ID NO: 526 DNA sequence

Nucleic Acid Accession #: NM_024423.1

Coding sequence: 64..2590

1 11 21 31 41 51
 15 GGCAGGTCTC GCTCTCGGCA CCCTCCCGGC GCCCGCGTTC TCCTGGCCCT GCCCGGCATC 60
 CCGATGGCCG CCGCTGGGCC CCGGCGCTCC GTGCGCGGAG CCGTCTGCCT GCATCTGCTG 120
 CTGACCTCTG TGATCTTCAG TCGTGATGGT GAAGCCTGCA AAAAGGTGAT ACTTAATGTA 180
 CCTTCTAAAC TAGAGGCAGA CAAATAAATT GGCAGAGTTA ATTTGGAGA GTGCTTCAGG 240
 TCTGCAGACC TCATCCGCTC AAGTGATCCT GATTTCAGAG TTCTAAATGA TGGGTCACTG 300
 20 TACACAGCCA GGGCTGTTGC GCTGTCTGAT AAGAAAAGAT CATTTACCAT ATGGCTTTCT 360
 GACAAAAGGA AACAGACACA GAAAGAGGTT ACTGTGCTGC TAGAACATCA GAAGAAGGTA 420
 TCGAAGACAA GACACACTAG AGAACTGTT CTCAGGCGTG CCAAGAGGAG ATGGGCACCT 480
 ATTCTTGCT CTATGCAAGA GAATTCCTTG GCCCTTTCC CATTGTTTCT TCAACAAGTT 540
 GAATCTGATG CAGCACAGAA CTATACTGTC TTCTACTCAA TAAGTGGACG TGGAGTTGAT 600
 25 AAAGAACCTT TAAATTTGTT TTATATAGAA AGAGACACTG GAAATCTATT TTGCACTCGG 660
 CCTGTGGATG GTGAAGAATA TGATGTTTTT GATTTGATTG CTTATGCGTC AACTGCAGAT 720
 GGATATTGAG CAGATCTGCC CCTCCCACTA CCCATCAGGG TAGAGGATGA AAATGACAAC 780
 CACCTGTTTT TCACAGAAGC AATTATAAAT TTGAAGTTT TGGAAAGTAG TAGACCTGGT 840
 ACTACAGTGG GGGTGGTTTG TGCCACAGAC AGAGATGAAC CGGACACAAT GCATACGCGC 900
 30 CTGAATATCA GCATTTTGCA CGACAGACCA AGGTCACTG GGCTCTTTTC TGTGCATCCC 960
 AGCAGAGGCG TAATCACCAC AGTCTCTCAT TATTTGGACA GAGAGGTGTG AGACAAGTAC 1020
 TCATTGATAA TGATCTTACA AGACATGGAT GGCCAGTTTT TTGGATTGAT AGGCACATCA 1080
 ACTTGTATCA TAACAGTAAC AGATTCAAAT GATAATGCAC CCATCTTCAG ACAAATAGCT 1140
 TATGAAGCAT TTGTAGAGGA AATGTCATT AATGTGGAAA TCTTACGAAT ACCTATAGAA 1200
 35 GATAAGGATT TAATTAACAC TGCCAATTGG AGAGTCAATT TTACCATTTT AAAGGGAAT 1260
 GAAAATGGAC ATTTCAAATC CAGCACAGAC AAAGAACTA ATGAAGGTGT TCTTTCTGTT 1320
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 GAAGCGCCAT TTGCTAGAGA TATTCACAGA GTGACAGCCT TGAACAGAGC CTTGGTTACA 1440
 GTTCATGTGA GGGATCTGGA TGAGGGGCGT GAATGCACCT CTGCAGCCCA ATATGTGCGG 1500
 40 ATTAAGAAAA ACTTAGCAGT GGGTCAAAAG ATCAACGGCT ATAAGGCATA TGACCCCGAA 1560
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 ATTGATGAAA TTTCAAGGTC AATCATAACT TCCAAAATCC TGGATAGGGA GGTGAAACT 1680
 CCCCAAAATG AGTTGTATAA TATTACAGTC CTGGCAATAG ACAAAGATGA TAGATCATGT 1740
 ACTGGAACAC TTGCTGTGAA CATTGAAGAT GTAAATGATA ATCCACCAGA AATACTTCAA 1800
 45 GAATATGTAG TCATTGCAA ACCAAAATG GGGTATACCG ACATTTTAGC TGTGTATCCT 1860
 GATGAACCTG TCCATGAGC TCCATTTTAT TTCAGTTTGC CCAATACTTC TCCAGAAATC 1920
 AGTAGACTGT GGAGCCTCAC CAAAGTTAAT GATACAGCTG CCCGTCTTTC ATATCAGAAA 1980
 AATGCTGGAT TTCAAGATAA TACCATTCTT ATTACTGTAA AAGACAGGCG CGGCCAAGCT 2040
 GCAACAAAAT TATTCTGTGT TAATCTGTGT GAATGTACTC ATCCAACTCA GTGTCTGTGCG 2100
 50 ACTTCAAGGA GTACAGGAGT AATACTTGGG AAATGGGCAA TCCTTGCAAT ATTACTGGGT 2160
 ATAGCACTGC TCTTTTCTGT ATTGCTAAT TTAGTATGTG GAGTTTTTGG TGCAACTAAA 2220
 GGGAAACGTT TTCCTGAAGA TTTAGCACAG CAAAACCTTA TTATATCAAA CACAGAAGCA 2280
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 55 GAAATGATGA AAGGAGGAAA CCAGACCTTG GAATCTGCC GGGGGGCTGG GCATCATCAT 2460
 ACCCTGGACT CCTGCAGGCG AGGACACACG GAGGTGGACA ACTGCAGATA CACTTACTCG 2520
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 65 TCTCAAACCT CAGCACTGGA ATTAAGGTCT CTAAGCATC TGCTCTTTT TTTTCTTACG 3060
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 75 TTCTGTTTTC TGTGGGAAGG AAATAGGGAA TCCAATGGAA CAGTAGCTTT GCTTTCAGT 3660
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 ATAACAAAAA CATTTTAAAA CTTACCTTTA CTGAAGTTAA ATCTCTATT GCTGTTTCTA 3840
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 80 ATGTCTCTTA AACCTGAAGC CCACAAACTT GACACCTGAT CAGGTCTGGG AGCTACAAAA 4020
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 AGGCCTTGTG GGCCCTCTTC TTTGGGCTTT CTGCTAAAGC AACACCTCCA GCAGAGATTC 4140
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 CTTTCTCCAG AGAATTTTTT AAATAATAGA AGAAATAGAA ATTTTGAATG TATAAAGAA 4260
 85 AAAGATCAAG TTGATTTTAT AGAACAGAGG GAACCTTGGG AGAAAGCAGC CCAAGTAGGT 4320
 TATTTGTACA GTCAGAGGGC AACAGGAAGA TGCAGGCCCT CAAGGGCAAG GAGAGGCCAC 4380
 AAGGAATATG GGTGGGACTA AAAGCAACAT CGTCTGCTTC ATACTTTTTC CTAGGCTTGG 4440

	CAC	TGC	CTT	TCT	TC	CA	GG	CCA	TGG	CA	AA	CT	GCC	AT	TG	AG	T	CC	GG	T	G	AG	GG	GA	TC	AG	4500
	CCA	AC	CT	CT	CT	AT	GG	CT	CAT	T	CA	CC	CT	TAT	T	GG	AG	T	GA	GA	AT	CA	AG	GA	CT	GA	4560
	TGC	AT	G	T	GA	GT	CT	GA	AG	GC	AT	TT	T	G	CA	GG	A										4620
5	AGG	CAT	TC	AT	TC	AT	GG	AA	TT	GT	T	G	T	AT	T	CC	T										4680
	CT	AT	GA	AA	TT	A	AT	G	CC	CT	AT	T	A	A	T	CT	G										4740
	TG	AC	CC	T	AAA	T	AT	CT	AT	GT	T	TT	TA	GA	CT	T	A										4800
	TT	G	AG	AC	GA	CG	GT	CT	GC	CT	T	G	AC	CA	AG												4860
	CT	GA	A	AG	CT	C	CG	CT	CC	CG	G	GT	TC	AT	GC	CA											4920
10	GAC	T	AC	AG	GC	CC	CA	CC	AC	CC																	4980
	TT	CA	CT	GT	GT		TAG	CC	AG	GA	T																5040
	TCC	CA	A	AG	TG		CT	GG	AT	TAC																	5100
	GT	CG	CT	CT	CT		TT	TA	AT	GT	TA																5160
	TC	AT	CT	TT	GA		AA	TA	CT	CA	AC																5220
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	TG	TA	ACC	AGA			AG	CC	AG	TT	GT																5340
	CCC	AC	T	C	ACC		GAT	CA	AAA	ACC																	5400
	TCA	AA	G	AG	CA		ACC	AG	GA	TCA																	5460
	TG	AA	C	T	GC	T		GA	AA	AC	CC																5520
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	TC	CT	T	A	T	A	T	G																			5640
	AG	CT	T	T	C	A	T	T																			5700
	TT	T	T	C	T	T	A	T	A																		5760
	TT	T	A	A	C	A	G	A																			5820
25	CT	G	C	T	T	A	A	A																			5880
	AA	T	A	A	A	A	A	A																			5940
	TT	T	A	C	A	G	A	T																			6000
	TT	T	A	G	A	G	A	T																			6060
30	GA	A	A	T	A	G	A	A																			6120
	TC	AT	T	A	T	A	TC	A																			6180
	TT	GA	AG	C	A	C	A																				6240
	GT	AT	T	A	A	A	A	G																			6300
	AC	A	G	G	G	G	T	T																			6360
	C	A	G	G	C	A	A	T																			6420
35	G	A	C	A	G	A	T	G																			6480
	GG	A	G	T	GT	GC	T																				6540
	AA	AG	C	C	T	T	A	C																			6600
	AC	CA	T	A	T	T	T																				6660
	AT	AC	C	G	G	A	T																				6720
40	GT	T	G	A	G	A	A	C																			6780
	AC	T	T	C	T	G	T																				6840
	AT	G	A	C	A	A	C	A																			6900
	AC	A	T	A	G	A	A	C																			6960
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Seq ID NO: 527 Protein sequence
Protein Accession #: NP_077741.1

	1	11	21	31	41	51	
50	MAA	AGP	RRSV	RGAV	CLHLL	TLV	IFSRDGE
	ADL	IR	SSDP	FRVL	NDG	SVY	TARA
	KTR	HRET	VL	RRAK	RRWAP	I	PCSMQ
55	EPL	NLFY	IER	DTGN	LFC	TRP	VDRE
	PVF	TE	AIYN	EVLE	SSRP	PGT	TVGV
	TGV	ITV	SHY	LDRE	VVDK	YS	LIMKV
	EAF	VEEN	AFN	VEIL	EIP	IED	KDL
60	KPL	NYEEN	AFN	VEIL	EIP	IED	KDL
	KEN	LAV	GSKI	NGY	KAYD	PEN	RNGN
	KNEL	YNIT	VL	AIDK	DRS	CT	GTLA
	EPV	HGA	PFY	SLP	NTS	PEIS	RLWS
	TKL	LR	VNLCE	CTH	P	QCRAT	SRST
65	KRF	PED	LAQ	NLI	ISNT	EAP	GDDR
	MMK	GNQ	TL	SCR	GAG	HHT	LDS

Seq ID NO: 528 DNA sequence
Nucleic Acid Accession #: NM_001941.2
Coding sequence: 64..2754

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	CCG	ATGG	CCG	CGT	GGG	CCC	CGCT
	CTG	ACCT	CTG	TGAT	CTT	CAG	TCGT
75	CC	TTCT	AAAC	TAG	AGG	CAG	CAAA
	CTG	CAG	ACC	TCAT	CCG	CTC	AAGT
	TAC	ACAG	CCCA	GGG	CTG	TGT	GCTG
	GAC	AAA	AGGA	AAC	AGAC	ACA	GAA
80	TCG	AGAC	ACAA	GAC	CACT	AG	AGAA
	ATT	CTT	GTCT	CTAT	GCA	AGA	GAAT
	GAAT	CTG	ATG	CAG	CA	GAA	CTAT
	AAAG	AAC	CTT	TAA	ATT	TGTT	TTAT
	CC	TG	GGAT	G	TGA	GA	GAAT
85	GG	AT	TTCA	G	AT	CTG	CC
	CAC	CTG	TTG	CA	CA	AGG	CA
	ACT	AC	AGT	GG	G	TG	CC
	CTG	AA	ATAC	A	G	AT	CA

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AGCACAGGCG TAATCACCAC AGTCTCTCAT TATTGGACA GAGAGGTTGT AGACAAGTAC 1020
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 GATGAACCTG TCCATGGAGC TCCATTTTAT TTCAGTTTTC CCAATACTTC TCCAGAAATC 1920
 AGTAGACTGT GGAGCCTCAC CAAAGTTAAT GATACAGCTG CCCGTCTTTC ATATCAGAAA 1980
 AATGTCTGGAT TTCAAGATA TACCATTCTCT ATTACTGTAA AAGACAGGGC CGGCCAAGCT 2040
 GCAACAAAAT TATTGAGAGT TAATCTGTGT GAATGTACTC ATCCAACTCA GTGTGTCGG 2100
 ACTTCAAGGA GTACAGGAGT AATACTTGGG AAATGGGCAA TCCTTGCAAT ATTACTGGGT 2160
 ATAGCACTGC TCTTTCTGT ATTGCTAAT TTAGTATGTG GAGTTTGTGG TGCACATAAA 2220
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 CTTGGAGAGC ATAGAGTGTG CTCCTGCCAAT GGATTTATGA CCCAACTAC CAACAACCT 2340
 AGCCAAAGTT TTGTGGTAC TATGGGATCA GGAATGAAAA ATGGAGGGCA GGAAACCAAT 2400
 GAAATGATGA AAGAGGAAAA CCAGACCTTG GAATCTGCC GGGGGGCTGG GCATCATCAT 2460
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 GAGTGGCACA GTTTTACTCA ACCCGTCTC GGTGAAAAAT TGCATCGATG TAATCAGAAT 2580
 GAAGACCCGA TGCCATCCCA AGATTATGTC CTCACTTATA ACTATGAGGG AAGAGGATCT 2640
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 AACAGACAAC TGGTAAATCT CAAACTCCAG CACTGGAATT AAGGTCTCTA AAGCATCTGC 3000
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 ACTGAATTA ATTAATAATG TTGCAGCTCA TAAAGAAATG GGACTCACCC CTACTGCCT 3240
 ACCAAATTC TTTGACTTTG GAGGCAAAAT GTGTTGAAGT GCGCTATGAA GTAGCAATTT 3300
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 TAACCATGTC CTCCTAGAGT TTAGAGGCTA GAGGGAGCTG AGGGGAGGAT CTTACTGAAA 3900
 GCACCTCGGG GAGATTGATT GTCTTAAAC CTAAGCCCCA CAAACTTGAC ACCTGATCAG 3960
 GTCTGGGAGC TACAAAATTT CATTTTCTC CTCACTGCC TCTCTGAG TGCCATTGGC 4020
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 ATTAAGAGTA TTAGAAGGTG GTTATAATTG CAGAGTATTC CATGAATAGT AACTGACAC 6180

WO 02/086443

5 AGGGGTTTTA CTTTGAGGAC CAGTGTAGTC AAGGGAAAAC ATGAGTTAAA AAGAAAAGCA 6240
 GGCAATATTG CAGTCTTGAT TCTGCCACTT ACAGGATAGA TAATGCCTGA ACTTTAATGA 6300
 CAAGATGATC CAACCATAAA GGTGCTCTGT GCTTCACAGT GAATCTTTTC CCCATGCAGG 6360
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 AGCCTTACAT TTTAATATAG GTTGAACCAA AATTTCAATT CCAGTAACTT CTATTGTAAC 6480
 CATTATTTTT GTGTATGTCT TCAAGAATGT TCATTGGATT TTTGTTTGTG ATAGTAAAAA 6540
 ACCGGATACA TTTCACGTGT CCTTCAGTAT TGATTGGTGT GAATATTGGG TCATAATGGT 6600
 TGAGAAGCAT GGACACTAGA GCCAGAAATG TGGATATGA ATCCTGGATC TGTCACTTAC 6660
 10 TTCTGTGTGA CCTTTGAAAG GCTACTTATT TCCTCTCTTA GCTTCTCAT TAAAATCAAT 6720
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 ATAGAACACT GCCTGCACAT AGTAAAGAAA TTATAAGTGT GAGGTAGTTG GTAAAATTAT 6840
 GTAGTTGGAT ATACTACCGA ACAATATCTA ATCTCTTTT AGGGAAATAA AGTTTGTGCA 6900
 TATATATAAT CCCGAAACAT G

15 Seq ID NO: 529 Protein sequence
 Protein Accession #: NP_001932.1

20 1 11 21 31 41 51
 MAAAGPRRSV RGAVCLHLL TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS 60
 ADLIRSSDDP FRVLNDGGSVY TARAVALSDK KRSFTIWLSD KRXQTQKEVT VLLEHQKKVS 120
 KTRHRTETVL RRAKRWRWPI PCSMQENSLG PFPLFLQQVE SDAAGNYTVF YSISGRGVDK 180
 EPLNLFYIER DTGNLFCTRP VDREYDVFD LIAYASTADG YSADLPPLP IRVEDENDNH 240
 25 PVFTEAIYNF EVLESSRPGT TVGVVCAADR DEPDTHMTRL KYSILQQTFR SPGLFSVHPS 300
 TGVITTVSHY LDREVVDKYS LIMKVQMDMG QFFGLIGTST CIITVTDSDN NAPTFRQNAY 360
 EAFVEENAFN VEILRIPIED KDLINTANWR VNFTILKGNE NGHFKISTDK ETNEGVLSSV 420
 KPLNYEENRQ VNLEIGVUNE APPARDIPRV TALNRALVTV HVRDLDEGFE CTAAQYVRI 480
 KENLAVGSXI NGYKAYDPEN RENGNGLYKK LHDPKGWITI DEISGSITS KLLDREVETP 540
 30 KNELYNITVL AIDKDDRSCT GTLAVNIEDV NDNPFILQE YVVICPKMG YTDILAVDPD 600
 EPVHGAPFFY SLPNTSPKIS RLWSLTKVND TAARLSYQKN AGFQEYTIPI TVKDRAGQAA 660
 TKLLRVNLCE CTHPTQCRAT SRSTGVILGK WAILAILGI ALLFSVLLTL VCGVFGATRG 720
 KRFPEDLAQO NLIISNTAP GDDRVCSSANG FMTQTNNSS QGFCGTMGSG MKNGGQETIE 780
 MMKGNQTLB SCRGAGHHT LDSCRGGHTE VDNCRITYSE WHSFTQPRLG EKLHRCNQNE 840
 35 DRMPSQDYVL TYNYEGRGSP AGSVGCCSEK QEEDGLDFLN NLEPKFITLA EACTKR

40 Seq ID NO: 530 DNA sequence
 Nucleic Acid Accession #: NM_016583.2
 Coding sequence: 72..842

45 1 11 21 31 41 51
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 TAAGAGCAAA GATGTTTCAA ACTGGGGGCC TCATTGTCTT CTACGGGCTG TTAGCCCAAGA 120
 CCATGGCCCA GTTTGGAGGC CTGCCCCGTC CCTCGACCA GACCTGCCC TTGAATGTGA 180
 ATCCAGCCCT GCCCTTGAGT CCCACAGGTC TTGCAGGAAG CTTGACAAAT GCCCTCAGCA 240
 ATGGCCTGCT GTCTGGGGGC CTGTTGGGCA TTCTGGAAAA CCTTCCGCTC CTGGACATCC 300
 50 TGAAGCCTGG AGGAGGTACT TCTGGTGGCC TCCTTGGGGG ACTGCTTGGG AAAGTGACGT 360
 CAGTGATTCC TGGCCTGAAC AACATCATTG ACATAAAGGT CACTGACCCC CAGCTGCTGG 420
 AACTTGGCCT TGTGCAGAGC CCTGATGGCC ACCGTCTCTA TGTCAACATC CCTCTCGGCA 480
 TAAAGTCCCA AGTGAATACG CCCCTGGTCC GTGCAAGTCT GTTGAGGCTG GCTGTGAAGC 540
 TGGACATCAC TGCAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGGTCC 600
 TTGGTGACTG CACCCATTCC CCTGGAAGCC TGCAAATTC TCTGCTTGAT GGACTTGGCC 660
 55 CCCTCCCCAT TCAAGGTTCT CTGGACAGCC TCACAGGGAT CTTGAATAAA GTCCCTGCCTG 720
 AGTTGGTTCA GGGCAACGTG TGCCCTCTGG TCAATGAGGT TCTCAGAGG TTGGACATCA 780
 CCCTGGTGCA TGACATTGTT AACATGCTGA TCCACGAGT ACAGTTGTGC ATCAAGGTCT 840
 AAGCCTTCCA GGAAGGGGCT GGCCTCTGCT GAGCTGCTC CCAGTGTCTC CAGATGGCTG 900
 GCCCATGTGC TGGAAAGTCA CACAGTTGCC TTCTCTCCGA GGAACCTGCC CCCTCTCCTT 960
 60 TCCCACCAGG CGTGTGTAAC ATCCCATGTG CCTCACCTAA TAAATGGCT CTCTCTCTGC 1020
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

65 Seq ID NO: 531 Protein sequence
 Protein Accession #: NP_057667.1

70 1 11 21 31 41 51
 MFQTGGLIVE YGLLAQTMAG FGGLPVPLDQ TLPLNVNPAL PLSPITGLAGS LTNALSNGLL 60
 SGLLGILEN LPLLDILKPG GGTSGGLLGG LLGKVTSVIP GLNNIIDIKV TDPQLLELGL 120
 VQSPDGHRLY VTIPGLIKLG VNTPLVGASL LRLAVKLDT AEILAVRDQK ERIHLVLGDC 180
 75 THSPGSLQIS LLDGLGPLFI QGLLDSLTGI LNKVLPPLVQ GNVCPVNEV LRGLDITLVH 240
 DIVNMLIHGL QFVIKV

80 Seq ID NO: 532 DNA sequence
 Nucleic Acid Accession #: NM_004363.1
 Coding sequence: 115..2223

85 1 11 21 31 41 51
 CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT 60
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 TCTCCCTCGG CCCCTCCCCA CAGATGGTGC ATCCCTGGC AGAGGCTCCT GCTCAGAGCC 180
 TCACTTCTAA CCTTCTGGAA CCCGCCACAC ACTGCCAAGC TCATATTGTA ATCCAGCCCG 240
 TTCAATGTGC CAGAGGGGAA GGAGGTGCTT CTACTTGTCC ACAATCTGCC CCAGCATCTT 300
 85 TTTGGCTACG GCTGTGTACA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT 360
 GTAATAGGAA CTCAACAAGC TACCCAGGG CCCGCATACA GTGGTCGAGA GATAATATAC 420
 CCCAATGCAT CCTGCTGAT CCAGAACATC ATCCAGAATG ACACAGGATT CTACACCCCTA 480

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CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCGG GGTATACCCG 540
 GAGCTGCCCA AGCCCTCCAT CTCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT 600
 GTGGCCTTCA CCTGTGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAT 660
 CAGAGCCTCC CGGTCAAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720
 TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAGT 780
 GCCAGGCGCA GTGATTCAGT CATCCTGAAT GTCCCTCTATG GCCCGGATGC CCCACCATT 840
 TCCCCTCTAA ACACATCTTA CAGATCAGGG GAAATCTGA ACCTCTCTGT CCACGCGACC 900
 TCTAACCCAC CTGCACAGTA CTCTTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 960
 GAGCTCTTTA TCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020
 AACTCAGACA CTGGCCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA 1080
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 CTCCCGGTCA GTCCCGAGCT GCAGCTGTCC AATGACAACA GGACCCCTAC TCTACTCAGT 1260
 GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAATT AAGTGTGAGC 1320
 CACAGCGACC CAGTCATCCT GAATGTCTCT TATGGCCAG ACACCCCTAC CATTTCCCCC 1380
 TCATACACTT ATTACCGTAT AGGGGTGAAC CTCAGCTCTC CTGCGCATGC AGCCTCTAAC 1440
 CCACCTGCAC AGTATTCTTG GCTGATTGAT GGAACATCC AGCAACACAC ACAAGAGCTC 1500
 TTTATCTCCA ACATCAGTGA GAAGAACAGC GGACTCTATA CCTGCCAGGC CAATAACTCA 1560
 GCGAGTGGCC CACAGCTGAG TACAGTCAAG ACAATCAGAG TCTCTGCGGA GCTGCCAAGC 1620
 CCTCCACTCT CCAGCAACAA CTCCAAACCC GTGGAGGACA AGGATGTCTG GGCCTTCACC 1680
 TGTGAACCTG AGGCTCAGTA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740
 GTCAGTCCCA GGCTGCAGCT GTCCAATGGC AACAGGACCC TCATCTATT CAATGTACA 1800
 AGAAATGAGC CAAGAGCCTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCGCAGT 1860
 GACCCAGTCA CCTGTGATG CCTCTATGGG CCGGACACCC CCATCATTTC CCCCCAGAC 1920
 TCGTCTTACC TTGCGGAGC GAACCTCAAC CTCTCTGCC ACTCGGCCCT TAACCCATCC 1980
 CGCAGTATT CTGCGGTAT CAATGGGATA CCGCAGAAC ACACACAAGT TCTCTTTATC 2040
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 AGACTCTGAC CAGAGATCGA GACCATCTA GCCAACATCG TGAAACCCCA TCTCTACTAA 2400
 AAATACAAAA ATGAGCTGGG CTGCTGTGGC CGCACCCTGA GTCCAGTTA CTCGGGAGGC 2460
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 ACTGCACTCC AGTCTGGCAA CAGAGCAAGA CTCCTCTCA AAAAGAAAAG AAAAGAACAC 2580
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 TAATTAATTT CATGGGACTA AATGAACATA TGAGGATTGC TGATCTTTA AATGTCTTGT 2760
 TTCCAGATT TCAGGAAACT TTTTCTCTT TAAGCTATCC ACTCTTACAG CAATTTGATA 2820
 AAATATACTT TGTGAACAA AATTGAGAC ATTACATT TCTCCCTATG TGGTCGCTCC 2880
 AGACTTGGGA AACTATTAT GAATATTAT ATTGTATGGT AATATAGTTA TTGCACAAGT 2940
 TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

Seq ID NO: 533 Protein sequence
 Protein Accession #: NP_004354.1

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1 11 21 31 41 51
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 HLFQSWYKRG ERVDGNRQII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFPY 120
 TLHVIKSDLV NEEATGQFRV YPELKPFSIS SNNSKPVEDK DAVAFTCEPE TQDATYLWNV 180
 NNQSLPVSPR LQLSNGNRTL TLFNVTRNDT ASYKCTQNP VSARRSDSVI LNVLYGPDAP 240
 TISPLNTSVR SGENLNLSCB AASNPPAQYS WFNVTGTFQQS TOELFIPNIT VNNSGSYTCQ 300
 AHNSTDGLNR TTVTTITVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NITYLWNVNN 360
 QSLPVSPRLQ LSNDRNLTL LSVTRNDVGP YECGIQNELS VDHSDPVLIN VLYGPDPTI 420
 SPSYTYRPG VNLDSLCHAA SNPPAQYSWL IDGNIQHTQ ELFISNITEK NSGLYTCQAN 480
 NSASGHSRRT VKTITVSREL PKPSISSNNS KPVEDKDAVA FTCEPEAQNT TYLWVWNGQS 540
 LPVSPRLQLS NGNRLTLFEN VTRNDARAYV CGIQNSVSN RSDPVTLDVL YGPDPTIISP 600
 PDSSYLSGAN LNLSCHSASN PSPQYSNRIN GIPOQHTQVL FIAKITPNNN GTYACFVSNL 660
 ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI

Seq ID NO: 534 DNA sequence
 Nucleic Acid Accession #: NM_006952.1
 Coding sequence: 11..793

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1 11 21 31 41 51
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 ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180
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 TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTCATTC TGATGTTTAT 300
 AGTATATGCC TTTGAAGTGG CATCTTGAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
 ACCCAACCTC TCTCTGAAGC AGATGCTAGA GAGGTACCAA AACACAGCC CTCCAACAA 420
 TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480
 CAATTGCTGT GGCCTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC 540
 TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
 AGAACCTCTC AACCTGGAGG CTGTGAAACT AGGCGTGCTT GGTTTTATCA ACAATCAGGG 660
 CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG 720
 ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCTGGGT ACCATGTCTT ACTGGAGCAG 780
 AATTGAATAT TAAGAA

Seq ID NO: 535 Protein sequence
 Protein Accession #: NP_008883.1

85

1 11 21 31 41 51

MAKDNSTVRC PQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW 60
 IGIFVIGICLF CLSVLGIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL 120
 FLKQMLERYQ NMSPPNDDQ WKNGVTKTW DRLMLQDNCC GVNPGSDWQK YTSAPRTENN 180
 DADYFPPRQC CVMNMLEKPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVANFGFAI 240
 LCWTFWVLLG TMFYWSRIEY

Seq ID NO: 536 DNA sequence
 Nucleic Acid Accession #: NM_002638.1
 Coding sequence: 120..473

1 11 21 31 41 51
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 GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAACACCTT CCTGACACCA 120
 TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCTCAT CGCTGGGACG CTGGTTCTAG 180
 AGGCAGCTGT CACGGGAGTT CTGTTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
 TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG 300
 CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360
 TCCGGTGGCG CATGTTGAAT CCCCCTAACC GCTGCTTGA AGATACTGAC TGCCAGGAG 420
 TCAAGAAGTG CTGTGAAGGC TCTTGCAGGA TGGCCTGTTT CGTTCCTCCAG TGAAGGGAGC 480
 CGGTCTTGGC TGCACCTGTG CCGTCCCGAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540
 TGCTGCCCTT CCCCTTCCCA CACTGTCCAT TCTTCTCCC ATTCAGGATG CCCACGGCTG 600
 GAGCTGCCCT TCTCATCCAC TTTCAATAA A

Seq ID NO: 537 Protein sequence
 Protein Accession #: NP_002629.1

1 11 21 31 41 51
 | | | | |
 MRASSFLIVV VFLIAGTLVL EAAVTGVPVK GQDTVKGKRP FNGQDPVKGQ VSVKGQDKVK 60
 AQEPVKGPVS TKPSCPIIL IRCAMLNPPN RCLKDTCFPG IKKCEGSCG MACFVPQ

Seq ID NO: 538 DNA sequence
 Nucleic Acid Accession #: NM_001793.2
 Coding sequence: 71..2560

1 11 21 31 41 51
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 CTCTGCAGCC ATAGGGGCTCC CTGCTGGACC TCTCGCTCT CTCTCTCTC TCAGGTTTG 120
 CTGGCTGCAG TGGCGGCGCT CCGAGCCGTG CCGGGCGGTC TTCAAGGAGG CTGAAGTGAC 180
 CTTGGAGGCG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAG TATTCATGGG 240
 TGCCCTTGGG CAAGAGCCAG CTCTGTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
 TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
 ATCCAAACCT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
 TGAATAATGC AAGGTCCTCT TCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480
 AGACACCAAG ATTTTCTACA GCATCACGGG GCGGGGGGCA GACAGCCCC CTGAGGGTGT 540
 CTTGCTGTGA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
 GATTGCCAAG TATGAGTCTT TTGGCCACGC TGTGTCAGAG AATGGTGCT CAGTGGAGGA 660
 CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
 GGACACCTTC CGAGGGGAGT TCTTAGAGGG AGTCCTACCA GGTACTTCTG TGATGCAGGT 780
 GACAGCCAGG GATGAGGATG ATGCCATCTA CACTACCAAT GGGGTGGTTG CTACTCCAT 840
 CCATAGCCAA GAACCAAGG ACCCACAGCA CCTCATGTTT ACCATTACC GGAGCACAGG 900
 CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAGAA GTCCCTGAGT ACACACTGAC 960
 CATCCAGGCC ACAGACATGG ATGGGGAAGG CTCACCAACC ACGGCAGTGG CAGTAGTGGA 1020
 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
 GCCTGAGAA GTAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140
 CAACTACCA GCGTGGGCGT CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
 TACCATCACC ACCCACTCTG AGAGCAACCA GGGCATCTCT ACAACCAAGG AGGGTTTGGG 1260
 TTTGAGGCC AAAAACCCAG ACACCTCTGA CGTTGAAGTG ACCAAGAGG CCCCTTTTGT 1320
 GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
 ACCTGTGTTT GTCCCAACCT CCAAGTGTGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
 GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGCTACCG 1500
 CATCCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560
 TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTGTGAGG AACACATCT ATGAAGTCAT 1620
 GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680
 ACTGATTGAT GTCAATGACC ATGGCCCACT CCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
 CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
 CCTTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
 GGAAGGTGAC ACAGTGTGCT TGTCCCTGAA GAAGTTCTCT AAGCAGGATA CATATGACGT 1920
 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCACTGT 1980
 GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAGGGAG GTTTCATCCT 2040
 CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGGTGTCTG TTTTGTGTTG 2100
 GAGAAAGAAG CGGAAGATCA AGGAGCCCTT CCTACTCCCA GAAGATGACA CCGTGACAA 2160
 CGTCTTCTAC TATGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
 GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTTCTC CGCAATGAGC TGGCACCAAC 2280
 GATCATCCCG ACACCCATGT ACCGTCTCTG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
 TATAATTGAG AACCTGAAG CCGCTAACAC AGACCCCA CAACCCCTCT ACAGCACCTT 2400
 CTTGTGTGTC GACTATGAGG GCAGCGGCTC CGACCGCCG TCCCTGAGCT CCTCACCTC 2460
 CTCGCGCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCGCTTCAA 2520
 GAAGCTGGCA GACATGTACG GTGGCGGGA GGACGACTAG GCGGCCTGCC TGCAGGCTG 2580
 GGGACCAACG CTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCTCC TTCAGCTGAG 2640
 GACTTCGAGG ATGTCTAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
 ACGTTAGAGT GGTGTCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
 AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCCTCAG AGGCCAAGTT TCCAGAAGCC 2820
 TCTTACCTGC CGTAAATGTC TCAACCTGT GTCCCTGGGC TGGGCCTGCT GTGACTGACC 2880
 TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940

TTTTTTAAT GCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000
 GCTGGGCCCA CTGGCCGTCC TGCATTCTCT GTTTCACAGC CCCAATGCCT CCCATTCCGA 3060
 TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTT TATTTTCCCT 3120
 GTTGCCTTGC TATAGATGAA GGGTGAGGAC AATCGTGAT ATGTACTAGA ACTTTTTTAT 3180
 TAAAGAACT TTTCCAGAA AAAAA

Seq ID NO: 539 Protein sequence
 Protein Accession #: NP_001784.2

1 11 21 31 41 51
 MGLPRGPLAS LLLQLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFPGCPG 60
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIPPSKR ILRRHKRDWV VAPISVPENG 120
 KGFFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVPAV EKETGWLLLN KPLDREEIAK 180
 YELFGHAYSE NGASVEDPMN ISIIIVTDQND HKPKFTQDFT RGSVLEGLVP GTSVMQVTAT 240
 DEDDAIYTYN GVVAYSISHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TDMGDGSGTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP 360
 ANRATYLMHG GDDGDHFTIT THPESNQGIL TTRKGLDPEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
 DPAGWLAMP DSGQVTVAGT LDREDEQFVR NNIEVVMVLA MDNGSPPTTG TGTLLTLTID 540
 VNDHGFVPEP RQITICNOSP VRQVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKKPL KQDTYDVHLS LSDHGNKEQL TVIRATVCDG HGHVETCPGP WKGGFILPVL 660
 GAVLALLFLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVFI YGEEGGGEED QDYDITQLHR 720
 GLEARPEVVL RNDVAPTIIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDITLLVF 780
 DYEGSGSDAA SLSLSTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

Seq ID NO: 540 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..672

1 11 21 31 41 51
 ATGAGGCTCC AAAGACCCCG ACAGGCCCCG GCGGGTGGGA GCGCGCGCGC CCGGGCGGG 60
 CGGGGCTCCC CCTACCGGCC AGACCCGGGG AGAGGCGCGC GAGAGCTGCG AAGGTTCCAG 120
 AAGGGCGGGG AGGGGGCGCC GCGCGCTGAC CCTCCTCTGG CACCGCTGGG GACGATGGCG 180
 CTGCTCGCCT TGCTGTGTTG CGTGGCCCTA CCGCGGGTGT GGACAGACGC CAACCTGACT 240
 GCGAGACAAC GAGATCCAGA GGAATCCAGC CGAACGAGCG AGGGTGACAA TAGAGTGTGG 300
 TGTATGTTT GTGAGAGAGA AAACACTTTC GAGTGCAGG ACCCAAGGAG GTGCAATGG 360
 ACAGAGCCAT ACTGCGTTAT AGCGGCCGTG AAAATATTTC CACGTTTTTT CATGTTTGGC 420
 AAGCAGTGCT CCGCTGTGTT TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480
 CTCCTGGAAG AGCCCAAGCC CTCTCTTTAC CTCAGGTGTT GTAAAAATTC CTACTGCAAT 540
 TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAGAGAA ATGCTGGGAG CATGGGTGAG 600
 AGCTGTGGTG GCGTGTGGCT GGCATCCTC CTGCTGCTGG CCTCCATTGC AGCCGCCCTC 660
 AGCCTGTCTT GA

Seq ID NO: 541 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MRLQRPRQAP AGGRRAPRGG RGSFYRDPDG RGARRLRRPQ KGGEGAPRAD PPWAPLGTMA 60
 LLALLLVVAL PRVWTDANLT ARQRPEDDSQ RTDEGDNVWV CHVCERENTF ECQNPRRCWK 120
 TEPYCVIAAV KIFPRPFMVA KQCSAGCAAM ERPKPEEKRF LLEBPMPPFY LKCKIRYCN 180
 LBGPPINSSV FKEYAGSMGE SCGGLWLAIL LLLASIAAGL SLS

Seq ID NO: 542 DNA sequence
 Nucleic Acid Accession #: XM_035292.2
 Coding sequence: 53..1576

1 11 21 31 41 51
 GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60
 TGCGGGCCCG AAGCGGCGCG CGCTAGCGGC GCGGCGCGCC GAGGAGAAGG AAGAGGCGCG 120
 GGAGAAGATG CTGCGCGCCA AGAGCGCGGA CCGCTCGCGC CCGGCAGGCG AGGGCGAGGG 180
 CGTGACCTCG CAGCGGAACA TCACGCTGCT CAACGCGCTG GCCATCATCG TGGGACCAT 240
 TATCGGCTCG GGCATCTTCG TGACGCCAC GGGCGTGCTC AAGGAGGCG GCTCGCGGG 300
 GCTGGCGCTG GTGGTGTGGG CCGCGTGGCG CGTCTCTCC ATCGTGGGCG CGCTCTGCTA 360
 CGCGGAGCTC GGCACCAACA TCTCCAAATC GGGCGGCGAC TACGCCTACA TGCTGGAGGT 420
 CTACGGCTCG CTGCGCGCCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCGGCGCTTC 480
 ATCGCAGTAC ATCGTGGCCC TGGTCTTGG CACCTACCTG CTCAGCGCGC TCTTCCCCAC 540
 CTGCCCGGTG CCGGAGGAGG CAGCCAAAGT CGTGGCCTCG CTCTGCGTGC TGCTGCTCAC 600
 GGCGGTGAAC TGCTACAGCG TGAAGGCGCG CACCGGGTTC CAGGATGCCT TTGCGCGCG 660
 CAACTCCTCG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720
 TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAATGGATG TGGGGAACAT 780
 TGTGTGGCA TTATACAGCG GCCTCTTTCG CTATGGAGGA TGAATTACT TGAATTGCT 840
 CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTG GCCATCATCA TCTCCTTGCC 900
 CATCGTGACG CTGCTGTACG TGCTGACCAA CCTGGCCTAC TTCACCAACC TGTCCACCGA 960
 GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGAATTCGGG AACTATCACG TGGGCGTCAT 1020
 GTCTGGATTC ATCCCGTCT TCGTGGGCGT GTCTGCTTC GGCTCCGCTA ATGGGTCCCT 1080
 GTTCACATCC TCCAGGCTCT TCTTGTGGG GTCCCGGGA GGCACCTGCT CCTCATCCT 1140
 TCCCATGATC CACCCACAGC TCCTCACCCC CGTGGCGTCC CTCGTGTTC CGTGTGTGAT 1200
 GACGCTGCTC TACGCTTCT CCAAGGACAT CTCTCCGCT ATCAACTTCT TCAGCTTCTT 1260
 CAACTGGCTC TACGCTTCT TGGCCATCAT CGGCTGATC TGGCTGCGCC ACAGAAAGCC 1320
 TGAGCTTGA CGGCCATCA AGGTGAACCT GGCCCTGCT GTGTCTTCA TCCTGGCCTG 1380
 CCTCTTCTG ATCGCGTCT CTCTCTGGA GACACCGTG GAGTGTGGCA TCGGCTTCA 1440
 CATCATCCTC AGCGGGCTGC CCGTCTACTT CTCTGGGCT TGGTGGAAAA ACAAGCCCA 1500
 GTGGCTCTC CAGGCGATCT TCTCCAGGAC CGTCTGTGT CAGAAGCTCA TGCAGTGTG 1560

CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

Seq ID NO: 543 Protein sequence
Protein Accession #: XP_035292.2

1	11	21	31	41	51	
MAGAGPKRRA	LAAPAAEKE	EAREKMLAAK	SADGSAPAGE	GEGVTILQRNI	TLLNGVAIIV	60
GTIIGSGIFV	TPTGVLKEAG	SPGLALVVA	ACGVFSIVGA	LCYAEIGTTI	SKSGGDYAYM	120
LEVYGSIPAF	LKLWIELLII	RPSSQYIVAL	VFATYLLKPL	PPTCPVPEEA	AKLVACLCLV	180
LLTAVNCYSV	KAATRVQDAF	AAAKLLALAL	IILLGFVQIG	KGDVSNLDPN	FSFEGTKLDV	240
GNIVLALYSY	LFAYGGWNYL	NFVTEEMINP	YRNLFPLAII	SLPIVTLVYV	LTNLAYFTTL	300
STEQMLSSAA	VAVDFGNVHL	GUMSWIIPVF	VGLSCFGSVN	GSLEPTSSRLF	FVGSREGHLP	360
SLLSMIHPQL	LTPVPSLVFT	CVMTLLYAFS	KDIFSVINFF	SFFNWLVCAL	AIIGMIWLRH	420
RKPELERPIK	VNLALPVFFI	LACLFLIAVS	PWKTPVECGI	GFTIILSGLP	VYFFGVWKN	480
KPKWLLQGIF	STTVLCQKLM	QVVPQBT				

Seq ID NO: 544 DNA sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 168..989

1	11	21	31	41	51	
TAAAAAGCAA	AAGAATTCGC	GGCCGCGTCG	ACACGGGCTT	CCCCGAAAAC	CTTCCCCGCT	60
TCTGATATG	AAATTCAGC	TGCTTGTCTGA	GTCTTATTGC	CGGCTGCTGG	GAGCCAGGAG	120
AGCCCTGAGG	AGTAGTCACT	CAGTAGCAGC	TGACGCGTGG	GTCCACCATG	AACCTGGAGTA	180
TCTTTGAGGG	ACTCTGAGT	GGGTCAACA	AGTACTCCAC	AGCCTTTGGG	CGCATCTGGC	240
TGTCTCTGGT	CTTCATCTTC	CGCGTGTCTG	TGTACTCTGT	GACGGCCGAG	CGTGTGTGGA	300
GTGATGACCA	CAAGGACTTC	GACTGCAATA	CTCGCCAGCC	CGGCTGCTCC	AACGTCTGCT	360
TTGATGAGTT	CTTCCCTGTG	TCCCATGTGC	GCCTCTGGGC	CCTGCAGCTT	ATCCTGTGTA	420
CATGCCCTTC	ACTGCTGTG	GTCATGCACG	TGGCCTACCG	GGAGGTTTCA	GAGAAGAGGC	480
ACCGAGAAGC	CCATGGGGAG	AACAGTGGGC	GCCTCTACCT	GAACCCCGGC	AAGAAGCGGG	540
GTGGGCTCTG	GTGGACATAT	GTCTGCAGCC	TAGTGTTCAA	GGCGAGCGTG	GACATCGCCT	600
TTCTCTATGT	GTTCCACTCA	TTCTACCCCA	AATATATCCT	CCCTCTGTGT	GTCAAGTGCC	660
ACGCAGATCC	ATGTCCTAAT	ATAGTGGACT	GCTTCACTTC	CAAGCCCTCA	GAGAAGAACA	720
TTTTCACTTC	CTTCATGTG	GCCACAGCTG	CCATCTGCAT	CCTGCTCAAC	CTCGTGGAGC	780
TCATCTACCT	GGTGAAGCAG	AGATGCCACG	AGTGCTGGC	AGCAAGGAAA	GCTCAAGCCA	840
TGTGCACAGG	TCATCACCCC	CACGGTACCA	CCTCTTCTCT	CAACAAGAC	GACCTCTCTT	900
CGGGTGACCT	CATCTTCTCT	GGCTCAGACA	GTCTCTTCTC	TCTCTTACCA	GACCGCCCCC	960
GAGACCATGT	GAAGAAACC	ATCTTGTGAG	GGGCTGCCTG	GACTGTGCTG	GCAGGTGGGG	1020
CCTGGATGGG	GAGGCTCTAG	CATCTCTCAT	AGGTGCAACC	TGAGAGTGGT	GGAGCTAAGC	1080
CATGAGGTAG	GGGCAGGCAA	GAGAGAGGAT	TCAGACGCTC	TGGGAGCCAG	TTCTAGTCC	1140
TCAACTCCAG	CCACCTGCCC	CAGCTCGACG	GCACTGGGCC	AGTTCCCTCT	CTGCTCTGCA	1200
GCTCGGTTTC	CTTTCTAGA	ATGGAAATAG	TGAGGGCCAA	TGC		

Seq ID NO: 545 Protein sequence
Protein Accession #: NP_005259.1

1	11	21	31	41	51	
MNWSIFEGLL	SGVKNYSTAF	GRWLSLVFI	FRVLVYLVA	ERVNSDDHKD	FDCNTRQPGC	60
SNVCFDEFPF	VSHVRLWALQ	LILVTCPSLL	VVMHVAYREV	QEKRRHREAHG	ENSGRLYLNP	120
GKKRGGIWWT	YVCSLVFKAS	VDIAFLVVFH	SFYPKYILEP	VVKCHADPCP	NIIVDCFISKP	180
SEKNIFTLFM	VATAICILL	NLVELIYLV	KRCHECLAAR	KAQAMCTGHH	PHGTTSSCKQ	240
DDLSSGDLIF	LGSDSHPLLL	PDRPRDHVKK	TIL			

Seq ID NO: 546 DNA sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 26..457

1	11	21	31	41	51	
CGGGCGAAGC	AGCGCGGCA	GCGAGATGCA	GCACCGAGGC	TTCCTCTCTC	TCACCTCTCT	60
CGCCCTGCTG	GCGCTCACCT	CCGCGGTGCG	CAAAAAGAAA	GATAAGGTGA	AGAAGGGCGG	120
CCCGGGGAGC	GAGTGCCTG	AGTGGGCTG	GGGCGCTG	ACCCCGAGCA	GCAAGGATTG	180
CGGCGTGGGT	TTCCGCGAGG	GCACCTGCGG	GGCCGAGACC	CAGCGCATCC	GGTGCAGGGT	240
GCCCTGCAAC	TGGAAGAAGG	AGTTTGGAGC	CGACTGCAAG	TACAAAGTTG	AGAACTGGGG	300
TGCGTGTGAT	GGGGGACAG	GCACCAAGT	CCGCCAAGGC	ACCCTGAAGA	AGGCGCGCTA	360
CAATGCTCAG	TGCCAGGAGA	CCATCCGCGT	CACCAAGCCC	TGCACCCCCA	AGACCAAGGC	420
AAAGGCCAAA	GCCAAGAAAG	GGAAGGGAAG	GGACTAGACG	CCAAGCCTGG	ATGCCAAGGA	480
GCCCTGGTGT	TCACATGGGG	CCTGGCCACG	CCCTCCCTCT	CCCAGGCCCG	AGATGTGACC	540
CACCAAGTCC	TTCTGTCTGC	TGTTAGCTT	TAATCAATCA	TGCCCTGCCT	TGTCCCTCTC	600
ACTCCCGAGC	CCACCCCTTA	AGTGCCCAAA	GTGGGGAGGG	ACAAGGGATT	CTGGGAAGCT	660
TGAGCCTCCC	CCAAAGCAAT	GTGAGTCCCA	GAGCCCGCTT	TTGTTCTTCC	CCACAATTCC	720
ATTACTAAGA	AACACATCAA	ATAAAGTGAC	TTTTTCCCCC	CAATAAAAGC	TCTTCTTTT	780
TAATAT						

Seq ID NO: 547 Protein sequence
Protein Accession #: NP_002382.1

1	11	21	31	41	51	
MQHRGFLLLT	LLALLAL TSA	VAKKDKVKK	GGPGSECAEW	ANGPCTPSSK	DCGVGFREGT	60
CGAQTQRIIC	RVPCNWKKEF	GADCKYKFEN	WGACDGGTGT	KVRQGTLLKA	RYNAQCQETI	120
RVTKPCTPKT	KAKAKAKKKG	GKD				

Seq ID NO: 548 DNA sequence

Nucleic Acid Accession #: NM_006783.1
Coding sequence: 1..786

5 1 11 21 31 41 51
| | | | | |
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACACTC CACCAGCATC 60
GGGAAGGTGT GGATCACAGT CATCTTTATT TTCCGAGTCA TGATCCTAGT GGTGGCTGCC 120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTGCTCTGCA ACACACTGCA ACOGGGATGC 180
10 AAAAAATGTGT GCTATGACCA CTTTTCCTCC GTGTCCCACTA TCCGGCTGTG GGCCTCCAG 240
CTGATCTTCG TCTCCACCCC AGCGCTGCTG GTGCCCATGC ATGTGGCCTA CTACAGGCAC 300
GAAACCACTC GCAAGTTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
ATTAAAAAGC ACAAGGTTTCG GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420
TTTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCTT TTACAATGGG 480
TACCACCTGC CTGGGTGTTT GAAATGTGGG ATTGACCCCT GCCCAACCTT TGTGTACTGC 540
15 TTTATTCTA GGCCAAACAGA GAAGACCGTG TTTACCATTT TTATGATTTT TCGCTCTGTG 600
ATTTGCATGC TGCCTAAAGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTTAGG 660
AGATCAAGA GAGCACAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
CAGAAATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
AGCTAA

Seq ID NO: 549 Protein sequence
Protein Accession #: NP_006774.1

25 1 11 21 31 41 51
| | | | | |
MDWGLTHTFY GGVNKHSTSI GKVNITVIFI FRVMILVVAA QEVWGDEQED FVCNTLQPGC 60
KNVCYDHFPP VSHIRLWALQ LIFVSTPALL VAMHVAYYRH ETTRKFRGRG KRNDFKDIED 120
IKKHVKRIEG SLWWTYTTSSI PFRIIFEAAP MYVFPYLYNG YHLPWVLKCG IDPCPNLVDIC 180
FISRPTKTV TITPMISASV ICMLLNVAEL CYLLKVCPR RSKRAQTQKN HPNHALKESK 240
30 QNEMNELISD SQQNAITGFP S

Seq ID NO: 550 DNA sequence
Nucleic Acid Accession #: NM_002571.1
Coding sequence: 99..587

35 1 11 21 31 41 51
| | | | | |
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCTCCTGC 60
TCACCTCTGG GCTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
40 AGGACCTGGA GCTCCCAAGG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
ACATCTCCCT CATGGCGACA CTGAAGGCCC CTCTGAGGGT CCACATCACC TCACTGTTGC 240
CCACCCCGGA GGACAACCTG GAGATCGTTC TGCACAGATG GGAGAACAAAC AGCTGTGTTG 300
AGAAGAGAGT CCTTGGAGAG AAGACTGGGA ATCCAAGAA GTTCAAGATC AACTATACGG 360
TGGCGAACGA GGCACCGCTG CTCGATACTG ACTACGACAA TTTCTGTGTT CTCTGCCTAC 420
45 AGGACACCAC CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCTGTGTTG 480
AGGACGATGA GATCATGCGAG GGATTTCATCA GGGCTTTTCA GCGCCCTGCC AGGCACCTAT 540
GGTACTTGCT GGACTTGAAG CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCCGCTT 600
CCAGGAAGAC CAGACTCCCA CCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCCTGCCC 660
50 TTCAAAGAA TAACCACAGC TCAGAAGACG ATGACGTGGT CATCTGTGTC GCCATCCCTT 720
TCTCTGTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAACC CTTGGAGCAT G

Seq ID NO: 551 Protein sequence
Protein Accession #: NP_002562.1

55 1 11 21 31 41 51
| | | | | |
MDIPQTKQDL ELPLKAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPPT EDNLEIVLHR 60
WENNSCVEKK VLGEKTGNPK KFKINYTVAN EATLLDITDYN NFLPLCLQDT TTPIQSMMQ 120
60 YLARVLVEDD EIMQGFIRAP RPLPRHLWYL LDLKQMEEPK RF

Seq ID NO: 552 DNA sequence
Nucleic Acid Accession #: NM_006500.1
Coding sequence: 27..1967

65 1 11 21 31 41 51
| | | | | |
ACTTGCGTCT CGCCCTCCGG CCAAGCATGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC 60
70 TCGCGCCTG CTGCTGCTGT CCTCGCGTGG CGGGTGTGCC CGGAGAGGCT GAGCAGCCTG 120
CGCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCTCTCCC 180
AGTCCCAAGG CAACCTCAGC CATGTCGACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC 240
TCATCTTCCG TGTGCGCCAG GGCCAGGGCC AGAGCGAACC TGGGGAGTAC GAGCAGCGGC 300
TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCCTGACTCA AGTCACCCCC CAAGACGAGC 360
75 GCATCTTCTT GTGCCAGGGC AAGCGCCCTC GGTCGCCAGG GTACCGCATC CAGCTCCGCG 420
TCTCAAAGC TCCGAGGAG CCAAAATATC AGTCAACCC CCTGGGCATC CTTGTGAACA 480
GTAAGGAGCC TGAGGAGGTG GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCTCTCAG 540
TCATCTGGTA CAGAATGGC CGGCCTCTGA AGGAGGAGAA GAACCGGGTC CACATTCAGT 600
CGTCCAGAC TGTGGAGTCG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC 660
TGGTTAAAGA AGACAAAGAT GCCCAGTTT ACTGTGAGCT CAATACCGG CTGCCCAAGT 720
80 GGAACCATAT GAAGGAGTCC AGGGAAGTCA CCGTCCCTGT TTTCTACCCG ACAGAAAAAG 780
TGTGGCTGGA AGTGGAGCCC GTGGGAATGC TGAAGGAAGG GGACCGCTG GAAATCAGGT 840
GTTTGGCTGA TGGCAACCTT CCACCACTC TCAGCATCAG CAAGCAGAAC CCCAGCACCA 900
GGGAGGCGGA GGAAGAGACA ACCAACGACA ACGGGGTCTT GGTGCTGGAG CCGCCCGGA 960
AGGAACACAG TGGGCGCTAT GAATGTCAAG CCTGGAATT GGACACCATG ATATCGCTGC 1020
85 TGAGTGAAC ACAGGAACAT CTGGTGAAT ATGTGTCTGA GTCGAGAGT AGTCCCGAG 1080
CCCTGAGAG ACAGGAAGGC AGCAGCCTCA CCTGACCTG TGAGGCAGAG AGTAGCCAGG 1140
ACCTCGAGTT CCAGTGGCTG AGAGAAGAGA CAGACCAGGT GCTGGAAAGG GGGCCTGTGC 1200

5	TTCAAGTTGCA	TGACCTGA	CGGGAGGCAG	GAGGCGGCTA	TCGCTGCGTG	GGCTCTGTGC	1260
	CCAGCATACC	CGGCTGAAC	CGCACACAGC	TGGTCAAGCT	GGCCATTITT	GGCCCCCCTT	1320
	GGATGGCATT	CAAGGAGAGG	AAGGTGTGGG	TGAAAGAGAA	TATGGTGTG	AATCTGTCTT	1380
	GTGAAGCGTC	AGGGCACCCC	CGGCCCACCA	TCTCTGGAA	CGTCAACGGC	ACGCCAAGTG	1440
	AAACAAGACCA	AGATCCACAG	CGAGTCTCTGA	GCACCTTGAA	TGTCTCTGTG	ACCCCGGAGC	1500
	TGTTGGAGAC	AGGTGTTGAA	TGCAACGGCT	CCAAACGACCT	GGGCAAAAGC	ACCAGCATCC	1560
	TCTTCTCTGA	GCTGTCTAAT	TTAACCACCC	TCACACCAGA	CTCCAAACAC	ACCACTGGCC	1620
	TCAGCACTTC	CACCTGCCAGT	CCTCATACCA	GAGCCACACG	CACCTCCACA	GAGAGAAAGC	1680
10	TGCCGGAGCC	GGAGAGCCGG	GGCGTGGTCA	TCGTGGCTGT	GATTGTGTGC	ATCCTGGTCC	1740
	TGGCGTGTCT	GGGCGCTGTC	CTCTATTTC	TCGTATAAGAA	GGGCAAGCTG	CCGTGCAGGC	1800
	GCTCAGGGAA	GCAGGAGATC	ACGCTGCCCC	CGTCTCGTAA	GACCGAATCT	GTAGTTGAAG	1860
	TTAAGTCAGA	TAAGCTCCCA	GAAGAGATGG	GCCTCTCTGA	GGGCAGCAGC	GGTGACAAGA	1920
	GGGCTCCGGG	AGACCAGGGA	GAGAAATACA	TCGATCTGAG	GCATTAGCCC	CGAATCACTT	1980
15	CAGCTCCCTT	CCCTGCCCTG	ACCATTCCCA	GCTCCCTGCT	CACCTCTCTC	TCAGCCAAAG	2040
	CTCTCCAAAG	GACTAGAGAG	AAGCCTCCTG	CTCCCTCAC	CTGCACACCC	CCTTTCAGAG	2100
	GGCCACTGGG	TAGGAGCTG	AGGACCTCAC	TTGGCCCTGC	AAGCCGCTTT	TCAGGGACCA	2160
	GTCACACACC	ATCTCTCTCA	CGTTGAGTGA	AGCTCATCCC	AAGCAAGSAG	CCCCAGTCTC	2220
	CCGAGCGGGT	CAGGAGAGTT	CTTGCAAGAAC	GTGTTTTTTC	TTTACACACA	TTATGGCTGT	2280
20	AAATACCTGG	CTCTGCCAG	CAGCTGAGCT	GGTAGCCTC	TCTGAGCTGG	TTTCTGCCCC	2340
	CAAAAGCTGG	CTTCCACCAT	CCAGGTGCAC	CACCTGAAGT	AGGACACACC	GGAGCCAGGC	2400
	GCCTGTCTAT	GTGGAAGTGC	GCTGTTTACA	CCGCTCCGGG	AGAGCACCC	AGCGGCATCC	2460
	AGAAGCAGCT	GCAGTGTGTC	TGCCACACCC	CTCTGCTCG	CCTCTTCAAA	GTCTCTCTGT	2520
	ACATTTTTTC	TTTGTCTAGA	AGCCAGGAAC	TGGTGTCTAT	CCTTAAAGAA	TACGTGCCGG	2580
25	GGCCAGGTGT	GGTGGCTCAC	GCCTGTAATC	CCAGCACTTT	GGGAGGCCGA	GGCGGGCGGA	2640
	TCACAAAGTC	AGGACGAGAG	CATCTGGCT	AACACGGTGA	AACCTGTCT	CTACTAAAAA	2700
	TACAAAAAAA	AATTAGCTAG	CGGTAGTGGT	TGGCACCTAT	AGTCCCAAGT	ACTCGGAAGG	2760
	CTGAAGCAGC	AGAATGGTAT	AATCCAGGA	GGTGGAGCTT	GCAGTGAGCC	GAGACCGTGC	2820
	CACCTGCACT	CAGCCTGGGC	AAACACGCGA	GACTCCGTCT	CGAGGAAAAA	AAAAGAAAAA	2880
30	ACCGGTACCT	GGGTGAGGA	AGCTGGGCGC	TGTTTTGAG	TTCAAGTGAA	TTAGCCTCAA	2940
	TCCTCCGTGT	CACCTGTCTC	CATAGCCCTC	TTGATGGATC	ACGTAAAACT	GAAAGGCAGC	3000
	GGGAGCAGCA	CAAAAGCTAG	GTCTACACTG	TCCTTCTATG	GGATTAAAGC	TATGGTTATA	3060
	TTAGCACCAA	ACTTCTACAA	ACCAAGCTCA	GGGCCCCAAC	CCTAGAAAGG	CCCAAAATGAG	3120
	AGAATGGTAT	TTAGGGATGG	AAAACGGGGC	CTGGCTAGAG	CTTCGGGTGT	GTGTGTCTGT	3180
35	CTGTGTGTAT	GCATACATAT	GTGTGTATAT	ATGGTTTTGT	CAGGTGTGTA	AATTTGCAAA	3240
	TTGTTTCCTT	TATATATGTA	TGTATATATA	TATATGAAAA	TATATATATA	TATGAAAAAT	3300
	AAAGCTTAAT	TGTCCAGAAA	AATCATACAT	TGCTTTTTTA	TTCTACATGG	GTACCCAGG	3360
	AACTGGGGG	CCTGTGAAGC	TACAACCAAA	AGGCACACAA	AACCGTTTCC	AGTTGGCAGC	3420
	AGAGATCAGG	GGTTACCTCT	GCTTCTGAGC	AAATGGCTCA	AGCTCTACCA	GAGCAGACAG	3480
40	CTACCCTACT	TTTACGACAG	AAAACGTCCT	GTATGACGCA	GCACGAAGGG	CCTGGCAGGC	3540
	TGTTAGCAGG	AGCTATGTCC	CTTCTATCG	TTTCCGTCCA	CTT		

Seq ID NO: 553 Protein sequence
Protein Accession #: NP_006491.1

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	GLPRLVCAFL	LAACCCCPRV	AGVPGAEQEP	APELVEVEVG	STALLKCGLS	QSQGNLSHVD	60
	WFSVHKEKRT	LIFRVQGGG	QSEFGEYEQR	LSLQDRGATL	ALTQVTPQDE	RIFLCQKRP	120
	RSQERYIQLR	VVKAPPEENI	QVNPLGIPVN	SKPEEVEATC	VGRNGYPIPO	VIWYKNGRPL	180
50	KEEKVRVHIQ	SSQTVESSGL	YTLQSLKAQ	LVKEDKDAQF	YCELNYRLPS	GNHMKESREV	240
	TVPVFPYPTK	VNLEVEPVGM	LKEGDRVEIR	CLADGNPPPH	FSISKQNPST	REAEETITND	300
	NGVLVLEPAR	KEHSGRYECQ	AWNLDTMISL	LSEPOELLVN	YVSDVRVSPA	APERQEGSSL	360
	TLTCEAESST	DLFEQWLRREE	TDQVLERGPV	LQLHDLKREA	GGGYRCVASV	PSIPGLNRTQ	420
	LVKLAIFFGP	WMAFKERKVV	VKENMVLNLS	CEASGHPRPT	ISWNVNGTAS	EQDQDPQVRL	480
55	STLNLVLTPE	LELETGVECTA	SNDLGNKNTSI	LFLELVNLT	LTPDSNTTGT	LSTSTASPHT	540
	RANSTSTERK	LPEPESRGVV	IVAVIVCILV	LAVLGAVLYP	LYKKGKLPCR	RSQKQBITLP	600
	PSRKTELVEE	VKSDKLPEEM	GLLQSSGSDK	RAPGDQGEKY	IDLRH		

Seq ID NO: 554 DNA sequence
Nucleic Acid Accession #: NM_003183.3
Coding sequence: 165..2639

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	GCTAGGCCGG	GCAGATCCCG	TCCTCCCCCG	ATGTGAGCAG	TTTTCCGAAA	CCCGCTCAGG	120
	CGAAGGCTGC	CCAGAGAGGT	GGAGTCGGTA	GCGGGGCCCG	GAACATGAGG	CAGTCTCTCC	180
	TATTCTTGAC	CAGCGTGGTT	CCTTTCGTGC	TGGCGCGCGG	ACCTCCGGAT	GACCCGGGCT	240
70	TCGCCCCCA	CCAGAGACTC	GAGAAGCTTG	ATTCTTTGCT	CTCAGACTAC	GATATTCTCT	300
	CTTTATCTAA	TATCCAGCAG	CATTCCGTAA	GAAAAAGAGA	TCTACAGACT	TCAACACATG	360
	TAGAAACACT	ACTAACTTTT	TCAGCTTTGA	AAAGGCATT	TAAATTATAC	CTGACATCAA	420
	GTACTGAACG	TTTTTTCACAA	AATTTCAAGG	TCGTGGTGGT	GGATGGTAAA	AACGAAAGCG	480
	AGTACACTGC	AAAATGGCAG	GACTTCTTCA	CTGGACACGT	GGTTGGTGAG	CCTGACTCTA	540
	GGGTCTTAGC	CCACATAAGA	GATGATGATG	TTATAATCAG	AATCAACACA	GATGGGGCCG	600
75	AAATATAACT	AGAGCCACTT	TGGAGATTGG	TTAATGATAC	CAAAAGACAAA	AGAATGTTAG	660
	TTTATAAATC	TGAAGATATC	AAGAATGTTT	CACGTTTGCA	GTCTCCAAAA	GTGTGTGGTT	720
	ATTTAAAGT	GGATAATGAA	GAGTTGCTCC	CAAAAGGTTT	AGTAGACAGA	GAACCACTG	780
	AAGAGCTTGT	TCATCGAGTG	AAAAGAAGAG	CTGACCCAGA	TCCCATGAAG	AACACGTGTA	840
	AAATATTGGT	GGTAGCAGAT	CATCGCTTCT	ACAGATACAT	GGGCAGAGGG	GAAGAGAGTA	900
80	CAACTACAAA	TACTTAATAA	GAGCTAATTG	ACAGAGTTGA	TGACATCTAT	CGGAACACTT	960
	CATGGGATTA	TGCGAGTTTT	AAAGGCTATG	GAATACAGAT	AGAGCAGATT	CGCAATTCTCA	1020
	AGTCTCCACA	AGAGGTAAAA	CCTGGTGAAA	AGCACTACAA	CATGGCAAAA	AGTTACCCAA	1080
	ATGAAGAAAA	GGATGCTTGG	GATGTGAAGA	TGTTGCTAGA	GCAATTATAG	TTTGATATAG	1140
	CTGAGGAAGC	ATCTAAAGTT	TGCTTGGCAC	ACCTTTTCAC	ATACCAAGAT	TTTGATATAG	1200
85	GAACCTCTTG	ATTAGCTTAT	GTTGGCTCTC	CCAGAGCAAA	CAGCCATGGA	GGTGTGTTGC	1260
	CAAAAGGCTA	TTATAGCCCA	GTTGGGAAGA	AAAATATCTA	TTTGAATAGT	GGTTTGACGA	1320
	GCACAAAGAA	TTATGTTAAA	ACCATCCTTA	CAAAGGAAGC	TGACCTGGTT	ACAACTCATG	1380

	AATTGGGACA	TAATTTTGA	GCAGAACATG	ATCCGGATGG	TCTAGCAGAA	TGTGCCCCGA	1440
	ATGAGGACCA	GGGAGGGAAA	TATGTCATGT	ATCCCATAGC	TGTGAGTGGC	GATCAGCAGA	1500
	ACAATAAGAT	TTTTTCAAAC	TGCAGTAAAC	AATCAATCTA	TAAGACCATT	GAAAGTAAGG	1560
5	CCGAGGAGTG	TTTTCAAGAA	CGCAGCAATA	AAGTTTGTGG	GAACCTCGAGG	GTGGATGAAG	1620
	GAGAAAGAGT	TGATCCTGGC	ATCATGTATC	TGAACAAACA	CACCTGCTGC	AACAGCGACT	1680
	GCACGTTGAA	GGAAAGGTGTC	CAGTGCAAGT	ACAGGAACAG	TCCTTGCTGT	AAAAACTGTC	1740
	AGTTTGAGAC	TGCCCAGAA	AAGTGCCAGG	AGGCGATTAA	TGCTACTTGC	AAAGGCGTGT	1800
	CCTACTGCAC	AGGTAATAGC	AGTGAGTGCC	CGCCTCCAGG	AAATGCTGAA	AATGACACTG	1860
10	TTTGCTTGA	TCTTGGCAAG	TGTAAGGATG	GGAAATGCAT	CCCTTCTGTC	GAGAGGGGAA	1920
	AGCAGCTGGA	GTCCTGTGCA	TGTAATGAAA	CTGCAAACTC	CTGCAAGGTG	TGCTGCAAGG	1980
	ACCTTCTCG	CCGCTGTGTG	CCCTATGTGC	ATGCTGAACA	AAAGAAGCTTA	TTTTTGAGGA	2040
	AAGGAAAGCC	CTGTACAGTA	GGATTTTGTG	ACATGAATGG	CAATGTGAG	AAACGAGTAC	2100
	AGGATGTAAT	TGAACGATTT	TGGGATTTCA	TTGACCAGCT	GAGCATCAAT	ACTTTTGGAA	2160
	AGTTTTTAC	AGACAAATC	GTTGGGTCTG	TCTGTGTTT	CTCCTTGATA	TTTGGGATTC	2220
15	CTTTCAGCAT	TCTTGTCCAT	TGTGTGGATA	AGAAATTTGA	TAAACAGTAT	GAATCTCTGT	2280
	CTCTGTTTCA	CCCCAGTAAC	TGCGAAATGC	TGAGCAGCAT	GGATTCTGCA	TGCGTTTCGA	2340
	TTATCAAACC	CTTTCCTCGC	CCCCAGACTC	CAGGCCGCTC	GCAGCCTGCC	CCTGTGATCC	2400
	CTTCGGCGCC	AGCAGCTCCA	AACTGGGACC	ACCAGAGAAT	GGACACCATC	CAGGAAGACC	2460
20	CCAGCACAGA	TCCCAATAG	GACGAGGATG	GGTTTGAGAA	GGACCCCTTC	CCAAATAGCA	2520
	GCACAGCTGC	CAAGTCATT	GAGGATCTCA	CGGACCATCC	GGTCCGCGAG	AGTGAAGAGG	2580
	CTGCTCTCT	TAACTGTGAG	GTGCTAAGAC	CAAGAAGACA	GAGTGCTAAT		2640
	TTAGTTCTCA	GCTCTTCTGA	CTTAAGTGTG	CAAAATATTT	TTATAGATTT	GACCTACAAA	2700
	TCAATCACAG	CTTGATTTT	GTGAAGACTG	GGAAAGTACT	TAGCAGATGC	TGGTCATGTG	2760
25	TTTGAACCTC	CTGCAGGTAA	ACAGTTCTTG	TGTGGTTTGG	CCCTTCTCCT	TTTGAAGAGG	2820
	TAAAGTGAAA	GTGAATCTAC	TTATTTTGAG	GCTTTCAGTG	TTTAGTTT	AAAATATCTT	2880
	TTGACCTGTC	TGCAAAATAC	AGAAATACAC	GCTGGATTGG	GTTATGAATA	TTTACGTTTT	2940
	TGTAAATTA	TCTTTTATAT	TGATAACAGC	ACTGACTAGG	GAAATGATCA	GTITTTTTTT	3000
	ATACACTGTA	ATGAACCGCT	GAATATGAAG	CATTTGGCAT	TTATTTGTGA	GAAAAGTGGG	3060
30	ATAGTTTTTT	TTTTTTTTTT	TTTTTTTTTG	CTTCAACTAA	AAACAAAGGA	GATAAATTTA	3120
	GTATACATTC	TATCTAAAT	GTGGGTCTAT	TTCTAGTTAT	TACCCAGAGT	TTTTATGTAG	3180
	CAGGAAATAT	ATATATCTAA	ATTTAGAAAT	CATTTGGGTT	AATATGGCTC	TTTATAATTC	3240
	TAAGACTAAT	GCTCAGAAC	TAACCACTAC	CTTACAGTGA	GGGCTATACA	TGGTAGCCAG	3300
	TTGAATTTAT	GGAATCTACC	AACTGTTTAG	GGCCCTGATT	TGCTGGGCAG	TTTTTCTGTA	3360
35	TTTTATAAGT	ATCTTCATGT	ATCCCTGTTA	CTGATAGGGA	TACATGTCTT	AGAAAATTTCA	3420
	CTATTGGCTG	GGAGTGGTGG	CTCATGCCGT	TAATCCAGC	ACTTGGAGAG	GCTGAGGTTG	3480
	CGCCACTACA	CTCCAGCCTG	GGTGACAGAG	TGAGATCTGC	CTC		

Seq ID NO: 555 Protein sequence
Protein Accession #: NP_003174.2

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45	QSTHVELLL	TPSALKRHF	LYLTSSTERF	SONFKVVVD	GKNESEYAK	WQDFPTGHVV	120
	GEPDSRVLAH	IRDDVIRI	NTDGAENIE	PLWRPVNDTK	DKRMLVYKSE	DIKNVRLQS	180
	PKVCGYLKVD	NEELPLKGLV	DREPPPEELVH	RVKRRADPDF	MKNCTCKLLV	ADHRFPYRIM	240
	RGEESTTNY	LIELIDRVDD	IYRNTSWDNA	GFKGYGQIE	QIRILKSPQE	VKPGKEHYNM	300
	AKSYFNEEKD	ANDVIMLEQ	PSFDIAEEAS	KVCLAHLEPT	QDFDMGTGLL	AYVGSPPRNS	360
50	HGGVCPKAYY	SPVGKKNYL	NSGLTSTKNY	GKTIILTKEAD	LVTTHLELHN	FGAEHDPDGL	420
	AECAPNEDQG	PGYVMYPYIAV	SGDHENNMKF	SNCSKQSIYK	TIESKAQECF	QERSNKVCGN	480
	SRVDEGEBCD	PGIMVLNNDT	CNSDCTLKE	GVQCSDRNSP	CKKNCQFETA	QKKCQBAINA	540
	TCKGVSVCYTG	NSSECPPPGN	AENDTVCLDL	GKCKDQKCIPI	FCEREQQLS	CACNETDNCS	600
	KVCCRDLSGR	CPYVYDAQK	NPLFRKGKPC	TVGFCDMNGK	CEKRVQDVIE	RFNDFIDQLS	660
55	INTFGKFLAD	NIVGSVLVFS	LIFWIPFSIL	VHCVDKLLDK	QYESLSLFHP	SNVEMLSSMD	720
	SASVRIIKPP	PAPQTPGRLO	PAPVIPSAPA	APKLDHQRM	TIQEDPSTDS	HMEDGFEKED	780
	PPFNSTAAK	SFEDLTDPHV	ARSEKAASPK	LQRQNRVNSK	ETEC		

Seq ID NO: 556 DNA sequence
Nucleic Acid Accession #: NM_021832.1
Coding sequence: 164..2248

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	GAAAGGCTGCC	CAGAGAGGTG	GAGTCGGTAG	CGGGGCGGGG	AACATGAGGC	AGTCTCTCCT	180
	ATTCTGAGCC	AGCGTGGTTC	CTTTCGTGCT	GCGCCGCGGA	CCTCCGGATG	ACCCGGGCTT	240
	CGGCCCCAC	CAGAGACTCG	AGAAAGCTTGA	TTCTTTGCTC	TCAGACTACG	ATATTCTCTC	300
70	TTTATCTAAT	ATCCAGCAGC	ATTCGGTAAG	AAAAAGAGAT	CTACAGACTT	CAACACATGT	360
	AGAAACACTA	CTAATTTTTT	CAGCTTTGAA	AAGGCATTTT	AAATTATACC	TGACATCAAG	420
	TACTGAACGT	TTTTTACAAA	ATTTCAAGGT	CGTGGTGGTG	GATGGTAAAA	ACGAAAGCGA	480
	GTACACTGTA	AAATGGCAGG	ACTTCTTCAC	TGGACACGTG	GTTGGTGAGC	CTGACTCTAG	540
	GGTTCTAGCC	CACATAAGAG	ATGATGATGT	TATAATCAGA	ATCAACACAG	ATGGGGCCGA	600
75	ATATAACATA	GAGCCACTTT	GGAGATTGTT	TAATGATACC	AAAGACAAAA	GAATGTTAGT	660
	TTATAAATCT	GAAGATATCA	AGAATGTTTC	ACGTTTGACG	TCTCCAAAAG	TGTGTGGTTA	720
	TTTAAAGAGT	GATAATGAAG	AGTTGCTCCC	AAAAGGGTTA	GTAGACAGAG	AACCACTGTA	780
	AGAGCTTGTT	CATCGAGTGA	AAAGAAGAGC	TGACCCAGAT	CCCATGAAGA	ACACGTGTAA	840
	ATTATTGGGT	GATGAGTATG	ATCGCTTCTA	CAGATACATG	GGCAGAGGGG	AAGAGAGTAC	900
80	AACACAAAT	TACTTAATAG	AGCTAATTGA	CAGAGTTGAT	GACATCTATC	GGAACTCTTC	960
	ATGGGATAAT	GCAGGTTTTA	AAGGCTATGG	AATACAGATA	GAGCAGATTG	GCATTCTCAA	1020
	GTCTCCACAA	GAGGTAAAC	CTGGTGAAAA	GCACTACAAC	ATGGCAAAAA	GTTACCCAAA	1080
	TGAAGAAAAG	GATGCTTGGG	ATGTGAAGAT	GTGTCTAGAG	CAATTTAGCT	TTGATATAGC	1140
85	TGAGGAAGCA	TCTAAAGTTT	CTTGGGCA	CCTTTTCA	TACCAAGATT	TTGATATGGG	1200
	AACCTTTGGA	TTAGCTTATG	TTGGCTCTCC	CAGAGCAAA	AGCCATGGAG	GTGTTTGTCC	1260
	AAAGGCTTAT	TATAGCCAG	TTGGGAAGAA	AAATATCTAT	TTGAATAGTG	GTTTGACGAG	1320
	CACAAAGAA	TATGGTAAAA	CCATCCTTAC	AAAGGAAGCT	GACCTGGTTA	CAACTCATGA	1380
	ATTGGGACAT	AATTTTGGAG	CAGAACATGA	TCCGATGGT	CTAGCAGAA	GTGCCCCGAA	1440

5 TGAGGACCAAG GGAGGGAAAT ATGTCAATGTA TCCCATAGCT GTGAGTGGCG ATCACAGAGAA 1500
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 CCAGGAGGTGT TTTCAAGAAC GCAGCAATAA AGTTTGTGGG AACTCGAGGG TGGATGAAGG 1620
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 CACGTGTAAG GAAGGTGTCC AGTGCAAGTGA CAGGAACAGT CCTTGTCTGA AAAACTGTCA 1740
 GTTTGAGACT GCCCAGAAGA AGTGCCAGGA GCGGATTAAT GCTACTTGCA AAGGCGGTGC 1800
 CTAAGTCACA GGTAAATAGCA GTGAGTGCCC GCCTCCAGGA AATGCTGAAG ATGACACTGT 1860
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 35 3421 GCTGAGGTTG CGCCACTACA CTCAGCCTG GGTGACAGAG TGAGATCTGC CTC

Seq ID NO: 557 Protein sequence
 Protein Accession #: NP_068604.1

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 GEPDSRVLAH IRDDVIRI NTDGAENIE PLWRFVNDK DKRMLVYKSE DIKNVSRLOS 180
 45 PKVGYLKVND NEELLPKGLV DREFFELVH RVKRRADPDF MKNTCKLLV ADHRFYRYMG 240
 RGEESTTNY LIELIDRVDD IYRNTSWDNA GFKGVGQIE QIRILKSPQE VKPGEKHYNM 300
 AKSYPNEEKD AWDVKMLLEQ FSPDIABEAS KVCLAHLFY QDFDMGTLEL AYVGSPRANS 360
 HGVCPKAYT SPVGKKNLYL NSGLTSTKNY GKTLTKEAD LVTTHELGHN FGAEDHPDGL 420
 AECAPNEDQG GKYVMPIAV SGGHNNKMF SNCSKQSIYK TIESKAQECF QERSNKVCGN 480
 50 SRVDEGEEDC PGIMYLNNDT CCNSDCTLKE GVQCSDRNSP CCKNCQFETA QKKCQEAINA 540
 TCKGVSYCTG NSSECPPPGN AEDDTVCLDL GKCKDGKICP FCEREQQLS CACNETDNSC 600
 KVCCRDLSGR CVPYVDAEQK NPLRLKGP KC VRVCDMNGK CEKRVQDVIE RFNDFIDQLS 660
 INTFGKPLAD NIVGSVLVFS LIFWIPFSIL VHCV

Seq ID NO: 558 DNA sequence
 Nucleic Acid Accession #: NM_004994.1
 Coding sequence: 20..2143

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 65 CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCCTGCGC TGCTGCTTCT 240
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5
10
15

Seq ID NO: 559 Protein sequence
Protein Accession #: NP_004985.1

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RFSEGRGSRP QGFILADKW PALPRKLDV FEEPLSKLF FFSGRQVWVY TGASVLGPRR 600
LDKLLGLADV AQVTGALRSV RGKMLLFSGR RLWRFDVKAQ MVDPRSASEV DRMFPGVPLD 660
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Seq ID NO: 560 DNA sequence
Nucleic Acid Accession #: NM_000213.1
Coding sequence: 127..5385

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	GGCGGGAAGT	CCCAGGTCTC	CTACCGCACA	CAGGATGGCA	CCGCGCAGGG	CAACCGGGAC	3240
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20	GGCAGCCACA	GGCCCCAGCG	CTCCGATGAC	ACTGAGCACC	TGGTGAATGG	CCGGATGGAC	4260
	TTTGCTTCC	CGGGCCAGCA	CACCTCCCTG	CACAGGATGA	CCACGACCAG	TGCTGCTGCC	4320
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	ACACGGGACT	ACAACCTCACT	GACCCGCTCA	GAACACTCAC	ACTCGACCAC	ACTGCCGAGG	4440
25	GACTACTCCA	CCCTCACCTC	CGTCTCCTCC	CACGACTCTC	GCCTGACTGC	TGGTGTGCCC	4500
	GACACGCCCA	CCCGCCTGGT	GTTCTCTGCC	CTGGGGCCCA	CATCTCTCAG	AGTGAGCTGG	4560
	CAGGAGCCGC	GGTGGCAGCG	GGCTACAGTG	TGGAGTACCA	GCTGCTGAAC	GCTGCTGAAC	4620
	GGCGGTGAGC	TGCATCGGCT	CAACATCCCC	AACCTCGCCC	AGACCTCGGT	GGTGTGGAA	4680
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40	GGAAACCTTA	GCACCCACAT	GGACCAACAG	TTCTTCCAAA	CTTGACCGCA	CCCTGCCCCA	5400
	CCCCCGCCAT	GTCCCACTAG	CGGTCTCTCC	GACTCTCTCT	CCGGAGCCTC	CTCAGCTACT	5460
	CCATCTTGG	ACCCCTGGGG	GCCCAAGCCA	CCCGCATGCA	CAGAGCAGGG	GCTAGGTGTG	5520
	TCCTGGGAGG	CATGAAGGGG	GCAAGGTCCG	TCCTCTGTGG	GCCCAAACTT	ATTTGTAAAC	5580
45	AAAGAGCTGG	GAGCAGCACA	AGGACCCAGC	CTTTGTTCTG	CATTATATAA	ATGGTTTTCG	5640
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Seq ID NO: 561 Protein sequence
Protein Accession #: NP_000204.1

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55	QTAVCTRDIG	WRPDSTHLV	FSSTESAFHYE	ADGANVLAGI	MSRNDERCHL	DTTGTYYTQYR	300
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	BAFNRIKSNL	DIRALDSPRG	LRTEVTSKMF	QKTRTGSFHI	RRGEVGIYQV	QLRALEHVDG	420
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	CSBGSWGQTC	NCSTGSLSDI	QPCLEGEDEK	PCSGRGECQC	GHCVCYGEGR	YEGQFCEYDN	540
60	FQCPRTSGFL	CNDRGRCSMG	QCVCPEGWTC	PSCDCPLSNA	TCIDSNGGIC	NGRGHCECGR	600
	CHCHQQLSYT	DTICEINYSY	IHPGLCEDLR	SCVQCQAWGT	GEKKGRITCEE	CNFKVKMVDK	660
	LKRAEEVVVR	CSFRDEDDDC	TVSYTMEGDG	APGPNSTVLV	HKKDCPPGGS	FWWLIFLLLL	720
	LLPLALLLLL	LCWKYCACCK	ACLALLPCCN	RGHMVGPKED	HYMLRENLMA	SDHLDTPLMR	780
65	SGNLKGRDVG	RWKVTNNMQR	PGFATHAASI	NPTLVVPYGL	SLRLARLCTE	NLLKPDTRC	840
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	LTEKQVEQRA	PHDLKVAPGY	YTLTADQDAR	GMVEFQEGVE	LVDVRVPLFI	RPEDDDEKQL	960
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70	VQLSNPKFGA	HLGQPHSTTI	IIRDPDELDR	SFTSQMLSSQ	PPPHGDLGAP	QNPNAKAAGS	1140
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	AQGEPPYSSL	VSCRTHQEVF	SEPGRLAFNV	VSSVTYQLSW	AEPAETNGEI	TAYEVCYGLV	1260
	NDDNRPPIGPM	KKVLVDNPKN	RMLLIENLRE	SQPYRYTVKA	RNGAGWGPER	EAIINLATQP	1320
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75	PPGSTNSLHR	MTTTSAAAYG	THLSPHVPHR	VLSTSTSLTR	DYNSLTRSEH	SHSTTLPRDY	1440
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	ELHRLNIPNP	AQTSVVVEDL	LPNHSYVFRV	RAQSQEWNRG	EREGVITIES	QVHPQSPLCP	1560
	LPGSAFTLST	PSAFGLVFT	ALSPDSLQLS	WERPRRPNGD	IVGYLVTCM	AQGGGPATAP	1620
	RVDGDSFESR	LTVPLGSENV	PKYFKVQART	TEGFGPEREG	IITIESQDGG	PPFQLGSRAG	1680
80	LFQHPLOQSEY	SSITTTHTSA	TEPFLVDGPT	LGAQHLEARG	SLTRHVTQEP	VSRTLTTSST	1740
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Seq ID NO: 562 DNA sequence
Nucleic Acid Accession #: NM_013332.1
Coding sequence: 1..63

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25 Seq ID NO: 563 Protein sequence
 Protein Accession #: NP_037464.1

30 1 11 21 31 41 51
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 RSM

35 Seq ID NO: 564 DNA sequence
 Nucleic Acid Accession #: NM_023915.1
 Coding sequence: 250..1326

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65 Seq ID NO: 565 Protein sequence
 Protein Accession #: NP_076404

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 NQOPTEDNIH DCSKLKSPLG VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
 ISQSSRRKRKH NQIRVVVVAV FFTCFPLPYHL CRIPFTFSLH DRLLDESAQK ILYYCKEITL 300
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CTGATCATTG TCCTGGGTGT GATCCTAACC AAAGACAACT GCGCCCCCTGA AGAGGTTATC 660
TGGGAAGCGT TGAAGTGTAT GGGGGTGTAT GTTGGGAAGG AGCACATGTT CTACGGGGAG 720
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Protein Accession #: NP_005356.1

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LGLSCDSMLG DGHSMFKAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKEHMFYGE 240
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Seq ID NO: 568 DNA sequence
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Seq ID NO: 569 Protein sequence
Protein Accession #: NP_055215

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SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPPVVS CYNASDHVYK GCFDGNVTLT 180
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 Protein Accession #: NP_005320.1

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Seq ID NO: 572 DNA sequence
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Seq ID NO: 573 Protein sequence:
Protein Accession #: Eos sequence

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25	PVSVAEFTYT	TSVFGDDNKA	LSKSEIIYGN	ETELQIPSPN	EMVYPSESTV	MPNMYDNVKN	1080
	LNASLOETSV	SISSTKGMFP	GLAHTTTKV	FDHEISQVPE	NNFSVQPTH	VSQASGDTSL	1140
	KPVLANSSEP	ASDDPASSEM	LSPSTQLLEY	ETSASFSTEV	LQPSFQASD	VDTLTKTVLP	1200
	AVPSDPILVE	TPKVDKISST	MLHLIVSNSA	SSENMLHSTS	VPVFDVSPTS	HMHSASLQGL	1260
	TISYASEKYE	PVLLKSESSH	QVPSLYSND	ELFQTANLEI	NQAHPPKGRH	VFATPVLSID	1320
30	EPLNTLNLKL	HSSEKDLTST	KSSVTGKVFA	GIPTVASDTP	VSTDHSPVPIG	NGHVAITAVS	1380
	PHRDGVSST	KLLFPSSKATP	ELSHSAKSDA	GLVGGGDEGD	TDDGDDDDDD	DRGSDGLSIH	1440
	KCMSCSYRE	SQEKVMNDSD	THENSLMDQN	NPISYLSSEN	SEEDNRVTSV	SSDSQTMGDR	1500
	SPGKSPSANG	LSQKHNDCKE	ENDIQTGSAL	LPLSPESKAW	AVLTSDEESG	SGQQTSDSLN	1560
	ENETSTDPSF	ADTNEKDADG	ILAAAGDSEIT	PGFPQSPITS	VTSENSEVFH	VSEAEASNS	1620
35	HESRIGLAEG	LVLSKAGKAP	LVIVSALTPI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	1680
	VISTPPTPIF	PISDDVGAIP	IKHFPKHVAD	LHASSGPTTE	FETLKEFYQE	VQSCVTDLGI	1740
	TADSNHPND	KHNRYINIV	ADHRSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	1800
	QGPKLSTAED	FWRMIWEHNV	EVIVMITNLV	EKGRRKGDQY	WPADGSEEVG	NFLVTQKSVQ	1860
	VLAYTYVRNF	TLRNTKIKKG	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFFVRKAA	1920
40	AKRHAVGPVV	VHCSAGVGR	GTIYVLDLML	QQIQHEGTVN	IFGFLKHIRS	QRNYLVQTEE	1980
	QYVPIHDTLV	EALSLKETEV	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQLL	SQSNIIQSDY	2040
	SAALKQCNRE	KNRTSSIPV	ESRSRVGISSL	SGEGTDYINA	SYIMGYQSN	EFIIITQHPLL	2100
	HTIKDFWRMI	WDNNAQLVVM	IPDQGNMAED	EFVYWPKNDE	PINCSEFKVT	LMAEHKKCLS	2160
	NEEKLIQDQF	ILEATQDDYV	LEVRHFQCPK	WPNPDSPISK	TFELISVIKE	EAANRDGPMI	2220
45	VHDEHGGVTA	GTFCALTTL	HQLEKENSVD	VYQVAKMINL	MRPGVFADIE	QYQFLYKVIL	2280
	SLVSTRQEN	PSTSLDSNGA	ALPDGNIAES	LESIV			

Seq ID NO: 574 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-4518

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	CGGCGAGGGG	CCGCGAGACG	CTCGGAAATG	CGAATCTCAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCTCT	GCTTTGCGCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTGGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCTATCA	ATATTGATGA	AGATCTTACA	360
60	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	TTCATTAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTCAAGCGAG	GAGTTTCAGA	AATGGTGTTT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCACTCTG	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTITTTGAGGA	AGCAGTCAAA	660
65	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTITTTGGGA	GCAGGCTGCT	780
	TTAGATCCAT	TCTACTGTGT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTAC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTCTCTAC	AATGCAACAA	960
70	TCTGGTTATG	TCTATGCTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTT	CTCATACTCT	GGAAAGGAAG	AGATTCTATG	AGCAGTTTGT	1080
	AGTTTCAGAAC	CAGAAAATGT	TCAAGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTAC	1140
	TGGGAAAGAG	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGACGT	TTTGTACACC	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
75	GGTGCTATTC	TCAATAATTT	GCTACCCAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACGT	AAGAAATAAT	CAAGGAGGAG	1440
	GAGAGGGGAA	AAGACATTGA	AGAAAGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAATCA	GAAAAAGGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TGCGATAGGG	1560
80	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACAA	GAGGAAGTGA	ATTCCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAAGTCA	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCCTT	GACTTCTCAG	ACTGTGACTG	AACCTGCCAC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACGT	TTCTTAGATC	TCCACATATG	1800
	AACTTGTCGG	GAGCTCGAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAAATA	TGAGGAGGAG	1860
	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
85	GCAACTTCTG	CTATCCCAAT	CATCTCTGAG	AACATATCCC	AAGGTATAT	ATTTCTCTCC	1980
	GAAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCCG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCAAGAGAA	TCAGTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100

	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTAATTA	CACTGAGATA	CGTGTGATG	AATCTGAGAA	GACAAACCAAG	2220
	TCCTTTTCTG	CAGGCCCACT	GATGTACACG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
5	CATTATTCTA	CCTTTGCCCT	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTGTGT	CTCCACGGCT	AACGTGGTAT	ACTCGCAGAC	AACCCAAACCG	2400
	GTATACAATG	CAGAGGCCAG	TAATAGTAGC	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	2460
	TTGGAATCCG	AGAAGAAGGC	AGTTATACCC	CTTGTGATCG	TGTGAGCCCT	GACTTTTATC	2520
	TGCTAGTGG	TTCTTGTGGG	TATTCTCATC	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	2580
10	TTTTACTTAG	AGGACAGTAC	ATCCCTAGTA	GTTATATCCA	CACCTCCAAAC	ACCTATCTTT	2640
	CCAATTTTCA	ATGATGTGGG	AGCAATTTCA	ATAAAGCACT	TTCCAAAGCA	TGTTGCAGAT	2700
	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	TTTGAGACAC	TGAAAGAGTT	TTACCAGGAA	2760
	GTGCAGAGCT	GTACTGTTGA	CTTAGGTATT	ACAGCAGACA	GCTCCAAACCA	CCCAGACAAC	2820
	AAGCACAAGA	ATCGATACAT	AAATATCGTT	GCCTATGATC	ATAGCAGGGT	TAAGTAGCA	2880
	CAGCTTGTGT	AAAAGGATGG	CAAACTGACT	GATTATATCA	ATGCCAAITTA	TGTTGATGGC	2940
15	TACAAACAGC	CAAAAGCTTA	TATTGCTGCC	CAAGGCCCAAC	TGAAATCCAC	AGCTGAAGAT	3000
	TTCTGGAGAA	TGATATGGGA	ACATAATGTG	GAAGTTATTG	TCATGATAAC	AAACCTCGTG	3060
	GAGAAAGGAA	GGAGAAATG	TGATCAGTAC	TGGCCTGCCG	ATGGGAGTGA	GGAGTACGGG	3120
	AACCTTCTGG	TCACTCAGAA	GAGTGTGCAA	GTGCTTGCCCT	ATTATACTGT	GAGGAATTTT	3180
20	ACTCTAAGAA	ACACAAAGAT	AAAAAAGGCG	TCCCAGAAAG	GAAGACCCAG	TGGACGTTGT	3240
	GTCACACAGT	ATCACTACAC	GCAGTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
	GTGCTGACCT	TGCTGGAGAA	GGCAGCCTAT	GCCAAGCGCC	ATGCAGTGGG	GCCTGTTGTC	3360
	GTCCACTGCA	GTGCTGGAGT	TGGAAGAAC	GGCACATATA	TTGTGCTAGA	CAGTATGTTG	3420
	CAGCAGATTC	AACACGAAGG	AACGTGCAAC	ATATTTGGCT	TCTTAAACCA	CATCCGTTCA	3480
25	CAAGAAGATT	ATTGTGTACA	AACGTAGGAG	CAATATGTCT	TCATTCTATG	TACACTGGTT	3540
	GAGGCCATAC	TTAGTAAGAA	AACGTAGGAG	CTGGACAGTC	ATATTCTATG	CTATGTTAAT	3600
	GCATCTCTCA	TTCTCTGACC	ACGAGGCAAA	ACAAAGCTAG	AGAAACAAAT	CCAGCTCCTG	3660
	AGCCAGTCAA	ATATACAGCA	GAGTGACTAT	TCTGCAGCCC	TAAAGCAATG	CAACAGGGAA	3720
	AAGAATCGAA	CTTCTCTAT	CATCCCTGTG	GAAGATCAA	GGGTTGGCAT	TTCATCCCTG	3780
30	AGTGGAGGAG	GCACAGACTA	CATCAATGCC	TCCTATATCA	TGGGCTATTA	CCAGAGCAAT	3840
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	TGGGACCAT	ATGCCCAACT	GGTGGTTATG	ATTCTCTGATG	GCCAAACAT	GGCAGAGAT	3960
	GAATTTGTTT	ACTGGCCAAA	TAAAGATGAG	CCTATAAATT	GTGAGAGCTT	TAAGGTCACT	4020
	CTTATGGCTG	AAGAACACAA	ATGCTCTATC	AATGAGGAAA	AACCTATAAT	TCAGGACTTT	4080
35	ATCTTAGAAG	CTACACAGGA	TGATTATGTA	CTTGAAGTGA	GGCAGCTTCA	GTGCTCTAAA	4140
	TGGCCAAATC	CAGATAGCCC	CATTAGTAAA	ACTTTTGAAC	TTATAAGTGT	TATAAAGAAA	4200
	GAAGCTGCCA	ATAGGGATGG	GGCTATGATT	GTTCTATGATG	AGCATGGAGG	AGTGACGGCA	4260
	GGAACTTTCT	GTGCTCTGAC	AACCCCTATG	CACCAACTAG	AAAAAGAAAA	TTCCGTGGAT	4320
	GTTTACCAGG	TAGCCAAAGT	GATCAATCTG	ATGAGGCCAG	GAGTCTTTGC	TGACATTGAG	4380
40	CAGTATCAGT	TTCTCTACAA	AGTGATCCTC	AGCCTTGTGA	GCACAAGGCA	GGAGAGAAAT	4440
	CCATCCACCT	CTCTGGACAG	TAATGGTGCA	GCATTCGCTG	ATGGAATAT	AGCTGAGAGC	4500
	TTAGAGTCTT	TAGTTTAAAC	CAGAAAGGGG	TGGGGGGACT	CACATCTGAG	CATTGTTTTT	4560
	CTCTTCTCAA	AATTAGGCAG	GAAATCAGT	CTAGTCTGT	TATCTGTTGA	TTTCCCATCA	4620
	CCTGACAGTA	ACTTTCATGA	CATAGGATTC	TGCCGCCAAA	TTTATATCAT	TAACAATGAT	4680
45	TGCTTTTTTG	CAAGACTTGT	AATTTACTTA	TTATGTTTGA	ACTAAAAATGA	TTGAATTTTA	4740
	CAGTATTTCT	CAAGAAATGAA	TTGTGGTATT	TTTTTCTGTA	TTGATTTTAA	CAGAAATTTT	4800
	CAATTTATAG	AGGTTAGGAA	TTCCAAACTA	CAGAAATGTT	TTGTTTTTAG	TGTCAAATTT	4860
	TTAGCTGTAT	TTGTAGCAAT	TATCAGGTTT	GCTAGAAATA	TAACTTTTAA	TACAGTAGCC	4920
	TGTAATAATA	ACACTCTTCC	ATATGATATT	CAACATTTTA	CAACTGCAGT	ATTCACTTAA	4980
50	AGTAGAAATA	ATCTGTTACT	TATTGTAAT	ACTGCCCTAG	TGCTCTCATG	GACCAAAATTT	5040
	ATATTTATAT	TTGTAGATTT	TTATATTTTA	CTACTGAGTC	AAGTTTTCTA	GTTCTGTGTA	5100
	ATTGTTTAGT	TTAATACAGT	AGTTCATTAG	CTGGTCTTAC	TCTACCAAGT	TTCTGCATTT	5160
	GTATTTGTTT	ACCTAAGTCA	TTAATTTTGT	TTGAGCATGT	AATTTTAACT	TTTGTGGAAA	5220
	ATAGAAATAC	CTTCAATTTT	AAGAAGTTT	TTATGAGAAAT	AACACCTTAC	CAACATTGTT	5280
55	TCAAATGGTT	TTTATCCAA	GAATTCGAAA	AATAAATATA	AATATTGCCA	TTAAAAAAA	5340
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Seq ID NO: 575 Protein sequence:
Protein Accession #: Eos sequence

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	QSPINIDEDL	TQNVNVLKKL	KFGGWDKTSL	ENTPIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
65	FKASKITPHW	GKCNMSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSFEBAV	KGKGLRLALS	180
	ILFEVGTEN	LDFAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDMIVFK	DTVISISESL	AVFCEVLTMQ	QSGVVMMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIHFAV	CSSEPEENVQA	DPENYTSLLV	TWERPRVVD	TMIEKFAVLY	QQLDGEDQTK	360
70	HEFLTDGQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLFP	420
	LIGTEBIIKE	EZEQKDIEEG	AIVNPGRDSA	TNQIRKKEBP	ISTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GRGDVPNTSL	NSTSPVTKL	ATEKDISLTS	QVTLELPHPT	VEGTSASLND	540
	GSKTVLRSFH	MNLGGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPEITITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NWVFPSSDTI	660
75	TAQPDVGSGR	ESPLQNTYTE	IRVDESEKTT	KSFSAQPVMS	QGPSVTDLEM	PHYSTFAYFP	720
	TEVTPHAFPT	SSRQDLVST	VNVVYSQTTQ	PVYNAEASNS	SHERIGLAE	GLESEKKAVI	780
	PLVIVSALTF	ICLVVLVGLL	IYWRKCFQTA	HFYLEDSTSP	RVISTPPTPI	PPISDDVGA	840
	PIKHFFKHVA	DLHASSGFTE	EPETLKEFYQ	EVQSCCTVDL	ITADSSNHDP	NKHKNNRYNI	900
	VAYDHSRVLK	AQLAEKDGKL	TDYINANYVD	GYNRPKAYIA	AQGPLKSTAE	DFWRMIWEHN	960
80	VEVIVMITNL	VEGRRKCDQ	YFADGSESEY	GNFLVTQKSV	QVLAYYTVRN	FTLRNTKIKK	1020
	GSQKGRPSGR	VVTQHYHTQW	PDMGVPEYSL	PVLTFVRKAA	YAKRHAVGPV	VVHCSAGVGR	1080
	TGTIYVLDSM	LQIQIHEGTV	NIFGFLKHIR	SQRNLYVQTE	EQYVFIHDTL	VEAILSKETE	1140
	VLDSDIHAYV	NALLIPGPAG	KTKLEKQFQL	LSQSNIQQSD	YSAALKQCNR	EKNRTSSII	1200
	VERSRVGISS	LSGEGTDYIN	ASYIMGYYS	NEFIITQHPL	LHTIKDFWRM	IWDHNAQLV	1260
	MIPDQGNMAE	DEPFVWPKND	EPINCESPKV	TLMAEHEKCL	SNEEKLIQD	FILEATQDDY	1320
85	VLEVRFQFQP	KWPNFDPIS	KTFELISVIK	EAAANRDGPM	IVHDEHGGVT	AGTFCALTTL	1380
	MHQLKENSIV	DVYQVAKMIN	LMRPGVFADI	EQYQFLYKVI	LSLVSTRQER	NPSTSLDSNG	1440
	AALPDGNIAE	SLESIV					

Seq ID NO: 576 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 148-4494

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10	CGGCGAGGGG	CCGCAGACCG	TCTGGAAATG	CGAATCTCAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTGGCTG	GTCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CACTGAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
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	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCACACT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCAGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
	GGAAAAAGGA	TCTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTG	720
20	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTAGTCT	GTTTTGGGAA	GCAGGCTGCT	780
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	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTCTTAC	AATGCAACAA	960
	TCTGTTATG	TCAATCTGAT	GGAATCTTAA	CAAAACAAAT	TTGAGAGCA	ACAGTACAA	1020
25	TCTCTAGAAC	AGGTGTTTTT	CTCATACACT	GGAAAGGAAG	AGATTATGTA	AGCAGTTTGT	1080
	AGTTCAGAAC	CAGAAATAT	TGAGGCTGAC	CCAGAGAAAT	ATACCAAGCT	TCTTGTATCA	1140
	TGGGAAAGAC	CTCAGAGCTG	TTATGATACC	ATGATTGAGA	AGTTTGACGT	TTTGTACACG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGTG	CAGATGGCTA	TCAAGACTTG	1260
	GGTGCTATT	TCAATGATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
30	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
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	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAATACA	GGAAAAAGGA	ACCCAGGATT	TCTACCACAA	CACACTACAA	TCGCATAGGG	1560
35	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACCAA	GAGGAAGTGA	ATTCTCTGGA	1620
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	ACAGAAAAAG	ATATTTCCTT	GACTTCTCAG	ACTGTGACTG	AAGTGCACCC	TCACTAGTGT	1740
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	GAAGAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCAAGAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
45	AGCTTTCTCC	AGACTAATTA	CACCTGAGATA	CGTGTGATG	AATCTGAGAA	GACAACCAAG	2220
	TCCTTTTCTG	CAGGCCAGT	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCAA	2280
	CATTATTCTA	CTTTGCTCTA	TTCCCAACT	GAGGTAAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAAACG	2400
	GTATACAATG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	2460
50	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	2520
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	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAAACAC	TATCTTTCCA	2640
	ATTTGAGATG	ATGTCGAGC	AATTCCTAAT	AAGCACTTTC	CAAGCATGT	TGCAGATTTA	2700
	CATGCAAGTA	GTGGGTTTAC	TGAAGAAATT	GAGGAAGTGC	AGAGCTGTAC	TGTTGACTTA	2760
55	GGTATTACAG	CAGACAGCTC	CAACCAACCA	GACAACAAGC	ACAAGAAATC	ATACATAAAT	2820
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	CTGACTGATT	ATATCAATGC	CAATATGTT	GATGGCTACA	ACAGACCAAA	AGCTTATATT	2940
	GCTGCCCAAG	GCCTCACTGA	ATCCACAGCT	GAAGATTCTT	GGAGAATGAT	ATGGGAACAT	3000
	AATGTGGAAG	TTATTGTCAT	GATAACAAAC	CTCGTGGAGA	AAGGAAGGAG	AAAATGTGAT	3060
60	CAGTACTGGC	CTGCCGATGG	GAGTGAGGAG	TACGGGAACT	TTCTGTCTAC	TCAGAAGAGT	3120
	GTGCAAGTGC	TTGCCATTAT	TACTGTGAGG	AATTTTACTC	TAAGAAACAC	AAAAATAAAA	3180
	AAGGGCTCCC	AGAAAGGAA	ACCCAGTGGG	CGTGTGGTCA	CACAGTATCA	CTACACGAG	3240
	TGGCCTGACA	TGGAGTATCC	AGAGTACTCC	CTGCCAGTGC	TGACCTTTGT	GAGAAAGGCA	3300
	GCCTATGCCA	AGGCCATCTG	AGTGGGGCCT	GTGTGCTGTC	ACTGCACTGC	TGGAGTTGGA	3360
65	AGAACAGGCA	CATATATTGT	GCTAGACAGT	ATGTTGCAGC	AGATTCAACA	CGAAGGAACT	3420
	GTCACATAT	TTGGCTTCTT	AAAACACATC	CGTTCCACAA	GAAATATTAT	GGTACAAACT	3480
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	ATCCTCAGCC	TTGTGAGCAC	AAGGCAGGAA	GAGAATCCAT	CCACCTCTCT	GGACAGTAAT	4440
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	TACTTATTAT	GTTTGAACCTA	AAATGATTGA	ATTTTACAGT	ATTTCTAAGA	ATGGAATTGT	4740
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Seq ID NO: 577 Protein sequence:
 Protein Accession #: EOS sequence

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Seq ID NO: 578 DNA sequence
 Nucleic Acid Accession #: EOS sequence
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Seq ID NO: 579 Protein sequence:
 Protein Accession #: EOS sequence

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Seq ID NO: 580 DNA sequence
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Seq ID NO: 584 DNA sequence
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Seq ID NO: 585 Protein sequence
Protein Accession #: NP_005679.1

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Seq ID NO: 586 DNA sequence
 Nucleic Acid Accession #: NM_001327.1
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 Protein Accession #: Eos sequence

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Seq ID NO: 590 DNA sequence
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Seq ID NO: 591 Protein sequence
Protein Accession #: NP_005553.1

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	PEGCTQCFCY	GHSASCRSSA	EYSVHKITST	FHQDVGWKA	VQRNGSPAKL	QWSQRHQDVF	240
	SSAQRDLFVY	FVAPAKFLN	QOVSYGQSL	FDYRVDGRGR	HPSAHDVILE	GAGLRITAPL	300
85	MPLGKTLPCG	LTKTYTFRLN	EHPNNWSPQ	LSYFEYRRL	RNLTLALRIRA	TYGEYSTGYI	360
	DNVTLISARP	VSGAPAPWVE	QCICPVGYKG	QFQDQCASGY	KRDSARLPGF	GTICPCNCOG	420
	GGACDPDTGD	CYSGDENPDI	ECADCPIGFY	NDPHDPRSC	PCPCNHNFS	SVMPEETEVEV	480

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Seq ID NO: 593 Protein sequence
 Protein Accession #: AAD16433.1

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Seq ID NO: 594 DNA sequence
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Seq ID NO: 595 Protein sequence
Protein Accession #: NP_006171.1

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20	GGCTGGTTGT	GGGCTTCTGG	AGGGCCGCTT	TGCGCTGTCC	CACGTCCTGC	AAATGCAGTG	600
	CCTCTCGGAT	CTGGTGCGAG	GACCCCTTCT	CTGGCATCGT	GGCATTTCGG	AGATTGGAGC	660
	CTAACAGTGT	AGATCTCTAG	AACATCACCG	AAATTTTCAT	CGCAAAACCAG	AAAAGGTTAG	720
	AAATCATCAA	CGAAGATGAT	GTTGAAGCTT	ATGTGGGACT	GAGAAATCTG	ACAATTGTGG	780
	ATTCTGGATT	AAAAATTTGT	GCTCATAAAG	CATTTCTGAA	AAACAGCAAC	CTGCAGCACA	840
25	TCAATTTTAC	CGGAACAATA	CTGACGAGTT	TGTCTAGGAA	ACATTTCCTG	CACCTTGACT	900
	TGCTGAAGAT	GATCCTGGTG	GGCAATCCAT	TTACATGCTC	CTGTGACATT	ATGTGGATCA	960
	AGACTCTCCA	GATCTCTTGT	TCCAGTCCAG	ACACTCAGGA	TTTGTACTGC	CTGAATGAAA	1020
	GCAGCAAGAA	TATCCCCCTG	GCAAACTCTG	AGATACCCAA	TTTGTGTTTG	CCATCTGCAA	1080
	ATCTGGCGCG	ACCTAACCTC	ACTGTGGAGG	AAGGAAAGTC	TATCACATTA	TCCTGTAGTG	1140
30	TGGCAGGTGA	TCCGTTTCCT	AATATGTATT	GGGATGTTGG	TAACCTGGTT	TCCAAACATA	1200
	TGAATGAAAC	AAGCCACACA	CAGGGCTCCT	TAAGGATAAC	TAACATTTCG	TCCGATGACA	1260
	GTGGGAAGCA	GATCTCTTGT	GTGGCGGAAA	ATCTTGTAGG	AGAAGATCAA	GATTCTGTGA	1320
	ACCTCACTGT	GCATTTTGCA	CCAACTATCA	CATTTCTCGA	ATCTCCAAAC	TCAGACCACC	1380
	ACTGTGTCAT	TCCATTCACT	GTGAAAGGCA	ACCCCAAACC	AGCGCTTCAG	TGTTTCTATA	1440
35	ACGGGGCAAT	ATTGAATGAG	TCCAAATACA	TCTGTACTAA	AATACATGTT	ACCAATCACA	1500
	CGGAGTACCA	CGGCTGCCTC	CAGCTGGATA	ATCCCACTCA	CATGAACAAT	GGGGACTACA	1560
	CTCTAATAGC	CAGGAATGAG	TATGGGAAGG	ATGAGAAACA	GATTTCGTGG	CACCTTCATG	1620
	GCTGGCCTGG	AATTGACGAT	GGTGCAAAAC	CAAATATCCG	TGATGTAATT	TATGAAGATT	1680
	ATGGAATGCG	AGCGAATGAC	ATCGGGGACA	CCACGAAACG	AAGTAATGAA	ATCCCTTCCA	1740
40	CAGACGTAC	TGATAAAACC	GGTCGGGAAC	ATCTCTCGGT	CTATGCTGTG	TGGTGATTGG	1800
	CGTCTGTGGT	GGGATTTTGC	CTTTTGTGTA	TGCTGTTTCT	GCTTAAAGTTG	GCAAGACACT	1860
	CCAGATTGGC	CATGAATGAG	TTCTCATGGT	TTGGATTGAG	GAAAGTAAAA	TCAAGACAAG	1920
	GTGTTGGCCC	AGCCTCCGTT	ATCAGCAATG	ATGATGACTC	TGCCAGCCCA	CTCCATCACA	1980
	TCTCCAAATG	GAGTAACACT	CATCTTCTTT	CGGAAGGTGG	CCCAGATGCT	GTCATTATTG	2040
45	GAATGACCAA	GATCCCTGTC	ATTGAAAATC	CCCAGTACTT	TGGCATCACC	AACAGTCAGC	2100
	TCAGGACGAA	CACATTTGTT	CAGCACATCA	AGCGACATAA	CATTGTTCTG	AAAAGGGAGC	2160
	TAGGCGAAGG	AGCCTTTGGA	AAAGTGTTC	TAGCTGAATG	CTATAACCTC	TGCTCTGAGC	2220
	AGGACAGATG	CTTGTTGGCA	GTGAAGACCC	TGAAGGATGC	CAGTGACAAT	GCAAGCAAGG	2280
	ACTTCCACCG	TGAGGCCGAG	CTCCTGACCA	ACCTCCAGCA	TGAGCACATC	GTCAAGTTCT	2340
50	ATGGCGTCTG	CGTGGAGGGC	GACCCCTCTA	TCATGGTCTT	TGAGTACATG	AAGCATGGGG	2400
	ACCTCAACAA	GTTTCTCAGG	GCACACGGCC	CTGATGCCGT	GCTGATGGCT	GAGGGCAACC	2460
	CGCCACGGGA	ACTGACGCGA	TGCGAGATGC	TGCATATAGC	CCAGCAGATC	GCCGCGGGCA	2520
	TGCTTACCTG	GGCGTCCGAG	CACCTTCGTG	ACCGCGATTG	GGCCACCAAG	AACTGCTTGG	2580
	TCGGGGAGAA	TGTGCTGGTG	AAAATCGGGG	ACITTTGGAT	GTCCCGGGAC	GTGTACAGCA	2640
55	CTGACTACTA	CAGGGTCGGT	GGCCACACAA	TGCTGCCCAT	TCGCTGGATG	CCTCCAGAGA	2700
	GCATCATGTA	CAGGAAATTC	ACGACGAAAA	GCGACGCTCT	GAGCCTGGGG	GTGCTGTTGT	2760
	GGGAGATTTT	CACCTATGGC	AAACAGCCCT	GGTACCAGCT	GTCAAACAAT	GAGGTGATAG	2820
	AGTGTATCAT	TCAGGGCCGA	GTCTCTGAGC	GACCCCGCAC	GTGCCCCCAG	GAGGTGTATG	2880
	AGCTGATGCT	GGGGTCTGGG	CAGCGAGAGC	CCCAATGAG	GAAAGAACATC	AAGGGCATCC	2940
60	ATACCCCTCT	TCAGAACTTG	GCCAAAGGCAT	CTCCGGTCTA	CCTGACATTC	CTAGGCTAGG	3000
	GCCTTTTTC	CCAGACCGAT	CCTTCCCAAC	GTACTCTCTA	GACGGGCTGA	GAGGATGAAC	3060
	ATCTTTTAAC	TGCCGCTGGA	GGCCACCAAG	CTGCTCTCCT	TCACTCTGAC	AGTATTAAAC	3120
	TCAAAGACTC	CGAGAAGCTC	TGAGGGGAAG	CAGTGTGTAC	TTCTTCAATC	ATAGACACAG	3180
	TATTGACTCT	TTTTTGGCAT	TATCTCTTTC	TCTCTTTCCA	TCTCCCTTGG	TTGTTCTTTT	3240
65	TTCTTTTTTT	AAATTTTCTT	TTTCTTCTTT	TTTTTCTGCT	TCCCTGCTTC	ACGATTCTTA	3300
	CCCTTTCTTT	TGAATCAATC	TGGCTTCTGC	ATTACTATTA	ACTCTGCATA	GACAAAGGCC	3360
	TTAACAAACG	TAATTTGTTA	TATCAGCAGA	CACCTCAGTT	TGCCCAACCAC	AACTAACAT	3420
	GCCTTGTGTT	ATTCCTGCCT	TTGATGTGGA	TGAAAAAAG	GGAACACAAA	TATTTCACCT	3480
	AAACTTTGTC	ACTCTGCTGT	TACAGATATC	GAGAGTTTCT	ATGGATTAC	TTCTATTAT	3540
70	TTATTATTAT	TACTGTTCTT	ATTGTTTTTG	GATGGCTTAA	GCCTGTGTAT	AAAAAGAGAA	3600
	ACTTGTGTTT	AATCTGTGAA	GCCTTTATCT	ATGGGAGATT	AAAAACAGAG	AGAAAGAGAA	3660
	TTTATTATGA	ACCGCAATAT	GGGAGGAACA	AAGACAACCA	CTGGGATCAG	CTGGTGTGAG	3720
	TCCTTACTTA	GGAAATACCT	AGCAACTGTT	AGCTGGGAAG	AATGTATTGG	GCACCTTCCC	3780
	CTGAGGACCT	TTCTGAGGAG	TAAAAAGACT	ACTGGCCTCT	GTGCCATGGA	TGATTCTTTT	3840
75	CCCATACCA	GAAATGATAG	CGTGCAAGTAG	AGAGCAAAGA	TGGCTTCCGT	GAGACACAAG	3900
	ATGGCGCATA	GTGTGCTCGG	ACACAGTTTT	GTCTTCTGTG	GTTGTGATGA	TAGCACTGGT	3960
	TTGTTTCTCA	AGCGCTATCC	ACAGAACTTT	TGTCAACTTC	AGTTGAAAAG	AGGTGGATTG	4020
	ATGTCAGAG	CTCATTTCCG	GGTCAGGTGG	GAAAGCC			

Seq ID NO: 597 Protein sequence
 Protein Accession #: AAL67965.1

	1	11	21	31	41	51	
85	MSSWIRWHGP	AMARLWGFCE	LUVGFWRAAF	ACPTSCCKCSA	SRIWCSDPSP	GIVAFPRLEP	60
	NSVDPENITE	IFIANQKRLK	INEDDVVEAY	VGLRNLTIIV	SGLKFAVHKA	FLKNSNLQHI	120
	NPTRNKLTSL	SRKHFRHLDL	SELILVGNPP	TCSCDIMWIK	TLQEAQSSPD	TQDLYCLNES	180
	SKNIPLANLQ	INCGLPSSAN	LAAPNLTVEE	GKSIITLSCSV	AGDPVPMNMY	DVGNLVSKHM	240

NETSHTQGS L RITN1SSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
 WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360
 LIAKNEYGKD EKQISAHFMG WFGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLLLKLARHS KPGMKDPSWF GFGKVKSRQG 480
 VGPASVISND DDSASPLHHI SNGSNTFSSS EGGPDVAIIG MTKIPVIEHP QYFGITNSQL 540
 KPDTFVQH1K RHNIIVLKRRL GEGAFGKVFL AECYNLCPEQ DKILVAVKTL KDASDNARKD 600
 FHREAE1LTN LQHEHIVKFY GVCVEGDPLI MVFEYMKHGD LNKFLRAHGP DAVLMAEGNP 660
 PTELTQSQML HIAQIIAAGM VYLASQHFVH RDLATRNCLV GENLLVKIGD FGMSRDVYST 720
 DYYRVGGHTM LPIRWMPPE IMYRKFTTES DVHSLGVVLM EIFTYKQPW YQLSNNEVIE 780
 CITQGRVLQR PRTCPQEVYE LMLGCWQREP HMRKNIKGIH TLLQNLAKAS PVYLDILG

Seq ID NO: 598 DNA sequence
 Nucleic Acid Accession #: AB052906
 Coding sequence: 74..814

1 11 21 31 41 51
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 CTCTGGGTCC TTAATGGCAG CAGCCGCCGC TACCAAGATC CTCTGTGTGC TCCCGCTTCT 120
 GCTCCTGCTG TCCGCTAGGT CCCGGGCTGG GCGAGCCGAC CCTCACTCTC TTGTGCTATGA 180
 CATCACCGTC ATCCCTAAGT TCAGACCTGG ACCACGGTGG TGTGCGGTTC AAGGCCAGGT 240
 GGATGAAAAG ACTTTTCTTC ACTATGACTG TGGCAACAAG ACAGTCACAC CTGTCAGTCC 300
 CCTGGGGAAG AAACCTAAATG TCACAACGGC CTGGAAGCA CAGAACCAG TACTGAGAGA 360
 GGTGGTGGAC ATACTTACAG AGCAACTGCG TGACATTCAG CTGGAGAATT ACACACCCAA 420
 GGAACCCCTC ACCCTGCAGG CCAAGATGTC TTGTGAGCAG AAAGCTGAAG GACACAGCAG 480
 TGGATCTTGG CAGTTCAAGT TCGATGGGCA GATCTTCTCT CTCTTTGACT CAGAGAAGAG 540
 AATGTGGACA ACGGTTATC CTGAGGCCAG AAAGATGAAA GAAAAGTGGG AGAATGACAA 600
 GGTGTGGGCC ATGTCCTTCC ATTACTTCTC AATGGGAGAC TGTATAGGAT GGCTTGAGGA 660
 CTCTCTGATG GGCATGGACA GCACCCCTGA GCCAAGTGCA GGAGCACCAC TCCCATGTCT 720
 CTCAGGCACA ACCCAACTCA GGGCCACAGC CACCACCTC ATCCTTTGCT GCCTCTCTAT 780
 CATCCTCCCC TGCTTCATCC TCCCTGGCAT CTGAGGAGAG TCCCTTAGAG TGACAGGTTA 840
 AAGCTGATAC CAAAGGCTC CTGTGAGCAC GGTCTTGATC AAACCTCGCC TTCTGTCTGG 900
 CCAGCTGCCC ACGACCTACG GTGTATGTCC AGTGGCTCC AGCAGATCAT GATGACATCA 960
 TGGACCCCAAT AGCTCATTCA CTGCCTTGAT TCCTTTTGCC AACAATTTTA CCAGCAGTTA 1020
 TACCTAACAT ATTATGCAAT TTTCTCTTGG TGCTACCTGA TGAATTCCT GCACCTAAAG 1080
 TTTCTGGCTG CTTAAACAAGA TATATCATT TCTTTCTTCT CTTTTTGTGT GGAAATCAA 1140
 GTACTTCTTT GAATGATGAT CTCTTCTTGG CAAATGATAT TGTCAAGTAA ATAATCACGT 1200
 TAGACTTCAG ACCTCTGGGG ATTCTTTCOG TGTCTGAAA GAGAATTTT AAATTATTTA 1260
 ATAAGAAAAA ATTTATATTA ATGATTGTTT CCTTTAGTAA TTTATTGTTT TGTACTGATA 1320
 TTTAAATAAA GAGTCTATT TCCCAAAAAA AAAAAAAAAA AA

Seq ID NO: 599 Protein sequence
 Protein Accession #: BAB61048.1

1 11 21 31 41 51
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 MAAAAATKIL LCLPLLLLLS GWSRAGRADP HSLCYDITVI PKFRPGPRWC AVQGVDEKT 60
 FLHYDCGNKT VTPSPPLGKK LNVTTAWKAQ NPVLREVVDI LTELRLDIQL ENYTPKEPLT 120
 LQARMSCEQK AEGHSSGSWQ FSPDQIPLL FDSEKRMWTT VHPGARKMKE KWENDKVAM 180
 SFHYFSMGDC IGWLEDFLMG MDSTLEPSAG APLAMSSGTT QLRATATTLI LCCLLIILPC 240
 FILPGI

Seq ID NO: 600 DNA sequence
 Nucleic Acid Accession #: NM_001898.1
 Coding sequence: 57..482

1 11 21 31 41 51
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 GGCTCTCACC CTCCTCTCCT GCAGCTCCAG CTTTGTGCTC TGCCCTCTGAG GAGACCATGG 60
 CCCAGTATCT GAGTACCCTG CTGCTCCTGC TGGCCACCTC AGCTGTGGCC CTGGCCTGGA 120
 CCCCCAAGGA GGAGGATAGG ATAATCCCGG GTGGCATCTA TAACGCAGAC CTCAATGATG 180
 AGTGGGTACA GCGTGCCCTT CACTTCGCCA TCAGCGAGTA TAACAAGGCC ACCAAGATG 240
 ACTACTACAG ACGTCCGCTG CCGGTACTAA GAGCCAGGCA ACAGACCGTT GGGGGGGTGA 300
 ATTAATCTCT CGACGTAGAG GTGGGCCGCA CCATATGTAC CAAGTCCAGC CCCAACTTGG 360
 ACACCTGTGC CTCTCCATGA CAGCCAGAAC TGCAGAAGAA ACAGTTGTGC TCTTTCGAGA 420
 TCTACGAAGT TCCCTGGGAG AACAGAAGGT CCCTGGTGAA ATCCAGGTGT CAAGAATCCT 480
 AGGGATCTGT GCCAGGCCAT TCGCACCAGC CACCACCCAC TCCCACCCCC TGTAGTGCTC 540
 CCACCCCTGC ACTGGTGGCC CCCACCTGC GGGAGGCCCT CCCATGTGCC TGCGCCAAGA 600
 GACAGACAGA GAAGGCTGCA GGAGTCCTTT GTTGCTCAGC AGGGCGCTCT GCCTCCCTC 660
 CTCCTTCTT GCTTCTTAATA GCCCTGTGAC ATGGTACACA CCCCCCACC TCCTGCAATT 720
 AAACAGTAGC ATCGCC

Seq ID NO: 601 Protein sequence
 Protein Accession #: NP_001889.1

1 11 21 31 41 51
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 MAQYLSTLLL LLATLAVALA WSPKEEDRII FGGIYNADLN DEWVQRALHF AISEYNKATK 60
 DDYRRPLRV LRARQQTGG VNYFFDVEVG RTICTKSQPN LDTCAFHEQP ELQKKQLCSF 120
 EIEYVWENR RSLVSRQCE S

Seq ID NO: 602 DNA sequence
 Nucleic Acid Accession #: NM_003976.2
 Coding sequence: 299..961

1 11 21 31 41 51
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CTCTGAGCTT CTCTGAGCCT TGTTTGCTCA TCTGGAAAAA GGGGATTAAA CCATTTACCT 60
CATGGAGTTG TGAAGAATA GCTGCAAAGC ACCTAACACA TAGTAAGGTT CCCAGTGCAG 120
CTACTTCTGC TGGGTGAGT CTAGCTGTGT AGGCCCCCTG TTCCTCACCT GGAGAAACTG 180
GGGTGGCAGG CCGTCCCCC ACAAAAGATA ACTCATCTCT TAATTGCAA GCTGCCCTCA 240
CAGGAGGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCCTGGTGT TGATAGAGAT 300
GGAACTTGGA CTTGGAGGCC TCTCCACGCT GTCCCACTGC CCCTGGCCTA GGCGGCAGCC 360
TGCCCTGTGG CCCACCTGG CCGCTCTGGC TCTGCTGAGC AGCGTCGAG AGGCCTCCCT 420
GGGCTCCGCG CCCCCAGCC CTGCCCCCGG CGAAGGCCCG CCGCTGTGCC TGGCGTCCCC 480
CGCCGCGCAC CTGCGGGGG GACGCAOAGC CCGCTGGTGC AGTGGAAAGAG CCCGGCGGCC 540
GCGCGCGCAG CCTTCTGGG CCGCGCCCCC GCGCCTGCA CCCCCTCTG CTCTTCCCCG 600
CGGGGGCCG GGGCGCGGG CTGGGGGGCC GGGCAGCGC GCTCGGGCAG CGGGGGCGCG 660
GGGCTGCCG CTGCGCTCGC AGCTGGTGCC GGTGCGCGCG CTCGCGCTGG GCCACCGCTC 720
CGACGAGCTG GTGCGTTTCC GCTTCTGCAG CCGCTCCTGC CGCCGCGCGC GCTCTCCACA 780
CGACCTCAGC CTGGCCAGCC TACTGGGCGC CGGGGCCCTG CGACCGCCCC CGGGCTCCCG 840
GCCCGTCAGC CAGCCCTGCT GCCAGCCAC GCGCTACGAA GCGGTCTCCT TCATGGACGT 900
CAACAGCACC TGGAGAAGC TGGACCGCT CTCGCCACC GCCTGCGGCT GCCTGGGCTG 960
AGGGCTCGCT CCAGGGCTTT GCAGACTGGA CCCTTACCGG TGGCTCTTCC TGCTGGGAC 1020
CCTCCCGCAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCCT CAAAGCTGAG 1080
AGGCCCTTAC CCGTGGGTGA TGGATATCAT CCCGGAACAG GTGAAGGGAG AACTGACTAG 1140
CAGCCCCAGA GCCCTCACCC TGCGGATCCC AGCCTAAAAG ACACAGAGA CCTCAGCTAT 1200
GGAGCCCTC GGCCTGAGT CTACAGACT CTGGCACTGG CCAGGCTCG AACCTGGGAC 1260
CCCTCCTCTG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCCGCCAGG CCTGTAGGG 1320
ACAGCATTTG AAGGACACAT ATTGCAGTTG CTTGGTTGAA AGTGCTCTGT CTGGAACCTG 1380
CCTGTACTCA CTCATGGGAG CTGGCCCC

Seq ID NO: 603 Protein sequence
Protein Accession #: NP_003967.1

1 11 21 31 41 51
MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
PAGHLPGGRT ARWCSSRRARR PPPQPSRPAP PPPAPPSALP RGGRARAGG PGSRARAAGA 120
RGCRRLRSQVL PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 604 DNA sequence
Nucleic Acid Accession #: NM_057091.1
Coding sequence: 783..1445

1 11 21 31 41 51
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GGACCCCCAA ATCTGCACGT ACCAGCAGTC AGCCGCCCCA CGCAGGGACC GGCTTACCCC 120
TCGCTCCCCG CCTCACTCA CTTTCTCCCG CCTCGGCCG GGCCTCCAGC CTCTCTACTT 180
CGCGTGTCTA CAAACTCAAC TCCCGGTTTC CGTGCTCTTC CACCGCTCGA GTTCTCTACT 240
CTCCATATCC GAGGGGCCCC TCCAGCATC TACCCCTTC CCAACCTCGG GGGACCTAGC 300
CAAGCTAGGG GGGACTGGAT CCGACGGGTG GAGCAGCCAG GTGAGCCCGC AAAGGTGGGG 360
CGGGGCAAGG GCGCTCCAG CCCCACCCCG GGATCTGGTG ACGCTGGGGC TGGAAATTGA 420
CACCGGACGG CTGCGGCGGC GGGCAGGAGG CTGCTGAGGG ATGGAGTTGG GCCCGGCCCC 480
GACACAAGGC CCGGGGGCTC CGCCAGCAGC AGGTCCCTCG GGCCTCCAGC CTCGCTGCCA 540
CCCGGGCCTG GAGCCCCACA CCCGAGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGCC 600
TAAAGAGAGC ACTGCCAGGT GTACAGTCTT GGGCATGCGC TGTTTGAGCT TCGGGGGAGA 660
GCCCGACATC CACCTCGCCG AAGGTGCCTA GAAGAACAAG GTGCAGGACC CCGTGTCTGC 720
TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GCGCTCTCTG GTGTTGATAG 780
AGATGGAAGT TGGACTTGGG GGCCTCTCCA CGCTGTCCCA CTGCCCCTGG CTTAGGCGGC 840
AGCCTGCCCC GTGGCCGCTC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGCCCT 900
CCCTGGGCTC CCGCGCCCGC AGCCCTGCCC CCGCGGAAGG CCCCCCGCCT GTCTTGGCGT 960
CCCCCGCGCG CCGCTGCGC GGGGACGCA CCGCCCGCTG GTGCAGTGGG AGAGCCCGGC 1020
GGCCCGCGCC GCAGCTTCT CCGCCCGCGC CCGCGCGGCC TGACCCCCA TCTGCTCTTC 1080
CCCGCGGGGG CCGCGCGGCC GGGGCTGGGG GCCCGGGCAG CCGCGCTCGG GCAGCGGGGG 1140
CGCGGGGCTG CCGCTGCGC TCGCAGCTGG TGCCGCTGCG CCGCTCGGC CTGGGCCACC 1200
GCTCCGACGA GCTGGTGGT TCCGCTTCT GCAGCGGCTC CTGCGCGCGC GCGCGCTCTC 1260
CACACGACCT CAGCCTGGCC AGCCTACTGG CCGCGGGGGC CTTGCGACCG CCCCCTGGCT 1320
CCCGGCCCGT CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG 1380
ACGTCAACAG CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCTGCG GGTGCTCTGG 1440
GCTGAGGGCT CGCTCCAGGG CTTTGAGAGC TGGACCTTCA CCGGTGGCTC TTCTTGCCTG 1500
GGACCTTCCC GCAGAGTCCC ACTAGCCAGC GGCTCAGCC AGGGACGAAG GCCTCAAAGC 1560
TGAGAGGGCC CTACCGTGGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAACCTG 1620
CTAGCAGCCC CAGAGCCCTC ACCCTGCGGA TCCCAGCCTA AAAGACACCA GAGACCTCAG 1680
CTATGGAGCC CTTTGGAGCC ACTTCTCACA GACTCTGGCA CTGCGCAGGC CTCGAACCTG 1740
GGACCCCTCC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT 1800
AGGGACAGCA TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGCC TGTGCTGGAA 1860
CTGGCCTGTA CTCATCTCAT GGAGCTGGCC CC

Seq ID NO: 605 Protein sequence
Protein Accession #: NP_003967.1

1 11 21 31 41 51
MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
PAGHLPGGRT ARWCSSRRARR PPPQPSRPAP PPPAPPSALP RGGRARAGG PGSRARAAGA 120
RGCRRLRSQVL PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 606 DNA sequence
Nucleic Acid Accession #: NM_057160.1

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5 1 11 21 31 41 51
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CACCTGGGTG CCTCTTTCT CCTGAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG 120
TGGCCCAACC TGGCGCTCT GGTCTGCTG AGCAGCGTCG CAGAGGCCTC CCTGGGCTCC 180
GCGCCCGCGA GCGCTGCCCC CCGCGAAGGC CCCCAGCCTG TCCTGGCGTC CCCCAGCGGC 240
CACCTGCGCG GGGACGACAC GCGCCGCTGG TGCAGTGGAA GAGCCCGCGG GCGCGCGCG 300
CAGCCTTCTC GCGCGCGGCC CCGCGCGCCT GCACCCCAT CTGCTCTTCC CCGCGGGGCG 360
CGCGCGCGCG GGGCTGGGGG CCGGGGAGC CGCGCTCGGG CAGCGGGGGC GCGGGGCTGC 420
CGCTGCGCTC CGCAGCTGGT GCGGTGCGC GCGCTCGGCC TGGGCCACCG CTCCGACGAG 480
CTGGTGGCTT TCCGCTTCTG CAGCGGCTCC TGCCGCGCG CCGCTCTCTC ACACGACCTC 540
AGCCTGGCCA GCCTACTGGG CCGCGGGGCC CTGCGACCGC CCGGGGCTC CCGGCCGCTC 600
AGCCAGCCCT GCTGCCGACC CACGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660
ACCTGGAGAA CCGTGGACCG CCTCTCGCC ACCGCTGCG GCTGCTGGG CTGAGGGCTC 720
GCTCCAGGGC TTTCAGACT GGACCTTAC CGGTGGCTCT TCCTGCTGG GACCTCTCCG 780
CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGGACGAAG CCTCAAAGCT GAGAGGCCCC 840
TACCGTGGG TGATGGATAT CATCCCGAA CAGGTGAAGG GACAACTGAC TAGCAGCCCC 900
AGAGCCCTCA CCTGCGGAT CACAGCCTAA AAGACACAG AGACCTCAGC TATGGAGCCC 960
TTGCGACCAA CTTCTCAGC ACTCTGGAC TGGCCAGGCC TCGAACCTGG GACCCCTCCT 1020
CTGATGAACA CTACAGTGGC TTAGGCATCA GCGCCGCGCC AGGCCCTGTA GGGACAGCAT 1080
TTGAAGGACA CATATTGCA TTGCTTGGTT GAAAGTGCCT GTGCTGGAAC TGGCCTGTAC 1140
TCACTCATGG GAGCTGGGCC C

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Seq ID NO: 607 Protein sequence
Protein Accession #: NP_476501.1

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30 1 11 21 31 41 51
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APRSPAPRPG PFPVLASPAH HLPGGRTARW CSGRRARRPP QPSRPAPPPP APPSALPRGG 120
RAARAGGPGS RARAAGARGC RLRSQLVFVR ALGLGHRSD LVRFRFCSSG CRRARSPHDL 180
LSLASLLGAG LRPPPGSRPV SQPCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG

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Seq ID NO: 608 DNA sequence
Nucleic Acid Accession #: NM_057090.1
Coding sequence: 29..715

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40 1 11 21 31 41 51
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GTGGCCCAACC TGGCGCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT CCTTGGGCTC 180
CGCGCCCGCG AGCCTTGCCC CCGCGCAAGG CCCCCGCGCT GTCTTGGGCT CCCCCGCGG 240
CCACTGCGCG GGGGAGACGA CCGCCGCTG GTGCACTGGA AGAGCCCGGC GCGCGCGGC 300
GCAGCCTTCT CCGCCCGCGC CCGCGCGGCC TGCACCCCA TCTGCTCTTC CCGCGGGGGG 360
CCGCGCGGCG GGGGCTGGGG GCGCGGCGC CCGCGCTCGG GCAGCGGGGG CCGGGGCTGC 420
CCGCTGCGCG TCGCAGCTGG TCGCGGTGCG CCGCTCGGCC CTGGGCCACC GCTCCGACGA 480
GCTGGTGGCT TCCGCTTCTC GCAGCGGCTC CTGCGCGCGC GCGCGCTCTC CACACGACCT 540
CAGCCTGGCG AGCCTACTGG CCGCGGGGCC CTGCGACCG CCGCGGGCTC CCGGGCCGCT 600
CAGCCAGCCC TGCTGCCGAC CCAAGCGCTA CGAAGCGGTC TCCTTCATGG ACCTCAACAG 660
CAGCTGGAGA CCGTGGGACC CCCTCTCGC CACCGCTGC GGCTGCTGG GCTGAGGGCT 720
CGCTCCAGGG CTTTCAGAC TGGACCTTA CCGGTGGCTC TTCTGCTGG GACCTCTCC 780
GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGAGCGAAG GCCTCAAAGC TGAGAGGCCC 840
CTACCGGTGG GTGATGGATA TCATCCCGA ACAGGTGAAG GGACAACTGA CTAGCAGCCC 900
CAGAGCCCTC ACCCTGCGGA TCCAGCCTA AAGACACCA GAGACCTCAG CTATGGAGCC 960
CTTGGAGCCC ACTTCTACA GACTCTGGCA CTGCGCAGGC CTCGAACCTG GACCCCTCCT 1020
TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT AGGGACAGCA 1080
TTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGGC TGTGCTGGAA CTGGCCTGTA 1140
TCACTCATGG GAGCTGGGCC C

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Seq ID NO: 609 Protein sequence
Protein Accession #: NP_476431.1

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65 1 11 21 31 41 51
| | | | |
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GPPPVLASPA GHLPGGRTAR WSGRRARRPP QPSRPAPPPP PAPPALPRG GRAARAGGPG 120
SRARAAGARG CRLRSQLVFV RALGLHRSR ELVRFRFCSSG SCRRARSPHD LSLASLLGAG 180
ALRPPPGSRP VSQPCRPTRY YEAVSFMDVN STWRTVDRLS ATACGCLG

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Seq ID NO: 610 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1746

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CGCTACCATG GCTGCCCTAG CGAGGTGACC TGCTCCAGGG CCTCCAGGT GAGGTGCACC 120
GGGGCACGCA TTGTGGCGGT GCCCACCCTC CTGCCCTGGA ACGCCATGAG CTGCAGATC 180
CTCAACACGC ACATCACTGA ACTCAATGAG TCCCGTTTCC TCAATATCTC AGCCCTCATC 240
GCCCTGAGGA TTGAGAAGAA TGAGCTGTG CGCATCACGC CTGGGGCTCT CCGAAACCTG 300
GGCTCGCTGC GCTATCTCAG CCTCGCCAAC AACAAGCTGC AGGTTCTGCC CATCGGCCTC 360
TTCCAGGGCC TGACAGCCT TGAATCTCT CTCTGTCCA GTAACCACTG GTTGCAGATC 420
CAGCCGGGCC ACTTCTCCA GTGCAGCAAC CTCAAGGAGC TGCAGTTGCA CGGCAACCAC 480
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	GGCAAGAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
	GTCTCTCCGC	TGTATGAGAA	CAGGCTCACG	GATATCCCCA	TGGGCACTTT	TGATGGGCTT	660
	GTAAACCTGC	AGGAACTGGC	TCTACAGCAG	AACCAGATTG	GACTGTCTCT	CCCTGGTCTC	720
5	TTCCACAACA	ACCAAACTCT	CCAGAGACTC	TACCTGTCCA	ACAACACAT	CTCCAGCTG	780
	CCACCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TACTCTCTTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTCTGG	CCCATGCCCA	ACCTGCCGGA	GCTTTGGCTC	900
	TATGACAACC	ACATCTCTTC	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCTCTGATT	TTAGCCGCAA	TCAGATCAGC	TTCTCTCTCC	CGGGTGCCTT	CAACGGGCTA	1020
10	ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCACCTG	AGGACCTGGA	CGGGAATGTC	1080
	TTCCGCGATG	TGGCCAACTC	GCAGAACATC	TCCCTGCAGA	ACAACTCCCT	CAGACAGCTC	1140
	CCAGGGAATA	TCTTGCCTCA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAACCCAG	1200
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	TATGACAATC	CCTGGAGGTG	TGACTCAGAC	ATCCTTCCCG	TCCGCAACTG	GCTCTGCTC	1320
15	AACCAAGCTA	GGTAACTGAC	GGACACTGTA	CCTGTGTGTT	TCAGCCACAG	CAATGTCCGA	1380
	GGCCAGTCCC	TCATTATCAT	CAATGTCAAC	GTGTCTGTTT	CAAGCGTCCA	TGTCCCTGAG	1440
	TGCTCTAGTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCCAG	1500
	TCCGTCTCTT	CTACCACTGA	GCTAACCAAG	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
	ATTACAGTCA	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCAGAG	CGGGCTGGCC	1620
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	TGTTGTCTGT	GCAAGAAAGG	GAGCCAAGCT	GTCTGTATGC	AGATGAAGGC	ACCAATAGAG	1740
	TGTTAAAGAG	CTTGGCTGGA	CGAGGGCTGG	GGAAATGATG	GACTGGAGGA	CCTGGGAATT	1800
	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGATTGCT	CTTTCTGGCC	1860
	CTAGATAAAG	GTGTGCTTAC	CTCTTCTGTA	CTTGCCTGAT	TCTCCCTGAG	AGAAGCAGGT	1920
25	CGTGCCGGAC	CTTCTCTAAA	TCAGGAAGAT	AGATCCAACT	GGCCATGGCA	AAAGCCCTGG	1980
	GGATTTCCGA	TTCTATACCC	TGGGCTTCTT	TCAGAGAGGG	TCTTCTCTCA	AATCCTCCCC	2040
	ACCTGTCTCT	CAGAACAAGC	CTTCCCTGCG	CCCAGGCCCC	CTCCGGGCTT	CTGTAGACTG	2100
	AGTTAGTCCA	CAGCTGTCTC	ACTTCGTGGG	AATAGTTCTC	CGCTGAGATA	GCCCCCTCTG	2160
	CCTAAGTATT	ATGTAAGTTG	ATTTCCTTTC	TTTTGTTTCT	CTTGTGTTCT	CTATGGCTTG	2220
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	TGAGTTCTCT	CCTCAAGAAA	GACTTCAAAC	CATTAACTAG	GTCTTCTTAA	AGCCGTCAAT	2340
	CAGCTGTGTT	TGGGAGTATG	TATGAAAGAG	AGAAGGAAAA	TCATGCCGCT	CAGTTCTCTG	2400
	AGACAGAAGA	GCCGTCTATC	GTGTCTCACT	TGTGATTTTT	ATCTGGAATA	GGAAGAAACA	2460
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35	TGAAAGTTT	AGCCCTTTAA	GGAAATGAAAT	CATGTAGAAAT	TTTGACTTTC	TAAAAACATT	2580
	AAAAACAGCT	TATTAATACG	GGATAGAGAA	AGAAATCTGG	TGCCCTGGGG	TCCCTGTGTT	2640
	CACCCCTAGA	TCTTTCTAAT	AAATTTTAA	TTGAAGCATG	TGAAGTGATC	STGCAGAAAA	2700
	GTGGGAACAT	GATAGTGTAT	GGCTTGTGTT	ATTTTCAACA	ACTGAACATA	CCTGTGTAAT	2760
	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCTGGGCT	TTTTCCAGTA	2820
40	GGAGATGGGG	GCTTCTGAAG	ATGGACTTAC	CTGGGACCTG	CCCCCATGTA	GCCAGGACGG	2880
	TCCCCCCACA	GTACGCTGTT	GCAAGAGGCC	CGTGGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
	TGTGGACAGG	GTGGCCTGAA	GTGGCCTGAA	CAGGAGATTT	TATTATATCT	GGAGACCTCT	3000
	AGAGACCCCT	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
	GTCCGTGCAG	CCACACCTTC	TTCCTTGCCA	GCAAGTTGTC	TGCGGCTCAT	CGGAGGCCCC	3120
45	TCCGCTGGGA	GCCTTCTATG	GACGTGATAT	GCCTGTATCT	GTCTTTAATT	TTTATCTTCT	3180
	ACTTAGGGGA	AGTGAATTCG	CTCAGAGATG	AGATCCTTTA	ATTGAAAACG	AAGTGTAAAG	3240
	GAATCTAGTG	TCTTTCTAAT	GTGGTAAAT	TCTCCATCAA	CATCACAGCT	AGCTGGCAGC	3300
	TGAATCTCAG	AATCTCACTT	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCACTAGTG	3360
	GTCTGGGGGG	TCCCTCTGCG	TGTGCTCTGG	TGTGGTCTGG	TAGGAGTTTG	AGTTGTTTGC	3420
50	TCCAGGGTTA	TTCTCTCTCT	CGAGTCACAG	TCACACGAAT	ACCTGCCTTC	TCTGGCTTTT	3480
	CTGCTATACA	CATATTACAG	TGGCGCTCAA	GAAGTTAGGC	TCATGGCAAC	GTGTGTCTTT	3540
	CTCTGGACAA	TGTTGCCCAT	TTACAGTGAA	ATGGAGAATT	TCAGGTCTCC	ACGTCTGCCC	3600
	AGGAAAGAAC	TTACGCTGAC	TCCACGGGGA	TCTGGAATTC	CACGACCAAT	CCCGATCGGC	3660
	TCTTATTAGC	TCCCTCTGAG	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
55	TCCGCTCTTA	TTAGCTCCCC	GCTCCACAAG	ACACCTGTGA	TCTGGAATTC	TACCACCAAT	3780
	CCCGATCGGC	TCTTATTAGC	TCCCGCTTCC	ACAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCAGG	TCTTCTTATG	TTTCCCTTTC	CAGTTCTCTG	ACAAAAAGTG	TCCAGAGGGC	3900
	TGTTTGCAAA	CACCTAGTGA	CTTGTAGCTT	TTTCAACCTC	TGTCCCAAGG	AATCTAGGAG	3960
	AGATGAGGCC	CGTCAGATGC	AAGAGATGTC	ATCCCCCAG	GGTCTCCCAAG	GCATTTCCAC	4020
60	ACTATTGGTG	GCACCTGGAG	GACATGCACC	AAGGCTTGCC	AGAGCCAACA	GGAAGTGAGC	4080
	CCAGAGCATG	GCACATGAGC	ATCACCCGCT	GATGGTGGCC	TGCTGTGCCT	GGTGCCAACA	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAAGCATG	GTTTGCCCAT	AGACCTGTCT	4200
	GGTGCTCCTG	TGAGTGGGCT	CCAGATGTCT	TTGTGCATAG	GCACAAGTGG	GCCAGGGCTG	4260
	GAGGGAGGTG	GGAAACCTCA	TCATCCGGTG	GGCCCTGCCA	ATCTTAACCC	AGAACCCCTA	4320
65	GGTATTCTCT	GCAGTAGCCA	TGACATTGGA	GCACCTTCTT	CTCCAGCCAG	AGGCTGACCT	4380
	GAGGGCCACT	GTCCTCAGAT	GACACCACCC	AGGAGCACCC	TAGGTGAGGG	GTGAGGGCCC	4440
	CCTTATGTGA	ACCTCTTGCC	TCTTCTTCTT	TCCCATCAGA	GTGGTTGGAT	GGAGCCATTG	4500
	GCCTCTTTTT	CTTACGCGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGGG	GTCTCCTTTC	CAACAGGATG	ATGCATTGTC	TCAATTCTCA	4620
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	CCTCTCTGTT	TACAGCTCCT	TGACAGTCCC	ACGCCCATCT	GGAGTGGGAG	CTGGGAGTTA	4740
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	TGACACAGTA	CTCTTCAAGC	ACTGAGCCTG	GATTTCTCTT	CTAGCCCTCA	GCACCCCTGC	4860
	GGTAGGAGTG	CGCCTCTAC	CCACTTGTGA	TGGGGTACAG	AGGCACCTGC	TCTTCTGCAT	4920
75	GGTGTTCAAT	AGGCTGGGAG	TTTTATTAT	CTCTTCAAAC	TTGTACAAAG	AGCTCATGGC	4980
	TTGTCTTGGG	CTTTCGTGAT	TAAACCAAAG	GAAATGGAAG	CCATTCCTCT	GTGCTCTCC	5040
	TTAGTCTTGG	TCATCAGAAC	CTCACTTGGT	ACCATATAGA	TCAAAGCTT	TGTAACCACA	5100
	GGAAAAAATA	AACCTTCCCA	TCCCTTAAAG	AATAGAATAG	TTTGTCCCTC	TCATGGGAAT	5160
	TGGGCTGTAT	GTATATTTGT	CTTCTCCTT	AGAAATTAGA	GATACAAAGG	TTCTACTTCT	5220
	AACTTTTCAT	GGACACAAAT	TCCACAACCT	TTCAGATGCT	GATGTAGAGC	TATTGGGAAA	5280
80	GAACCTTCAA	ACTCAGGAAG	TTTGACAGAG	GCAGACAGCT	AGAGATAACT	CGGGACCCAG	5340
	AGTTGGTCTG	CAGATGTTAG	ATGTATCCTA	GCTTTTAGCC	ATAAACCACT	CAAAGATTCA	5400
	GCCCCAGAT	CCCAAGTCA	GAACCTGAAT	TGCGTTGTTG	GGAAAGCCAG	AGTGGCCTTG	5460
	GGAAAGGAGC	CATGGCTGTG	GTTCAGAGAG	GGTGGGCTGG	CAAGCCACTT	CCGGGGAAAA	5520
	CTCCTTCCCG	CCAGGTTTTC	TTCTTCTCTT	AAGGAGAGAT	TGTTCTCACC	AACCCGCTGC	5580
85	CTTCATGCTG	CCTTCAAAGC	TAGATCATGT	TTGCTTGTCT	TAGAGAATTA	CTGCAATATC	5640
	GCCCCAGTGC	TTGGCGATGC	ATTATCAGAT	TTCTAGGCCC	TCAGGCTTTT	GTAGAGTGTG	5700
	AGCCCTGGTG	GGCAGGGTTG	GGGGGTCTGT	CTTCTGCTGG	ATGCTGCTTG	TAATCCATT	5760

GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 611 Protein sequence
Protein Accession #: BAB84587.1

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LNTHITELNE SPFLNISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKLQVLPIGL 120
PQGLDSLESL LLSSNQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAPD HLVGLTKLNL 180
GKNSLTHISP RVFQHLGNLQ VRLYENRLT DIPMGTFDGL VNLQELALQQ NQIGLLSPGL 240
FHNHNLQRL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRELWL 300
YDNHISLSPD NVFSNLRLQL VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLQDNV 360
FRMLANLQNI SLQNNRLRLQ PGNIPANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCLELRL 420
YDNPWRCDSD ILPLRNWLLL NQPRLTGDTV PVCFSANVR QQSLLIINVN VAVPSVHVPE 480
VPSYPETPHY PTPSYPTT SVSSTELTS FVEDYDLTT IQVTDDRSVW GMTQAQSGLA 540
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Seq ID NO: 612 DNA sequence
Nucleic Acid Accession #: XM_098151
Coding sequence: 1..447

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TCTGGAGTGG GAGCTGGGAG TCAGTGTGG AGAAGAAACA ACAAAGCCA ATTAGAACCA 180
CTATTTTAA AAAGTGCTTA CTGTGCACAG ATACTCTTCA AGCACTGGAC GTGGATTCTC 240
TCTCTAGCCC TCAGCACCCC TGCGGTAGGA GTCCGCCCTC TACCCACTTG TGATGGGGTA 300
CAGAGGCACT TGCTCTCTG CATGGTGTTC AATAGGCTGG GAGTTTTATT TATCTCTTCA 360
AACTTTGTAC AAGAGCTCAT GGCTTGCTT GGCCTTTCGT CATTAAACCA AAGGAAATGG 420
AAGCCATTCC CCTGTGCTC TCCTTAG

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Seq ID NO: 613 Protein sequence
Protein Accession #: XP_098151

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|      |      |      |      |      |
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LFLKSAYCAQ ILFKHWIWL SLALSTPAVG VPPLPTCDGV QRHLFLCMVF NRLGVLPFIS 120
NPFVQELMACL GLSSLNQKRW KPFFCCSP

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Seq ID NO: 614 DNA sequence
Nucleic Acid Accession #: NM_002658.1
Coding sequence: 77..1372

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GAGCGACTCC AAAGGCAGCA ATGAATTCA TCAAGTTCCA TCGAACTGTG ACTGCTCTAA 180
TGGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCAACATT CACTGGTGCA ACTGCCCAAA 240
GAAATTCAGG GGGCAGCACT GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG 300
TCACITTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCCCTGCC TGCCCTGGAA 360
CTCTGCCACT GTCCTTCAGC AAACGTACCA TGCCACAGA TCTGATGCTC TTCAGCTGGG 420
CCTGGGGAAA CATAATTACT GCAGGAACCC AGACAACCGG AGGCGACCTT GGTGCTATGT 480
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CACTGGCTTT GGAAGAGAGA ATTCTACCGA CTATCTCTAT CCGGAGCAGC TGAAGATGAC 1080
TGTGTGAAG CTGATTTCCC ACCGGGAGTG TCAGCAGCCC CACTACTACG GCTCTGAAAT 1140
CACCACCAA ATGCTATGTG CTGCTGACCC CCAATGGAAA ACAGATTCTT GCCAGGGAGA 1200
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TGTCTTTTTC TGGACTGAAG CCTGCAGGAG TTAAGAGGG CAGGGCATCT CCTGTGCATG 1680
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AATGTGGGAG CAGCGTTTG GGGAGCAGAG ACATAACGA CTTAGGGCA GGGCTCTGAT 1860
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ATCCCTTCTC TTAGCCTTAG TTCATCCAAT CCTCACTGGG TGGGGTGAGG ACCACTCCTT 2220
ACACTGAATA TTTATATTTC ACTATTTTTA TTTATATTTT TGTAATTTTA AATAAAGTG 2280
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Seq ID NO: 615 Protein sequence
Protein Accession #: NP_002649.1

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	HCEIDKSKTC	YEGNGHFYRG	KASTDTMGRP	CLPWSNATVL	QQTYYAHRSD	ALQLGLGKHN	120
	YCRNPDNRNR	PWCYVQVGLK	PLVQECMVHD	CADGKKPSSP	PEELKFQCCQ	KTLRPRFKII	180
10	GGEFTTIENQ	PWFAAIYRRH	RGGSVTVVCG	GSLISPCWVI	SATHCFIDYP	KKEDYIVYLG	240
	RSRLNSNTQG	EMKFEVENLI	LHKDYSADTL	AHHNDIALLK	IRSKEGRCQA	PSRTIQITICL	300
	PSMYNDPQFG	TSCEITGFGK	ENSTDYLYPE	QLKMTVVVKLI	SHRECQPHY	YGSEVTTKML	360
	CAADPQWKTD	SCQDSDGGPL	VCSLQGRMTL	TGIVSWGRGC	ALKDKPGVYT	RVSHFLPWIR	420
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Seq ID NO: 616 DNA sequence
Nucleic Acid Accession #: NM_024422.1
Coding sequence: 202..2907

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	GCTCCGGCCG	CGGCGCTCGC	CCCGCGGAGC	CCTCCTACCC	CGGCGCGACG	CTCGGCCGCG	180
25	GACCTGCCCC	GAGCCCTCTC	CATGGAGGCA	GCCCGCCCTC	CCGGCTCCTG	GAAAGGAGCC	240
	CTCTGCCGGC	TGCTCTCTGT	GACCTCTCGC	ATCTTAATAT	TTGCCAGTGA	TGCCTGCAAA	300
	AATGTGACAT	TACATGTTCC	CTCCAAACTA	GATGCCGAGA	AACCTGTTGG	TAGAGTTAAC	360
	CTGAAAGAGT	GCTTTACAGC	TGCAAACTTA	ATTCAATCAA	GTGATCCTGA	CTTCCAAATT	420
	TTGGAGGATG	GTTTCAGTCT	TACAACAAAT	ACTATTCTAT	TGCTCTCGGA	GAAAGAGAAGT	480
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	GAGCATCAAA	CAAGGTCTCT	AAAGAAAAGA	CATACTAAAG	AAAAAGTTCT	AAGGCGCGCC	600
	AAGAGAAGAT	GGGCTCCAAT	TCCTTGTTCC	ATGCTAGAAA	ACTCCTTGGG	TCCTTTTCCA	660
	CTTTTCCTTC	AACAGGTTCA	ATCTGACACG	GCCCAAAACT	ATACCATATA	CTATTCCATA	720
	AGAGGTCTCT	GAGTTGACCA	AGAACCTCGG	AATTTATTTT	ATGTGGAGAG	AGACACTGGA	780
35	AACCTGTATT	GTACTCGTCC	TGTAGATCGT	GAGCAGTATG	AATCTTTTGA	GATAATTGCC	840
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	GAGGATGAAA	ATGATAACTA	CCCAATTTTT	ACAGAAGAAA	CTTATACTTT	TACATTTTTT	960
	GAAATATGCA	GAGTGGGCAC	TACTGTGGGA	CAAGTGTGTG	CTACTGACAA	AGATGAGCCT	1020
40	GACACGATGC	ACACACGCCT	GAAGTACTCC	ATCATTGGGC	AGGTGCCACC	ATCACCCACC	1080
	CTATTTTCTA	TGCATCCAAC	TACAGGCGTG	ATCACCACAA	CATCATCTCA	GCTAGACAGA	1140
	GAGTTAATTT	CTCCAGATGG	GTGAAAAATA	AAAGTACAAG	ACATGGATGG	TCAGTATTTT	1200
	GGTCTACAGA	CAACTTCAAC	TTGTATCATT	AACATTGATG	ATGTAATGA	CCACTTGCCA	1260
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	CGTCTTTCTT	ATCAGAATGA	TCCTCCATT	GGCTCATATG	TAGTACCTAT	AACAGTGAGA	2160
	GATAGACTTG	GCATGTCTAG	TGTCACCTTA	TTGGATGTTA	CAGTGTGTGA	CTGCATTACC	2220
60	GAAATGACT	GCACACATCG	TGTAGATCCA	AGGATTGGCG	GTGGAGGAGT	ACAACCTTGA	2280
	AAGTGGGCCA	TCCTTGCAAT	ATTGTTGGGC	ATAGCATTGC	TCTTTTGCAT	CCTGTTTACG	2340
	CTGCTCTGTG	GGGCTTCTGG	GACGCTTAAA	CAACCAAAAG	TAATTTCTGT	TGATTAGCCG	2400
	CAGCAGAAC	TAATGTATAT	AAACACAGAA	GCTCCTGGAG	ATGACAAAAGT	GTATTCTGCG	2460
	AATGGCTTCA	CAACCCAAAG	TGTGGGCGCT	TCTGCTCAGG	GAGTTTGTGG	CACCGTGGGA	2520
65	TCAGGAATCA	AAAACGGAGG	TCAGGAGACC	ATCGAAATGG	TGAAAGGAGG	ACACCGAGCC	2580
	TCGGAATCCT	GCCGGGGGGC	TGGCCACCAT	CACACCTTGG	ACTCCTGCGG	GGGAGGACAC	2640
	ACGAGAGTGG	ACAACTGCAG	ATACACTTAC	TCGGAGTGGC	ACAGTTTATC	TCAGCCCGGT	2700
	CTTGGTGAAA	AAGTGTATCT	GTGTAATCAA	GATGAAAATC	ACAAGCATGC	CCAAGACTAT	2760
	GTCCCTGACAT	ATAACTATGA	AGGAAGAGGA	TCGGTGGCTG	GGTCTGTAGG	TTGTTGCAGT	2820
70	GAACGACAAG	AAGAAGATGG	GCTTGAATTT	TTGGATAATT	TGGAGCCCAA	ATTTAGGACA	2880
	CTAGCAGAAG	CATGCATGAA	GAGATGAGTG	TGTTCTAATA	AGTCTCTGAA	AGCCAGTGGC	2940
	TTTATGACTT	TTAAAAAATA	TTACAAACCA	AGAATTTTTT	AAAGCAGAAG	ATGCTATTTG	3000
	TGGGGGTTTT	TCTCTCATTA	TTTGGATGGA	ATCTCTTTGG	TCAAATGCAC	ATTTACAGAG	3060
	AGACACTATA	AACAAGTACA	CAAATTTTTC	AATTTTTCAC	TATTTTAAAA	TTACTTATCT	3120
75	TCTATCCAAG	GAGGTCTACA	GAGAAATTAA	AGTCTGCCTT	ATTGTTTACA	TTTGGGTATA	3180
	ATGACAACAG	CCAATTTATA	GTGCAATAAA	ATGTAATTAA	TTCAAGTCCT	TATTATAGAC	3240
	TATTTGAAGC	ACAACCTAAT	GGAAAATTGT	AGAGACCTTG	CTTAAACATT	ATCTCCAGTT	3300
	AATTAAGTGT	TCAATGTTGT	CTTGGAAACT	GTGTTTTCCT	TGAACATCTA	AAGTGTGTAG	3360
80	ACTGCATTCT	TGCTATTATT	TTATTCTTGT	AATGTGACCT	TTTCACTGTG	CAAAAGGGAGA	3420
	TTTCTAGCCA	GGCATTGACT	ATTACAATTT	CATT			

Seq ID NO: 617 Protein sequence
Protein Accession #: NP_077740.1

85	1	11	21	31	41	51	
	MEARPSGWSW	NGALCRLLLL	TLAILIFASD	ACKNVTLHVP	SKLDAEKLVG	RVNLKECPTA	60
	ANLIHSSDPD	FQILEDGSVY	TTNTILLSSE	KRSFTILLSN	TENQEKKKIF	VFLEHQTKVL	120

KKRHTKEKVL RRAKRRWAPI PCSMLENSLG PFPLFLQQVQ SDTAQNYTIY YSIRGPGVDQ 180
 EPRNLFYVER DTGNLYCTRF VDREQYESFE IIAFATTPDG YTPLEPLPLI IKIEDENDNY 240
 TIFTEETYTF TIFENCVRGT TVGQVCATDK DEEDTMHTRL KYSIIGQVPP SPTLFMSHPT 300
 TGVITTTSSQ LDRELIDKYQ LKIKVQMDMG QYFGLQTTST CIINIDVDND HLPFTPTSTY 360
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKONE NGNFKIVTDA KTNFVGLCVV 420
 KPLNVEEKQ MILIGUVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480
 KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVP RSLDREASTI 540
 KNGIYNITVL ASDQGRCTCT GTLQIILQDV NDNSPFIPKK TVIICKPTMS SAEIVAVDFD 600
 EPIHGPPPDF SLESSTSEVQ RMWRLKAIND TAARLSYQND PPFSGSYVPI TVDRRLGMS 660
 VTSLDVTLCD CITENDCTHR VDPRIQGGGV QLGKNAILAI LLGIALLFPI LFTLVCGASG 720
 TSKQPKVIPD DLAQONLIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVSGGIKNGG 780
 QETIEMVKGQ HQTSESCRGH GHHTLDSR GGHTEVDNCR YTVSEWSFT QPRLGEKVYL 840
 CNQDENHKA QDYVLTNYE GRGSVAGSVG CCSERQEDG LEFLDNLEPK FRTLAEACMK 900
 R

Seq ID NO: 618 DNA sequence
 Nucleic Acid Accession #: NM_004949.1
 Coding sequence: 202..2745

20 1 11 21 31 41 51
 CGCCAAAGGA AAAGCCCCTT GGATGAGAGG CAGGCGCTTC AGAGAAGCTA AGAAAAGCAC 60
 CTCTCCGCGC GCCCCACCTC CTCGCGCTCG CGCTCCTCCT GAGCAGCGGG CCCAGACTGC 120
 GCTCCGCGCG CGGCGCTGCG CCGCGGAGAG CCTCTACCCC CGGCGCGAGC CTCGCGCGCG 180
 GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCCC CCGGCTCCTG GAACGGAGCC 240
 CTCTGCGCGC TGCTCCTGCT GACCTCGCGC ATCTTAATAT TTGCCAGTGA TGCCTGCAAA 300
 AATGTGACAT TACATGTTC CTTCAAACCTA GATGCCGAGA AACTTGTGG TAGAGTTAAC 360
 CTGAAAGAGT GCTTTACAGC TGCAAACTCTA ATTCATTCAA GTGATCCTGA CTTCCAAATT 420
 TTGGAGGATG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGTCCTCGGA GAAGAGAAGT 480
 TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTGG 540
 GAGCATCAAA CAAAGGTCCT AAAGAAAAGA CATACTAAG AAAAAGTTCT AAGGCGCGCC 600
 AAGAGAAGAT GGGCTCCAAT TCCTTGTTCTG ATGTAGAGAA ACTCCTTGGG TCCTTTTCCA 660
 CTTTTCCTTC AACAGSTTCA ATCTGACACG GCCCAAACT ATACCATATA CTATTCCATA 720
 AGAGGTCTCG GAGTTGACCA AGAACCTCGG AATTTATTTT ATGTGGAGAG AGACACTGGA 780
 AACTTGTATT GTACTCGTCC TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840
 TTTGCAACAA GTACTACTGG GTATACTCCA GAACCTCCAC TGCCCTTAAT AATCAAAATA 900
 GAGGATGAAA ATGATACTA CCCAATTTT ACAGAGAGAA CTTATACTTT TACAATTTT 960
 GAAAATTGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT 1020
 GACACGATGC ACACACGCTT GAAGTACTCC ATCATTGGGC AGGTGCCACC ATCACCACC 1080
 CTATTTTCTA TGCATCCAAC TCAGGCGTGG ATCACCACAA CATCATCTCA GCTAGACAGA 1140
 GAGTTAATTG CAAAGTACCA GTTGAAAATA AAAGTACAA ACATGGATGG TCAGTATTTT 1200
 GGTCTACAGA CAACCTCAAC TTGTATCATT AACATTGATG ATGTAAATGA CCACTTGCCA 1260
 ACATTACTCA GACTTCTCTA TGTGACATCA GTGGAAGAAA ATACAGTTGA TGTGGAATAT 1320
 TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATACTG CTAAGTGGAG AGCTAATTAT 1380
 ACCATTTTAA AGGGCAATGA AATGGCAAT TTTAAATATG TAACAGATGC CAAAACCAAT 1440
 GAAGGAGTTC TTTGTGTAGT TAAGCCTTTG AATTATGAAG AAAAGCAACA GATGATCTTG 1500
 CAAATTTGGT TAGTTAATGA AGCTCCATT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560
 AGCAGAGCAA CAGTTACTGT TAATGTAGAA GATCAGGATG AGGGCCCTGA GTGTAAACCT 1620
 CCAATACAGA CTGTTGCGAT GAAAGAAAAT GCAGAAAGTG GAACAACAAG CAATGGATAT 1680
 AAAGCATATG ACCCAGAAAC AAGAAGTAGC AGTGGCATAA GGTATAAGAA ATTAAGTATG 1740
 CCAACAGGTG GGGTCAACAT TGTGAAAAT ACAGGATCAA TCRAAGTTT CAGAAGCCTG 1800
 GATAGAGAGG CAGAGACCAT CAAAATGGC ATATATAATA TTACAGTCTC TGATCAGAC 1860
 CAAGGAGGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGACGT GAATGATAAC 1920
 AGCCCATTC TACCTAAAAA GACAGTGATC ATCTGCAAA CCAACATGTC ATCTGCGGAG 1980
 ATTGTTGCGG TTGATCTCTG TGAGCCTATC CATGGCCAC CTTTGTACT TAGTCTGGAG 2040
 AGTTCTACTT CAGAAGTACA GAGAATGTGG AGACTGAAAG CAATTAATGA TACAGCAGCA 2100
 CGTCTTTCTC ATCAGAATGA TCCTCCATT GGCTCATATG TAGTACCTAT AACAGTGAGA 2160
 GATAGACTTG GCATGCTTAG TGTCACTTCA TTGGATGTTA CACTGTGTGA CTGCATTACC 2220
 GAAAATGACT GCACACATCG TGTAGATCCA AGGATTGGCG GTGGAGGAGT ACAACTTGGA 2280
 AAGTGGGCCA TCCTTGCAAT ATTGTTGGGC ATAGCATTGC TCTTTTGCAT CCGTITTACG 2340
 CTGGTCTGTG GGGCTTCTGG GAGCTCTAAA CAACCAAAAG TAATTCCTGA TGATTTAGCC 2400
 CAGCAGAAC TAATGTATC AAACACAGAA GCTCCTGGAG ATGACAAAGT GTATTCTGCG 2460
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 TCAGGAATCA AAAACGGAGG TCAGGAGACC ATCGAAATGG TGAAGGAGG ACACCAGACC 2580
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 CTATGAAGGA AGAGGATCGG TGGCTGGGTC TGTAGTTTGT TGCAGTGAAC GACAAGAGA 2880
 AGATGGGCTT GAATTTTGG ATAATTGGA GCCCAAATTT AGGACACTAG CAGAAGCATG 2940
 CATGAAGAGA TGAGTGTGTT CTAATAAGTC TCTGAAAGCC AGTGGCTTTA TGACTTTTAA 3000
 AAAAAATTAC AAACCAAGAA TTTTAAAG CAGAAGATGC TATTTGTGGG GGTTTTCTC 3060
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 AGTACACAAA TTTTCAATT TTTACATATT TTTAAATTAC TTATCTTCTA TCCAAGGAGG 3180
 TCTACAGAGA AATTAAGATC TGCTTATTT GTTACATTTG GGTATAATGA CAACAGCCAA 3240
 TTTATAGTGC AATAAAATGT AATTAATTCA AGTCCTTATT ATAGACTATT TGAAGCACA 3300
 CCTAATGGAA AATTGTAGAG ACCTTGCTTT AACATTATCT CCAAGTTAAT AAGTGTTCAT 3360
 GTGGTGCTTG GAACTGTGTT TTTTCTGAA CATCTAAAGT GTGTAGACTG CATTCTTGCT 3420
 ATTATTTTAT TCTTGTAAAT TGACCTTTTC ACTGTGCAAA GGGAGATTTC TAGCCAGGCA 3480
 TTGACTATTA CAATTCATT

Seq ID NO: 619 Protein sequence
 Protein Accession #: NP_004940.1

85 1 11 21 31 41 51
 MEAARPSGSW NGALCRLLLL TLAILIFASD ACKQVTLHVP SKLDAEKLVG RVNLKECFPTA 60

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 KKRHTKEKVL RRAKRRWAPI PCSMLNSLG PFPLFLQQVQ SDTAQNYTIY YSIRGPGVDQ 180
 EPRNLFFYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPLEPLPLI IKIEDENDNY 240
 PIFTEETYP TIFENCRVGT TVGQVCATDK DEPDTHMTRL KYSIIGQVPP SPTLFSMHPT 300
 TGVITTTSSQ LDRELIDKYQ LKIKVQDMQ QYFGLQTTST CIINIDVDND HLPFTFRTSY 360
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNFKIIVTDA KTNBGLVLCVV 420
 KPLNYEEKQQ MILQIGVNE APFSREASPR SAMSTATVTV NVEDQDEGFE CNPPIQTVRM 480
 KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAEI 540
 KNGIYNITVL ASDQGGRTCT GTLGIILQDV NDNSPFIKK TVIICKPTMS SAEIVAVDPD 600
 EPIHGPFFDF SLESSTSEVQ RMWRLKAIN TAARLSYQND PPFQSYVVP I TVDRRLGMSS 660
 VTSLDVTLCD CITENDCTHR VDPRIQGGGV QLKQWAILAI LLGIALLFICI LFTLVCGASG 720
 TSKQPKVIPD DLAQONLIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG 780
 QETIEMVKGG HQTSESCRG AHHHTLDSGR GGHTVEDNCR YTYSEHNSPT QPRLGEESIR 840
 GHTLIKN

Seq ID NO: 620 DNA sequence
 Nucleic Acid Accession #: NM_032545.1
 Coding sequence: 46..718

1 11 21 31 41 51
 AAACGTATCT TCAATGCACT AAGAGAAGGA GACTCTCAA CCAAAATGA CCTGGAGGCA 60
 CCATGTCAGG CTCTCTGTTA CGGTCACTTT GGCATTACAG ATCATCAATT TGGGAAACAG 120
 CTATCAAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGGTTG CCACTCAGAA 180
 GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCATTTC GGAGAGGTGA CTGGGAGCGC 240
 CGAGGGCTGG GGGCCGAGG AGCCGCTCCC CTACTCCCGG GCTTTCGGAG AGGGTGCCTG 300
 CGCGCGGCGG CGCTGCTGCA GGAACGGCGG TACTGCGTG CTGGGCGAGT TCTGCGTGTG 360
 CCGGCGCCAC TTCACCGGCC GCTACTGCGA GCATGACCA AGGCGCAGT AATGCGGCGC 420
 CCTGGAGCAC GGAGCCTGGA CCTCCGCGC CTGCCACCTC TGCAGGTGCA TCTTCGGGGC 480
 CCTGCACTGC CTCCTCTTCC AGACGCTGTA CCGCTGTGAC CCGAAAGACT TCCTGGCCTC 540
 CCACGCTCAC GGGCCGAGCG CGGGGGGCGG GCCCAGCCTG CTACTCTTGC TGCCCTGCGC 600
 ACTCTGACAC CGCTCTCTGC GCCCGGATGC GCCCGCGCAC CCTCGGTCCC TGGTCCCTTC 660
 CGTCTCTCAG CGGGAGCGGC GCCCTGCGG AAGGCCGGGA CTTGGGCATC GCCCTTAATT 720
 TTTATGTTG TAAATAATAG ATGTGTTAG TTTACCGTAA GCTGAAGCAC TGGGTGAATA 780
 TTTTATTGG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAATA AAAAAAATA 840
 AAAAAA

Seq ID NO: 621 Protein sequence
 Protein Accession #: NP_115934.1

1 11 21 31 41 51
 MTWRHHVRL FTVSLALQII NLGNSYOREK HNGGREEVTK VATQKHRQSP LNWTSSEHFE 60
 VTGSAEGWGP EEPLFYSRAF GEGASARPRC CRNGGTCTVLG SPCVCPAHFT GRYCEHDQRR 120
 SECGALEHGA WTLRACHLCR CTFGALHCLP LQTPDRCDPK DFLASHAHGP SAGGAPSLLL 180
 LLPCALHRL LRPDAPAPHR SLVPSVLQRE RRPCGRPGLG HRL

Seq ID NO: 622 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..390

1 11 21 31 41 51
 ATGAGGTTCA GTGTCTCAGG CATGAGGACC GACTACCCCA GGAGTGTGCT GGCTCCTGCT 60
 TATGTGTGAG TCTGTCTCCT CTCTCTGTGT CCAAGGGAAG TCATCGCTCC CGCTGGCTCA 120
 GAACCATGGC TGTGCCAGCC GGCACCCAGG TGTGGAGACA AGATCTACAA CCCCTGGAG 180
 CAGTGTCTGT ACAATGACGC CATCGTGTCC CTGAGCGAGA CCGGCCAATG TGGTCCCCC 240
 TGCACCTTCT GGCCTCTGCT TGAGCTCTGC TGTCTTGATT CCTTTGGCCT CACAAACGAT 300
 TTTGTGTGA AGCTGAAGGT TCAGGGTGTG AATTCACAGT GCCACTCATC TCCCATCTCC 360
 AGTAAATGTG AAAGAGGCCG GATATGTTAG

Seq ID NO: 623 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 MRFSVSGMRT DYPRSVLAPA YVSVCLLLLC PREVIAPAGS EPWLCQAPAP CGDKIYNFLE 60
 QCCYNDAIVS LSETRQCGPP CTFWPCFELC CLDSFGLTND FVVKLKVQGV NSQCHSSPIS 120
 SKCERGRIC

Seq ID NO: 624 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 51..1085

1 11 21 31 41 51
 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
 CCTCAGCCCC TCCTCTGAGA TTGCTGTGCC CCTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120
 TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
 ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TCGCCACAA CCTGCCCCAG AATCGTATTG 240
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
 TAGGAACCTA ACAAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGACA ATATACCCCA 360
 ATGCATCCCT GCTGATCCAG AACGTCACCC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC 480
 TGCCCAAGCC CTCTCATCTC AGCAACAAC CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
 CCTTCACCTG TGAACCTGAG GTTCAGAAAC CAACCTACCT GTGGTGGGTA AATGTCAGA 600
 GCCTCCCGGT CAGTCCCAAG CTGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA 660

	GCGTCAAAAG	GAACGATGCA	GGATCCTATG	AATGTGAAAT	ACAGAACCCA	GCGAGTGCCA	720
	ACCGCAGTGA	CCCAGTCACC	CTGAATGTCC	TCTATGGCCC	AGATGTCCCC	ACCATTTCCTC	780
	CCTCAAAAGG	CAATTACCGT	CCAGGGGAAA	ATCTGAACCT	CTCCTGCCAC	GCAGCCTCTA	840
5	ACCCACCTGC	ACAGACTCTC	TGGTTATCA	ATGGGACGTT	CCAGCAATCC	ACACAAGAGC	900
	TCTTTATCCC	CAACATCACT	GTGAATAATA	GCGGATCCTA	TATGTGCCAA	GCCCAATACT	960
	CAGCCACTGG	CCTCAATAGG	ACCACAGTCA	CGATGATCAC	AGTCTCTGGA	AGTGCTCTGT	1020
	TCCTCTCAGC	TGTGGCCACC	GTCGGCATCA	CGATTGGAGT	GCTGGCCAGG	GTGGCTCTGA	1080
	TATAGCAGCC	CTGGTGTATT	TTGATATTTT	CAGGAAGACT	GGCAGATTGG	ACCAGACCCT	1140
10	GAATTCTTCT	AGCTCCTCCA	ATCCCATTCT	ATCCCATTGGA	ACCACTAAAA	ACAAGGTCTG	1200
	CTCTGCTCCT	GAAGCCCTAT	ATGCTGGAGA	TGGACAACCT	AATGAAAAAT	TAAAGGGAAA	1260
	ACCCTCAGGC	CTGAGGTGTG	TGCCACTCAG	AGACTTCACC	TAACTAGAGA	CAGTCAAACT	1320
	GCAAACCATG	GTGAGAAATT	GACGACTTCA	CACATATGAC	AGCTTTTCCC	AAGATGTCAA	1380
	AACAAGACTC	CTCATCATGA	TAAGGCTCTT	ACCCCTTTT	AATTTGTCCT	TGCTTATGCC	1440
15	TGCTCTTTCT	GCTTGGCAGG	ATGATGCTGT	CATTAGTATT	TCACAAGAAG	TAGCTTCAGA	1500
	GGGTAACTTA	ACAGAGTGTC	AGATCTATCT	TGTCAATCCC	AACGTTTAC	ATAAAATAAG	1560
	AGATCCTTTA	GTGACCCAG	TGACTGACAT	TAGCAGCATC	TTTAAACACAG	CCGTGTGTTT	1620
	AAATGTACAG	TGTCCTTTT	CAGAGTTGGA	CTTCTAGACT	CACCTGTTCT	CACTCCCTGT	1680
	TTTAATTCAA	CCCAGCCATG	CAATGCCAAA	TAATAGAATT	GCTCCCTACC	AGCTGAACAG	1740
20	GGAGGAGTCT	GTGACGTTTC	TGACACTTGT	TGTTGAACAT	GGCTAAATAC	AATGGGTATC	1800
	GCTGAGACTA	AGTTGTAGAA	ATTAACAAAT	GTGCTGCTTG	GTTAAAAATG	CTACACTCAT	1860
	CTGACTCATT	CTTTATTTCT	TTTGTATCTT	GCCTAAGGTG	CGTAGTCCAA	1920	
	CTCTTGGTAT	TACCTCTCTA	ATAGTCATAC	TAGTAGTCAT	ACTCCCTGGT	GTAGTGTATT	1980
	CTCTAAAAGC	TTTAAATGTC	TGCTATGACG	CAGCCATCAA	ATAGTGAATG	GTCTCTCTTT	2040
25	GGCTGGAATT	ACAAAATGTC	GAGAAATGTG	TCATCAGGAG	AACATCATAA	CCCATGAAGG	2100
	ATAAAAGCCC	CAATGGTGG	TAACTGATAA	TAGCACTAAT	GCTTTAAGAT	TTGGTCACAC	2160
	TCTCACCTAG	GTGACGCGAT	TAGGCCAGTG	GTGCTAAATG	CTACATACTC	CAACTGAAAT	2220
	GTTAAGGAAG	AAGATAGATC	CAATTAATAA	AAATTAAATC	CAATTTAAAT	AAAAAAAGA	2280
	ACACAGGAGA	TTCAGTCTA	CTTGAGTTAG	CATAATACAG	AAGTCCCTTC	TACTTTAACT	2340
30	TTTACAAAAA	AGTAACCTGA	ACTAATCTGA	TGTTAAACCA	TGTATTATAT	TCTGTGGTTC	2400
	TGTTTCTCTG	TTCCAATTTG	ACAAAACCCA	CTGTCTCTGT	ATTGTATTGC	CCAGGGGGAG	2460
	CTATCACTGT	ACTTGTAGAG	TGGTGCTGCT	TTAATTCATA	AATCACAAT	AAAAGCCAA	2520
	TAGCTCTATA	ACT					

Seq ID NO: 625 Protein sequence
Protein Accession #: AA59907.1

	1	11	21	31	41	51	
40	MGPPSAPPCR	LHVPWKEVLL	TASLLTFWNP	PTTAKLTIES	TPFNVAEGKE	VLLLAHNLPO	60
	NRIGYSWYKG	ERVDGNLIV	GVVIGTQQAT	PGPAYSGRET	IYPNASLLIQ	NVTQNDTGFY	120
	TLQVIKSDLV	NEEATLQFHV	YPFLPKPSIS	SNNSPVDEK	DAVAFTCEPE	VQNTTYLWV	180
	NGQSLPVSFR	LQLSNGNMTL	TLLSVKRNDA	GSYECEIQNP	ASANRSDPVT	LNVLVGPDPV	240
	TISPSKANYR	PGENLNLSC	AASNPPAQYS	WFINGTFQQS	TQELFIPNIT	VNNSGSYMCQ	300
45	AHNSATGLNR	TTVTMITVSG	SAPVLSAVAT	VGITIGVLAR	VALI		

Seq ID NO: 626 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 1355..1657

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50	GGAGCTCAAG	CTCCTCTACA	AAGAGGTGGA	CAGAGAAGAC	AGCAGAGACC	ATGGGACCCC	60
	CCTCAGCCCC	TCCCTGTCAG	TGCAATGTCC	CCTGGAAGGA	GGTCTGCTC	ACAGCCTCAG	120
55	TTCTAACCTT	CTGGAACCCA	CCCACCACTG	CCAAGCTCAC	TATTGAATCC	ACGCCATTCA	180
	ATGTGCGAGA	GGGGAAGGAG	GTTCTTCTAC	TGCGCCCAAA	CCTGCCCCAG	AATCGTATTG	240
	GTTACAGCTG	GTACAAAGGC	GAAAGAGTGG	ATGGCAACAG	TCTAATTGTA	GGATATGTAA	300
	TAGGAACCTA	ACAAGCTACC	CCAGGGCCCC	CATACAGTGG	TGAGAGAGCA	ATATACCCCA	360
	ATGCATCCCT	GTCGATCCAG	AACGTCAACC	AGAATGACAC	AGGATTCTAT	ACCCCTACAAG	420
60	TCATAAAGTC	AGATCTTGTG	AATGAGAAG	CAACCGGACA	GTCCATGTA	TACCCGGAGC	480
	TGCCCAAGCC	CTCCATCTCC	AGCAACAAC	CCAACCCCGT	GGAGGACAAG	GATGCTGTGG	540
	CCTTCACCTG	TGAACCTGAG	GTTCAAGACA	CAACCTACCT	GTGGTGGGTA	AATGGTCAGA	600
	GCCTCCCGGT	CAGTCCCAGG	CTGCAGCTGT	CCAATGGCAA	CATGACCCCT	ACTCTACTCA	660
	GCGTCAAAAG	GAACGATGCA	GGATCCTATG	AATGTGAAAT	ACAGAACCCA	GCGAGTGCCA	720
65	ACCGCAGTGA	CCCAGTCACC	CTGAATGTCC	TCTATGGCCC	AGATGTCCCC	ACCATTTCCTC	780
	CCTCAAAAGC	CAATTACCGT	CCAGGGGAAA	ATCTGAACCT	CTCCTGCCAC	GCAGCCTCTA	840
	ACCCACCTGC	ACAGTACTCT	TGGTTTATCA	ATGGGACGTT	CCAGCAATCC	ACACAAGAGC	900
	TCTTTATCCC	CAACATCACT	GTGAATAATA	GCGGATCCTA	TATGTGCCAA	GCCCAATACT	960
	CAGCCACTGG	CCTCAATAGG	ACCACAGTCA	CGATGATCAC	AGTCTCTGGA	AGTGCTCTGT	1020
70	TCCTCTCAGC	TGTGGCCACC	GTCGGCATCA	CGATTGGAGT	GCTGGCCAGG	GTGGCTCTGA	1080
	TATAGCAGCC	CTGGTGTATT	TTGATATTTT	CAGGAAGACT	GGCAGATTGG	ACCAGACCCT	1140
	GAATTCTTCT	AGCTCCTCCA	ATCCCATTCT	ATCCCATTGGA	ACCACTAAAA	ACAAGGTCTG	1200
	CTCTGCTCCT	GAAGCCCTAT	ATGCTGGAGA	TGGACAACCT	AATGAAAAAT	TAAAGGGAAA	1260
	ACCCTCAGGC	CTGAGGTGTG	TGCCACTCAG	AGACTTCACC	TAACTAGAGA	CAGTCAAACT	1320
75	GCAAACCATG	CTGAGAAATT	GACGACTTCA	CACATATGAC	AGCTTTTCCC	AAGATGTCAA	1380
	AACAAGACTC	CTCATCATGA	TAAGGCTCTT	ACCCCTTTT	AATTTGTCCT	TGCTTATGCC	1440
	TGCTCTTTCT	GCTTGGCAGG	ATGATGCTGT	CATTAGTATT	TCACAAGAAG	TAGCTTCAGA	1500
	GGGTAACTTA	ACAGAGTGTC	AGATCTATCT	TGTCAATCCC	AACGTTTAC	ATAAAATAAG	1560
	AGATCCTTTA	GTGACCCAG	TGACTGACAT	TAGCAGCATC	TTTAAACACAG	CCGTGTGTTT	1620
80	AAATGTACAG	TGTCCTTTT	CAGAGTTGGA	CTTCTAGACT	CACCTGTTCT	CACTCCCTGT	1680
	TTTAATTCAA	CCCAGCCATG	CAATGCCAAA	TAATAGAATT	GCTCCCTACC	AGCTGAACAG	1740
	GGAGGAGTCT	GTGCACTTTC	TGACACTTGT	TGTTGAACAT	GGCTAAATAC	AATGGGTATC	1800
	GCTGAGACTA	AGTTGTAGAA	ATTAACAAAT	GTGCTGCTTG	GTTAAAAATG	CTACACTCAT	1860
85	CTGACTCATT	CTTTATTTCT	TTTGTATCTT	GCCTAAGGTG	CGTAGTCCAA	1920	
	CTCTTGGTAT	TACCTCTCTA	ATAGTCATAC	TAGTAGTCAT	ACTCCCTGGT	GTAGTGTATT	1980
	CTCTAAAAGC	TTTAAATGTC	TGCTATGACG	CAGCCATCAA	ATAGTGAATG	GTCTCTCTTT	2040
	GGCTGGAATT	ACAAAACCTCA	GAGAAATGTG	TCATCAGGAG	AACATCATAA	CCCATGAAGG	2100
	ATAAAAGCCC	CAATGGTGG	TAACTGATAA	TAGCACTAAT	GCTTTAAGAT	TTGGTCACAC	2160

WO 02/086443

PCT/US02/12476

TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAA CAATTAAAAA AAAAAAAGA 2280
ACACAGGAGA TTCCAGTCTA CTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT 2340
TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATAT TCTGTGGTTC 2400
TGTTCCTTGT TTCCAATTTG ACAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
CTATCACTGT ACTGTAGAG TGGTGTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
TAGCTCTATA ACT

Seq ID NO: 627 Protein sequence
Protein Accession #: AAA59908.1

1 11 21 31 41 51
MDSFSQDVKT RLLIMIRLLP PPNLSLLMPA SFAWQDDAVI SISQEVASEG NLTECQIYLV 60
NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELDI

Seq ID NO: 628 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 2370..2501

1 11 21 31 41 51
GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
CCTCAGCCCC TCCTCTGAGA TTGCATGTCC CCTGGAAGGA GGTCTGTCTC ACAGCTCAC 120
TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TCGCCACAA CCTGCCCCAG AATCGTATTG 240
GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
TAGGAACCTA ACAAGCTACC CCAGGGCCCC CATAAGTGG TCGAGAGACA ATATACCCCA 360
ATGCATCCCT GCTGATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACAGA 420
TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCGGAGGC 480
TGCCCAAGGC CTCCTATCTC AGCAACAAC CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
CCTTCACCTG TGAACCTGAG GTTCAGAAAC CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA 660
GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCAC 720
ACCGCAGTGA CCCAGTCAAC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCTC 780
CCTCAAAAGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840
ACCCACCTGC ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900
TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCATAACT 960
CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGTCTCTG 1020
TCCTCTCAGC TGTGGCCACC GTCCGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
TATAGCAGCC CTGGTGTATT TCGATATATT CAGGAAGACT GGCAGATTGG ACCAGACCCT 1140
GAATTCCTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
CTCTGTCTCT GAAGCCCTAT ATGCTGGAGA TGGACAACCT AATGAAAATT TAAAGGGAAA 1260
ACCCCTCAGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAAC 1320
GCAAAACCTG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380
AACAAGACTC CTCTATCTGA TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440
TGCCCTCTTC GCTTGGCAGG AGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500
GGGTAACCTA ACAGATGTG AGATCTATCT TGTCAATCCC AACGTTTAC ATAAAATAAG 1560
AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTAAACACAG CCGTGTGTTC 1620
AAATGTACAG TGGTCTCTTT CAGAGTTGGA CTCTTAGACT CACCTGTCTC CACTCCCTGT 1680
TTTAATTCAA CCCAGTCTGA CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740
GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGGAACAT GGCTAAATAC AATGGGTATC 1800
GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860
CTGACTCATT CTTTATCTTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920
CTCTTGGTAT TACCTCTCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
CTCTAAAAGC TTTAATGTCT TGCAATGACG CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
GGCTGGAATT ACAAACTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
ATAAAGGCC ATCAATGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160
TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAA CAATTAAAAA AAAAAAAGA 2280
ACACAGGAGA TTCCAGTCTA CTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT 2340
TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATAT TCTGTGGTTC 2400
TGTTCCTTGT TTCCAATTTG ACAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
CTATCACTGT ACTGTAGAG TGGTGTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
TAGCTCTATA ACT

Seq ID NO: 629 Protein sequence
Protein Accession #: AAA59909.1

1 11 21 31 41 51
MLTNVVISVV LPPCSNLTKP TVLVLYCPGG AITVLVEWCC FNS

Seq ID NO: 630 DNA sequence
Nucleic Acid Accession #: NM_016639.1
Coding sequence: 40..429

1 11 21 31 41 51
GCGGCGGGCG CAGACAGCGG CGGGCGCAGG ACGTGCACTA TGGCTCGGGG CTCGCTGCBC 60
CGGTTGTCTG GGTCTCTCGT GCTGGGGCTC TGGCTGGCGT TGGCTGCGTC CGTGGCCGGG 120
GAGCAAGCGC CAGGACCCGC CCCCTGCTCC CGCGGACGCT CCTGGAGCGC GGACCTGGAC 180
AAGTGCATGC ACTGCGCGTC TTGCAGGGCG CGACCGCACA GCGACTTCTG CCTGGGCTGC 240
GCTGCAGCAC CCGCTGCCCC CTTCGGGCTG CTTTGGCCCA TCCTTGGGGG CGCTCTGAGC 300
CTGACCTTCG TGCTGGGGCT GCTTTCTGCG TTTTGGTCTG GGAGACGATG CCGCAGGAGA 360
GAGAAGTTCA CCACCCCAT AGAGGAGACC GCGCGAGAGG GCTGCCACGC TGTGGCGCTG 420

ATCCAGTGAC AATGTGCCCC CTGCCAGCCG GGGCTCGCCC ACTCATCATT CATTATCCCA 480
 TTCTAGAGCC AGTCTCTGCC TCCCAGACGC GCGGGGAGCC AAGCTCCTCC AACCAACAGG 540
 GGGGTGGGGG GCGGTGAATC ACCTCTGAGG CCTGGGCCCA GGGTTCAGGG GAACCTTCCA 600
 AGGTGTCTGG TTGCCCTGCC TCTGGCTCCA GAACAGAAAG GGAGCCTCAC GCTGGCTCAC 660
 ACAAACAGC TGACACTGAC TAAGGAACCTG CAGCATTTGC ACAGGGGAGG GGGGTGCCCT 720
 CCTTCTTAG GACCTGGGGG CCAGGCTGAC TTGGGGGGCA GACTTGACAC TAGGCCCCAC 780
 TCACTCAGAT GTCCTGAAAT TCCACCACG GGGTCACCT GGGGGGTTAG GGACCTATTT 840
 TTAACACTAG GGGCTGGCCC ACTAGGAGGG CTGGCCCTAA GATACAGACC CCCCCAATC 900
 CCCAAAGCGG GGAGGAGATA TTTATTTTGG GGAGAGTTTG GAGGGGAGGG AGAATTTATT 960
 AATAAAGAA TCTTTAATTT TAAAAAATA AAAAAAAA

Seq ID NO: 631 Protein sequence
Protein Accession #: NP_057723.1

1 11 21 31 41 51
 MARGSLRRLL RLLVLGLWLA LRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCRARPH 60
 SDFCLGCAAA PPAPFRLLP ILGGALSLTF VLGLLSGLFV WRRCRREKRF TPIETGTGE 120
 GCPAVALIQ

Seq ID NO: 632 DNA sequence
Nucleic Acid Accession #: NM_003816.1
Coding sequence: 79..2538

1 11 21 31 41 51
 CGGCAGGGTT GGAATATGAT GGAAGAGGCG GAGGTGGAGG CGACCGAGTG CTGAGAGGAA 60
 CCTGCGGAAT CGGCCGAGAT GGGGTCTGGC GCGCGCTTTC CCTCGGGGAC CCTTCGTGTC 120
 CGGTGGTTGC TGTGTCTTGG CCTGGTGGCG CCAGTCTCTCG GTGCGGCGCG GCCAGGCTTT 180
 CAACAGACCT CACATCTTTC TTCTTATGAA ATTATAACTC CTGGGAGATT AACTAGAGAA 240
 AGAAGAGAAG CCCCTAGGCC CTATTCAAAA CAAGTATCTT ATGTTATTCA GGCTGAAGGA 300
 AAAGAGCATA TTATTCATT GGAAAGGAAC AAAGACCTTT TGCTGAAGA TTTGTGGTT 360
 TATACCTACA ACAAGGAAGG GACTTTAATC ACTGACCATC CCAATATACA GAATCATTTG 420
 CATTATCGGG GTATGTGGGA GGGAGTTTCAT AATTCATCCA TTGCTCTTAG CGACTGTTT 480
 GGACTCAGAG GTATGTCTGCA TTTAGAGAAT GCGAGTTATG GGATTGAACC CCTGCAGAAC 540
 AGCTCTCATT TTGAGCACAT CATTATTCGA ATGGATGATG TCTACAAAGA GCCTCTGAAA 600
 TGTGGAGTTT CCAACAAGGA TATAGAGAAA GAAACTGCAA AGGATGAAGA GGAAGAGCCT 660
 CCCAGCATGA CTCAGCTACT TCGAAGAAGA AGAGCTGTCT TGCCACAGAC CCGGTATGTG 720
 GAGCTGTTCA TTGTCTGAGA CAAGGAAAGG TATGACATGA TGGGAAGAAA TCAGACTGCT 780
 GTGAGAGAAG AGATGATTCT CCTGGCAAAC TACTTGGATA GTATGTATAT TATGTTAAAT 840
 ATTCGAATTG TGCTAGTTGG ACTGGAGATT TGGACCAATG GAAACCTGAT CAACATAGTT 900
 GGGGTGTCTG GTGATGTGCT GGGGAACTTC GTGCAGTGGC GGGAAAGATT TCTTATCACA 960
 CGTCGGAGAC ATGACAGTGC ACAGCTAGTT CTAAGAAGAG GTTTTGGTGG AACTGCAGGA 1020
 ATGGCATTGG TGGGAACAGT GTGTTCAAGG AGCCACGCGAG GCGGGATTAA TGTGTTTGA 1080
 CAAATCACTG TGGAGACATT TGCTTCCATT GTTGCTCATG AATTGGGTCA TAATCTTGA 1140
 ATGAATCAG ATGATGGGAG AGATTGTTCC TGTGGAGCAA AGAGCTGCAT CATGAATTCA 1200
 GGAGCATCGG GTTCCAGAAA CTTTAGCAGT TGCAGTCAG AGGACTTGA GAAGTTAACT 1260
 TTAATAAAG GAGGAACTG CCTTCTTAAT ATTCCAAGC CTGATGAAGC CTATAGTGCT 1320
 CCTCTCTGTG GTAATAAGTT GGTGGACGCT GGGGAAGAGT GTGACTGTGG TACTCCAAAG 1380
 GAATGTGAAT TGGACCTCTG CTGCGAAGGA AGTACCTGTA AGCTTAAATC ATTTGCTGAG 1440
 TGTGCATATG GTGACTGTGG TAAAGACTGT CGGTTCCTTC CAGGAGGTAC TTTATGCCGA 1500
 GGAAAAACCA GTGAGTGTGA TGTTCAGAG TACTGCAATG GTTCTTCTCA GTTCTGTGAG 1560
 CCAGATGTTT TTATTCAGAA TGGATATCCT TGCCAGAATA ACAAGCCTTA TTGCTACAAC 1620
 GGCATGTGCC AGATTATGTA TGCTCAATGT CAAGTCATCT TTGGCTCAAA AGCCAAGGCT 1680
 GCGCCCAAG ATGTTTTCAT TGAAGTGAAT TCTAAAGGTG ACAGATTGG CAATTGTGGT 1740
 TTCTCTGGCA ATGAATACAA GAAAGTGTCC ACTGGGAATG CTTTGTGTGG AAAGCTTCAG 1800
 TGTGAGAATG TACAAGAGAT ACCTGTATTT GGAATTGTGC CTGCTATTAT TCAAACGCCCT 1860
 AGTCAGAGCA CCAATGTTG GGGTGTGAT TTCCAGCTAG GATCAGATGT TCCAGATCCT 1920
 GGGATGTTA ACGAAGGCAC AAAATGTGGT GCTGGAAGA TCTGTAGAAA CTTCCAGTGT 1980
 GTAGATGCTT CTGTCTGTGA TTATGACTGT GATGTTTACA AAAAGTGTCA TGGACATGGG 2040
 GTATGTAATA GCAATAAGAA TTGTCACTGT GAAATGGCT GGGCTCCCCC AAATTGTGAG 2100
 ACTAAAGGAT ACGGAGGAAG TGTGGACAGT GGACCTACAT ACAATGAAAT GAATACTGCA 2160
 TTGAGGGACG GACTTCTGGT CTCTTCTTC CTAATTGTTT CCCTTATTGT CTGTGCTATT 2220
 TTTAICTTCA TCAAGAGGGA TCAACTGTGG AGAAGCTACT TCAGAAAGAA GAGATCACA 2280
 ACATATGAGT CAGATGGCAA AAATCAAGCA AACCCTTCTA GACAGCCGGG GAGTGTTCCT 2340
 CGACATGTTT CTCCAGTGAC ACCCTCCAGA GAAAGTCCCTA TATATGCAAA CAGATTGCA 2400
 GTACCAACCT ATGCAGCCAA GCAACCTCAG CAGTTCCCAT CAAGGCCACC TCCACCACAA 2460
 CGAAAGTAT CATCTCAGGG AAACCTTAAT CCTGCCCGTC CTGCTCCTGC ACCTCCTTTA 2520
 TATAGTTCCC TCACTTGATT TTTTAACTT TCTTTTGTCA AATGTCTTCA GGGAACTGAG 2580
 CTAATACCTT TTTTCTTCT TGATGTTTTC TTGAAAAGCC TTCTGTGTGC AACTATGAAT 2640
 GAAAAAATAA CACCACAAAA CAGACTTCAC TAACACAGAA AACACAGAAAC TGAGTGTGAG 2700
 AGTTGTGAAA TACAAGGAAA TGCAGTAAAG CCAGGGAATT TACAATAACA TTCCGTTTTC 2760
 CATCATTGAA TAAGTCTTAT TCAGTCATCG GTGAGGTTAA TGCACTAATC ATGGATTTTT 2820
 TGAACATGTT ATTGCAGTGA TTCTCAAAT AACTGTATTG GTGTAAGATT TTGTCTATTA 2880
 AGTGTTTAAG TGTATTCTG AATTTTCTAC CTTAGTTATC ATTAATGTAG TTCCTCATTG 2940
 AACATGTGAT AATCTAATAC CTGTGAAAA GACTAATCA GCTGCCAATA ATATCTAATA 3000
 TTTTTCATCA TGACAGCAAT AATAATCATC ATACTCTAGA ATCTTGTCTG TCACTCATA 3060
 CATGAATAAG CAAATATTGT CTTCAAAAAGA ATGCACAAGA ACCACAATTA AGATGTCATA 3120
 TTATTTTGAA AGTACAAAAT ATACTAAAAG AGTGTGTGTG TATTCACGCA GTTACTCGCT 3180
 TCCATTTTAA TGACCTTTCA ACTATAGGTA ATAACCTCTA GAGAAATTAA TTTAATATTA 3240
 GAATTTCTAT TATGAATCAT GTGAAAGCAT GACATTCGTT CACAATAGCA CTATTTTAAA 3300
 TAAATATATA GCTTTAAGGT ACGAAGTATT TAATAGATCT AATCAATAT GTTGATTCAT 3360
 GGCTATAATA AAGCAGGAGC AATTATAAAA TCTTCAATCA ATTGAACCTT TACAAAACCA 3420
 CTTGAGAATT TCATGAGCAC TTTAAATCT GAACTTCAA AGCTTGCTAT TAAATCATTT 3480
 AGAATGTTTA CATTTACTAA GGTGTGCTCG GTCATGTAAA ATATTAGACA CTAATATTTT 3540
 CATAGAAATT AGGCTGGAGA AAGAAGGAAG AAATGGTTTT CTTAAATACC TACAAAAAG 3600
 TTACTGTGGT ATCTATGAGT TATCATCTTA GCTGTGTAA AAATGAATTT TTACTATGGC 3660

AGATATGGTA TGGATCGTAA AATTTTAAGC ACTAAAAATT TTTTCATAAC CTTTCATAAT 3720
 AAAGTTTAAT AATAGGTTTA TTAAGTGAAT TTCATTAGTT TTTTAAAGT GTTTTGGTT 3780
 TGTGTATATA TACATATACA AATACAACAT TTACAATAAA TAAATACTT GAAATCTCA 3840
 AAAAAAAAAA AAAAAAAAAA AAAAA

Seq ID NO: 633 Protein sequence
 Protein Accession #: NP_003807.1

1 11 21 31 41 51
 MSGARPPSG TLRVRWLLLL GLVGPVLGAA RFGFOQTSHL SSYEIITPWR LTRERREAPR 60
 PYSKQVSIVI QAEGKEHIIH LERNKDLLPE DFVVYTYNKE GTLITDHPNI QNHCHYRGYV 120
 EGVHNSIAL SDGFLRGLL HLENASYGIE PLQNSSHFEH IYRMDVYK EPLKCGVSNK 180
 DIEKETAIDE EEEPPSMTQL LRRRAVLFPQ TRYVELPIV DKERYDMMGR NQTAVREMI 240
 LLANYLDSMY IMLNIRIVLV GLEIWTGNL INIVGGAGDV LGNFVQWREK FLITRRRHDS 300
 AQLVLKKGFG GTAGMARFVGT VCSRSAGGI NVFGQITVET FASIVAEHLG HNLGMNHDDG 360
 RDCSCGAKSC IMNSGASGSR NFSSCSAEDF EKLTNLKGGN CLLNPKPDE AYSAPSCGNK 420
 LVDAGEECDC GTPKCELDLP CCEGSTCKLK SFAECAYGDC CKDCRFLPGG TLRCRKTSEC 480
 DVPEYCNSSS QFCOPDVFIQ NGYPCQNNKA YCYNGMCQYY DAQCQVIFGS KAKAAPKDFC 540
 IEVNSGDRF GNCGFSNNEY KKCATGNALC GKLCQENVOE IPVFGIVPAI IQTPSRGTKC 600
 WGVDFQLGSD VPDPGMVNEG TKCGAGKICR NFQCVDAVL NYDCDVQKKC HGHGVCNSNK 660
 NCHCENGWAP PNCETKGYGG SVDSGPTYNE MNTALRDGLL VFFFLIVPLI VCAIFIFIKR 720
 DQLWRSYFRK KRSQTYESDG KNQANPSRQP GSVPRHVSFV TTPREVPIYA NFAVPTYAA 780
 KQPQFPSPRP PPPQPKVSSQ GNLIAPRAP APPLYSSLT

Seq ID NO: 634 DNA sequence
 Nucleic Acid Accession #: NM_002091.1
 Coding sequence: 56..503

1 11 21 31 41 51
 AGTCTCTGCT CTTCCAGGCC TCTCCGGCGC GCTCCAAGGG CTTCCTGTCG GGACCATGCG 60
 CGGCAGTGAG CTCCTGCTGG TCTGCTGGC GCTGGTCTCT TGCTAGCGC CCCGGGGGCG 120
 AGCGGTCCCG CTGCTGCTGG GCGGAGGGAC CGTGCTGACC AAGATGTACC CGCGGGGCAA 180
 CCCTGCGGCG GTGCGGCACT TAATGGGGAA AAAGAGCACA GGGGAGTCTT CTTCTGTTTC 240
 TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG 300
 GAATTTGCTG GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCAACCCAA 360
 GGCCTTGGGC AATCAGCAGC CTTCTGTTGA TACAGAGGAT AGCAGCAACT TCAAAGATGT 420
 AGGTTCAAAA GGCAGAGTTG GTAGACTCTC TGCTCCAGTG TCTCAACGTG AAGGAAGGAA 480
 CCCCAGCTG AACCAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAAACCCC 540
 TAAGAGACTG AGTTCTGCAA GCATCAGTTC TACGATCATC CAACAAGATT TCCTTGTCGA 600
 AAATATTGTA CTATTCTGTA TCTTTCATCC TTGACTAAAT TCGTGATTTC CAAGCAGCAT 660
 CTTCTGGTTT AAACCTGTTT GCTGTGAACA ATTGTGAAAC AGAGTCTTCC AATTAATGCT 720
 TTTTATATC TAGGCTACCT GTTGTGTTAGA TTCAAGGCCC CGAGCTGTGA CCATTCACAA 780
 TAAAGCTTA AACACAT

Seq ID NO: 635 Protein sequence
 Protein Accession #: NP_002082.1

1 11 21 31 41 51
 MRGSELPLVL LALVLCIAPR GRAVPLPAGG GTVLTMYPR GNHWAVGHLM GKKTGESSS 60
 VSERGSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPPQ PKALGNQPPS WDSEDSBNFK 120
 DVSGSKGVGR LSAPGSQREG RNPQLAQQ

Seq ID NO: 636 DNA sequence
 Nucleic Acid Accession #: NM_016522.1
 Coding sequence: 265..1299

1 11 21 31 41 51
 GCGGAAGCAG CGAGGAGGGA GCCCCTTTG GCCGTCTTCC GTGGAACCGG TTTTCCGAGG 60
 CTGGCAAAAG CCGAGGCTGG ATTTGGGGGA GGAATATTAG ACTCGGAGGA GTCTGCGCGC 120
 TTTTCTCTC CCCGCGCTC CCGGTGCGCG CGGGTTTACC GCTCAGTCCC CGCGCTCGCT 180
 CGGCACCCCA CCCACTTCCT GTGCTGCGCC GGGGGGCGTG TGCCGTGCGG CTGCGGAGT 240
 TCGGGGAAGT TGTGGCTGTC GAGAATGGGG GTCTGTGGGT ACCTGTTCCT GCCCTGGAAG 300
 TGCCCTCGTG TCGTGTCTCT CAGGCTGCTG TTCTTTGTAC CCACAGAGAT GCCCGTGCBC 360
 AGCGGAGATG CCACCTTCCC CAAAGCTATG GACAACGTGA CGGTCCGGCA GGGGGAGAGC 420
 GCCACCTTCA GGTGCACTAT TGACAACCGG GTCACCCGGG TGGCTGTGCT AAACCGCAGC 480
 ACCATCTCT ATGCTGGGAA TGACAAGTGG TGCTGTGATC CTGCGTGTGT CCTTCTGAGC 540
 AACACCCAAA CGCAGTACAG CATCGAGATC CAGAACGTGG ATGTGTATGA CGAGGGCCCT 600
 TACACCTGCT CGGTGCAGAC AGACAACACC CAAAGACCT CTAGGTTCCA CCTCATTTGT 660
 CAAGTATCTC CCAAAATTGT AGAGATTCT TCAGATATCT CCATTAATGA AGGGAACAAT 720
 ATTAGCCTCA CCGTCAATAG AACTGGTAGA CCAGAGCCTA CGGTACTTGT GAGACACATC 780
 TCTCCCAAG CGGTGGCTT TGTGAGTGA GACGAATACT TGGAAATTCA GGCATCACC 840
 CGGGAACAGT CAGGGGACTA CGAGTGCAGT GCCTCCAATG ACGTGGCCGC GCCCGTGGTA 900
 CGGAGAGTAA AGGTCAACGT GAACATATCA CCATACATTT CAGAAAGCAA GGGTACAGGT 960
 GTCCCGTGG GACAAAAGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA 1020
 TTCCAGTGGT ACAAGGATGA CAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGAA 1080
 AACAGACCTT TCCTCTCAAA ACTATCTTC TTCAATGTCT CTGAACATGA CTATGGGAAC 1140
 TACACTTGGC TGGCCTCCAA CAAGCTGGGC CACACCAATG CCAGCATCAT GCTATTTGGT 1200
 CCAGCGCGCG TCAGCGAGGT GAGCAACCGC ACGTGCAGGA GGGCAGGCTG CGTCTGGCTG 1260
 CTGCTCTCTC TGTCTTTCGA CTTGCTTCTC AAAATTTGAT GTGAGTGCCA CTTCCCCACC 1320
 CGGGAAGGCG TGCGCGCACC ACCACACCA ACACAACAGC AATGGCAACA CCGACAGCAA 1380
 CCAATCAGAT ATATACAAAT GAAATTAGAA GAAACACAGC CTCATGGGAC AGAAATTTGA 1440
 GGGAGGGGAA CAAAGAATAC TTTGGGGGGA AAAGAGTTTT AAAAAAGAAA TTGAAATTTG 1500
 CCTTGAGAT ATTTAGGTAC AATGGAGTTT TCTTTTCCCA AACGGGAAGA ACACAGCACA 1560

CCGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGGCAAG 1620
 GGCTCAGCCT CTCTGCCAC AGACTGCCCC CACGTGGAAC ATTCTGGAGC TGGCCATCCC 1680
 AAATTCATC AGTCCATAGA GACGAACAGA ATGAGACCTT CCGGCCCAAG CGTGGCGCTT 1740
 CCGGCCAAG CGTGGCGCTG CGGGCACTTT GGTAGACTGT GCCACCACGG CGTGTGTTGT 1800
 GAAACGTGAA ATAAAAAGAG CAAAAAATAA AAAAAAATAA

Seq ID NO: 637 Protein sequence
 Protein Accession #: NP_057606.1

1 11 21 31 41 51
 MGVCGLFLP WKCLVVVSLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID 60
 NRVTRVAVLN RSTILYAGND KWCLDPRLVL LSNTQTQYSI EIQNVVDVDE GPYTCVSVQTD 120
 NHPKTSRVHL IVQVSPKIVE ISSDISINEG NNISLTCTAT GRPEPTVTWR HISP KAVGFV 180
 SEDEYLEIQG ITRQSGDYE CSASNDVAAP VVRRVKVTVN YPPYISEAKG TGVVPVQKGT 240
 LQCEASAVPS AEFQNYKDDK RLIEGKKGVK VNRPFLLSKL IFFNVSEHDY GNYTCVASNK 300
 LGHTNASIML FPGAVSEVS NGTSRRAGCV WLLPLLVLHL LLKP

Seq ID NO: 638 DNA sequence
 Nucleic Acid Accession #: NM_012261.1
 Coding sequence: 203..1045

1 11 21 31 41 51
 GATTGTCTCT GCCAGCAGCT GTCGGTGCCG CGCTCGACAC CGAGTCCTAG CTAGGCGCTC 60
 ACAGAAATAG CGCTCCCTCC CTCCCTCTTC TCTGTCCGCC GCCTCTCGCT CACCCCGGCC 120
 CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCGGC CTCTGCAGCA GCACAGCCGG 180
 CCTCATTCGG GGCACCTGCA GTATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGACAG 240
 ACTTCGAGTT TCTCTGATGT TGTTCATATC AATGGCTCAA ATCATGGCA AACAAAGAGT 300
 GGAAATCTCT TCAGGCTCTT CCACTAACCC TGAAAAAGAT ATATTGTGG TCGCGGAAAA 360
 TGGGACGACG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG 420
 GGCCAGCAAC TACGTAGATC TGATCACAGA ACAGGCCGAT ATCGCATTGA CCGGGGAGAG 480
 TGAGGTGAAG GGCCTCTGTG GCCACAGCCA GTCGGAGCTG CAAGTGTCTT GGGTGGATCG 540
 CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAAGCCAC AACATGTCCA AGGGACCTGA 600
 GGCGACTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT 660
 CAAAGACGCA GTCACTGCTG GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCCTTGGT 720
 CACCCCGGCT GGGAGTCTCT ATGAGTGTCA AGCTCAACAA ACCATTTCAC TGGCCTCTAG 780
 TGATCCGCGA AAGACGGTCA CCATGATCCT GTCTCGGCTC CACATCCAAC CTTTGGACAT 840
 TATCTCAGAT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT 900
 GGAAGAAACC TTGCCCCGTA TTTTGGGGCT CATCTTGGGC CTCTCATCA TGGTAACACT 960
 CGCGATTAC CACGTCCACC ACAAAATGAC TGCCAAACAG GTGCAGATCC CTCGGGACAG 1020
 ATCCCACTAT AAGCAGATGG GCTAGAGGCC GTTAGGCAGG CACCCCTAT TCCTGCTCCC 1080
 CCAACTGGAT CAGGTAGAAC AACAAAGCA CTTTCCATC TTGTACACGA GATACACCA 1140
 CATAGCTACA ATCAAAACAG CTTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA 1200
 AACCCACGGA AGGGGGAGAC TCTTTCGGAT TTGTAGGGTG AAATGGCAAT TATTCTCTCC 1260
 ATGCTGGGGA GGAAGGAGAG AGGGTCTCAG ACAGCTTTGC TGCTCATGGT GGCTTGGCTT 1320
 TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCAAA AGTTTAGGGA 1380
 TTGAAACAT GCTTCTTGA GAGGAAACC CCTTTAGGTT CAGAAGAATA TGGGGTGCTT 1440
 TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAACC 1500
 TCATGCTCCC TCGAGCAAGA CCCTGAAAG TGATTATGTC TTCTGGCTGG CATTCTGCAT 1560
 GTTTAGTAGT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGAGT GCAGCACCAG 1620
 AAAACGACTA ATGTAATCAT GCAGAGTTGT TTGACTTCT TCCTGTGCCA GGTCCAAGTC 1680
 GGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AAATGAATA AAACACACTA 1740
 TTCTCTGGC

Seq ID NO: 639 Protein sequence
 Protein Accession #: NP_036193.1

1 11 21 31 41 51
 MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDFVW RENGTTCLMA 60
 EFAAKFIVFY DVWASNYVDL ITEQADIALT RGAEVKGRCG HSQSELQVFW VDRAYALKML 120
 FVKESHNSMK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHLS ALVTPAGKSY 180
 ECQAQQTISL ASSDPQRTVT MILSAVHIQF FDIISDFVFS ESHKCPVDER EQLEETLPLI 240
 LGLILGLVIM VTLAIYVHH KMTANQVQIP RDRSQYKHM

Seq ID NO: 640 DNA sequence
 Nucleic Acid Accession #: NM_002993.1
 Coding sequence: 64..408

1 11 21 31 41 51
 GGCACGAGCC AGTCTCCGCG CCTCCACCCA GCTCAGGAAC CCGCGAACCC TCTCTTGACC 60
 ACTATGAGCC TCCGCTCCAG CCGCGCGGCC CGTGTCCCGG GCTCTTCGGG CTCCTTGTGC 120
 GCGCTGCTCG CGCTGCTGCT CCGCTGAGC CCGCGGGGCG CCTCGCCAG CGCTGGTCTC 180
 GTCTCTGCTG TGCTGACAGA GCTGCGTTGC ACTTGTATTAC GCGTTACGCT GAGAGTAAAC 240
 CCCAAAACGA TTGTGTAACCT GCAGGTGTTT CCGCGAGGCC CGCAGTGCTC CAAGGTGGAA 300
 GTGGTAGCCT CCGTGAAGAA CGGGAAGCAA GTTTGTCTGG ACCCGGAAGC CCCTTTTCTA 360
 AAGAAAGTCA TCCAGAAAT TTTGGACAGT GGAACAAGA AAACTGAGT AACAAAAAG 420
 ACCATGCAAT ATAAATTTGC CAGTCTTCA GCGGAGCAGT TTTCTGGAGA TCCCTGGACC 480
 CAGTAAGAAT AAGAAGGAAG GGTGGTTTTT TTTCCATTTT CTACATGGAT TCCCTACTTT 540
 GAAGAGTGTG GGGGAAAGCC TACGCTTCTC CTTGAAGTTT ACAGCTCAGC TAATGAAGTA 600
 CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCTTTGG 660
 CAATTGACCA TATTGTGAGC AAGAATCAC TGGTTATTAG TCTTTCAATG AATATTGAAT 720
 TGAAGATAAC TATTGTATT CTATCATACA TTCCTTAAAG TCTTACCAG AAGCGTGTGG 780
 ATTTGATATG GAAATAATGT TTTATTAGTG TGCTGTTGAG GGAGGTATCC TGTGTTCTT 840
 ACTCACTCTT CTCATAAAT AGGAATATT TTAGTTCTGT TTTCTTGGG AATATGTTAC 900

TCTTTACCTT AGGATGCTAT TTAAGTTGTA CTGTATTAGA ACACTGGGTG TGTACATCCG 960
 TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AAATTTAAGT TCTGTAAGGG 1020
 CTAATATATT CTCTTCTCAT GGTTTTAGAT GTTTGATGTC TTCTTAGTAT GGCATAATGT 1080
 CATGATTTAC TCATTAAACT TTGATTTTGT ATGCTATTTT TTCACTATAG GATGACTATA 1140
 ATTCTGGTCA CTAATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTCC 1200
 TGATTGCTAA TTTACATAGA AATGATTCTT CTGGTTTTT TAAATAAAG CAAAATTAAAC 1260
 AATGATCTGT GCTCTGCAAA GTTTTGAAAA TATATTTGAA CAATTTGAAT ATAAATTCAT 1320
 CATTTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
 TTTAAAGGTT TTGACCATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
 AAATGCACT TTTATTTTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCTAT 1500
 TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAA AAAA

Seq ID NO: 641 Protein sequence

Protein Accession #: NP_002984.1

1 11 21 31 41 51
 MSLPSSRAAR VPGPSGSLCA LLALLLLLTP PGPLASAGPV SAVLTELRCT CLRVLRLVNP 60
 KITIGKLQVFP AGPQCSKVEV VASLKNGKQV CLDPEAPFLK KVIQKILDSG NKKN

Seq ID NO: 642 DNA sequence

Nucleic Acid Accession #: NM_013271.1

Coding sequence: 27..809

1 11 21 31 41 51
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 CCGGGGGCGT CGGCCTTTTG GTGCTGCTGC TGCTCGGCCT GTTTCGGCCG CCCCCCGCGC 120
 TCTGCGCGCG GCGCGTAAAG GAACCCCGCG GCCTAAGCGC AGCGTCTCCG CCCTTGGCTG 180
 AGACTGGCGC TCCTCGCGCG TTCCGGCGGT CAGTGCCCGG AGGTGAGCGG GCGGGGGCGG 240
 TGCAGGAGCT GCGCGCGGGC CTGGCGCATC TGCTGGAGGC CGAACGTCTG GAGCGGGCGC 300
 GGGCCGAGGC GCAGGAGGCT GAGGATCAGC AGGCGCGCGT CTTGGCGCAG CTGCTGCGCG 360
 TCTGGGGCGC CCCCOCGCAAC TCTGATCCGG CTCTGGGCCT GGACGACGAC CCGGACGCGC 420
 CTGCAGCGCA GCTCGCTCGC GCTCTGCTCC GCGCCCGCCT TGACCTTGCC GCCCTAGCAG 480
 CCCAGCTTGT CCCCOCGCGC GTCCCCGCGG CGGCGCTCCG ACCCGGCGCC CCGGTCTAGC 540
 ACGACGGGCT GATGCTGAGG GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC 600
 CCGAGCTGTT GAGGTACTTG CTGGACGCGA TTCTTGCGGG AAGCGCGGAC TCCGAGGGGG 660
 TGGCAGCCCC GCGCCGCGCT CGCCGTGCGG CCGACCAAGA TGTGGGCTCT GAGCTGCCCC 720
 CTGAGGGGCT GCTGGGGGCG CTGCTGCGTG TGAAACGCGT AGAGACCCCG GCGCCCCAGG 780
 TGCCTGCAAG CCGCCTCTTG CCACCTGAG CACTGCCCGG ATCCCGTGCA CCCTGGGACC 840
 CAGAAAGTGC CCGCCCATCC CGCCACCAAG ACTTCTCCCC GCCAGCACGT CCAGAGCAAC 900
 TTACCCCGGC CAGCCAGCCC TCTCACCCGA GGATCCCTAC CCGCTGGCCC ACAATAACAT 960
 GATCTGAGC

Seq ID NO: 643 Protein sequence

Protein Accession #: NP_037403.1

1 11 21 31 41 51
 MAGSPLLWGP RAGGVGLLV LLLGLFRPPP ALCARPVKEP RGLSAASPPL AETGAPRRFR 60
 RSVPRGEAAG AVQELARALA HLLAERQER ARAEAQEAED QARVLAQLL RVWGAPRNSD 120
 PALGLDDDDP APAQLARAL LRLRLDPAAL AAQLVPAPVP AAALRPRFPV YDDGPAGPDA 180
 EEAGDETCDV DPELLRLLG RILAGSADSE GVAAPRRLRR AADHDVGSSE PEGVLGALL 240
 RVKRLTPAP QVPARRLLPP

Seq ID NO: 644 DNA sequence

Nucleic Acid Accession #: NM_002214

Coding sequence: 681..2990

1 11 21 31 41 51
 CCCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCGAGAGCTT CTCCCTTGCC AGCCAGGACG 60
 CTGCCGACTT GTCTTTGCCG GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT 120
 GTTGGCTTCC CTGCCACCT GTGGAAGCAA CTGCGCTGAT TGATGCGCA CAGACTTTT 180
 TCCCTCGAC CTGCGCGCGG TACCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
 TAGGGTGGTT TCCCCCCAG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG 300
 CTAAGCTGAT TTATGAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCTTTCTT 360
 TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCCGGGCCCT 420
 TGGCCGTGCA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCGGTGCC GAGCCGGGAG 480
 GGCCGTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGCCC GCTTACCTGC ACCGCTTGCT 540
 CCGAGCCGCG GGGTCCGCT GCTAGGCCTG CGGAAAACGT CCTAGCGACA CTCGCCGCG 600
 GGCCCCGAGG TCGCCCGGGA GGCCGAGCCC GCGTCCGGAA GGCAGCCAGG CCGCGGGCGC 660
 GGGCGGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTTTACC GCTGCAITTG 720
 TCTGCTGCA AAACGACCGG CAGGTCCCG CCTCGTTCCT CTGGGCGAGC TGGGTGTTTT 780
 CACTTGTCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGATCTTCA AATGCAGCAT 840
 CCTGTGCCAG GTGCCCTTGC CTGGGTCCAG AATGTGGATG GTGTGTTCA GAGGATTTC 900
 TTTCAAGTGG ATCAAGAAAT GAACGTTGTG ATATTGTTT CAATTTAATA AGCAAAGGCT 960
 GCTCAGTTGA TTCATAGAA TACCCATCTG TGCAATGTTT AATACCCACT GAAATGAAA 1020
 TTAATACCCA GTGACACCA GGAGAAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA 1080
 ATTTTATGCT GAAAGTTTCT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTG 1140
 ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCCGTTGGA AACGATTAT 1200
 CTAGAAAAAT GGCATTTTTC TCCCGTGAAT TTCGTTCTGG ATTTGGCTCA TACGTTGATA 1260
 AAACAGTTTC ACCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT 1320
 ACAATTTAGA CTGCATGCCT CCCCATGGAT ACATCCATGT GCTGCTTTG ACAGAGAAC 1380
 TCACTAGATT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440
 AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGCTCTGTA AAGTCATATC GGATGGCGAA 1500
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560

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GCAAATTGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACACGCTCT 1620
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ACAACAACAT TAATGTCATC TTGTCAGTTC AAGGAAAACA ATTTTCATTG TATAAGGATC 1740
TTCTACCCCT CTGTCAGGCG ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACTCA 1800
ATAATTTGGT AGTGGAAAGCC TATCAGAAGC TCATTTTCAGA AGTGAAGATT CAGGTGGAAA 1860
ACCAGGTACA AGGCATCTAT TTAAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920
CAGGCATGGA AGGATGCAGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG 1980
TTACAATGAA AAAATGTGAT GTCCACAGGAG GAAAAAATA TGCAATAATC AAACCTATTG 2040
GTTTAAATGA AACCGCTAAA ATTCAATATC ACAGAAACTG CAGCTGTCTG TGTGAGGACA 2100
ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTCT AGATTCCAAG TGTTCACAGT 2160
GTGATGAGAA TAAATGTCAT TTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC 2220
ACAAGGATCA GCCTGTTTGC AGTGGTCSAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC 2280
ACAAAATTAA GCTTGGAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTG 2340
CATATCACCA TGAATAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400
GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460
TCAATTCAA GGGCAAGTG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520
GCACCGATCC CAGGAGCATC GGCCTCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT 2580
GCAAGGAAAA CTGGAATTGT ATGCAATGCC TTCACCTCA CAATTTGTCT CAGGCTATAC 2640
TTGATCAGTG CAACACCTCA TGTGCTCTCA TGGAAACAAC GCATTATGTC GACCAAACTT 2700
CAGAATGTTT CTCCAGCCCA AGCTACTTGA GAATATTTT CATCATTTTC ATAGTTACAT 2760
TCTTGATTGG TGTCTTAA TGTCTGATCA TTAGACAGGT GATACTACAA TGGAAATAGTA 2820
ATAAAATTAA GTCTCTATCA GATTACAGAG TGTGACGCTC AAAAAAGGAT AAGTTGATTG 2880
TGCAAGTGT TTGCAACAAG GCAGTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA 2940
TGGATATCAG CAAATTAATAT GCTCATGAAA CTTTCAGGTG CAACTTCTAA AAAAAGATT 3000
TTAAACACTT AATGGGAAAC TGGAAATTGT AATAATTGCT CCTAAAGATT ATAATTTTAA 3060
AAGTCACAGG GGGCAACAAA TTGCTCACGG TCATGCCAGT TGTGTTGTGT ACACCTCGAAC 3120
GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180
AAAAATGTGT TTACTACTGT TTGAGACTAG TGTGTTGTGA GCACCTTACT GTAATATATA 3240
ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300
TACCTGTTAT CCCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT 3360
CACTACAAGG GTACGATTAAT CCCTGCACTG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420
TATATTCTAA GGTTCGCAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG 3480
ATGAATAAAT GATTCTGTGT TCACCTTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA 3540
AAAGATTATT GCTTTTAA GGTGTAGATT TTATGCATGT GTGTTTATGG TTGCTTATT 3600
TTTGCAAGAT GGATACTAAT TCCAGCATTC TCTCTCTTT GCCTTTATGT TTTGTTTCT 3660
TTTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAACT GCTAAGTTAC 3720
TACTGCCATA AAAAATAAT AATACATGT CACTTTATCA GAATACTAGT TTTAAAGCT 3780
GAATGTAA

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Seq ID NO: 645 Protein sequence
Protein Accession #: NP_002205

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60

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1 11 21 31 41 51
MCGSALAPFT AAFVCLQND RGPASFLWAA WVFSVLVLGL QGEDNRCASS NAASCARCLA 60
LGEPCGWCVQ EDFISGGRS ERCDIVSNLI SKGCSVDSEI YPSVHVIIPT ENBINTQVTP 120
GEVSIQLRPG AEAANFMLKVH PLKKYPVDLY YLVDVSAASM NNIKLSNVG NDLSRKMAFF 180
SRDFRLGFGS YVDKTVSPYI SIHPERIHQ CSDYNLDCMP PHGYIHVLSL TENITEFEKA 240
VHRQKISGNI DTPEGGFDAM LQAAVCESHI GWRKEAKRL LVMTDQTSHL ALDSKLAGIV 300
VPNDGNCHLK NNIVVKSTTM EHPSLGQLSE KLIDNNINVI FAVGQKQFHW YKDLLFLLEP 360
TIAGEIESKA ANLNLNVEEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR 420
NVTNDEVLFP NVTVTMKKCD VTGKKNYAI KPFGNETAK IHIHRNCSQ CEDNRGPKGK 480
CVDETFLDSK CFQCDENKCH FDEDQFSSES CKSHKDPQVC SGRGVCVCGK CSCHKIKLKG 540
VYGKYCEKDD PSCPHYHGNL CAGHGECEAG RCQCPSGWEG DRQCPSSAAA QHCVNSKGVQ 600
CSGRGTVCVG RCECTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNLS QAILDQCKTS 660
CALMEQHYV DQTECFSP SYLRIFFIIF IVTFILIGLLK VLIIRQVILQ WNSNRIKSSS 720
DYRVSASKID KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETFRCNF

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Seq ID NO: 646 DNA sequence
Nucleic Acid Accession #: NM_003318.1
Coding sequence: 1..2574

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70
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1 11 21 31 41 51
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AGAGACATTA AAAATAAGTT TAAAAATGAA GACCTTACTG ATGAACCTAG CTGGAATAAA 120
ATTTCTGCTG ATACTACAGA TAACTCGGGA ACTGTTAACC AAATTATGAT GATGGCAAC 180
AAACCCAGAG ACTGGTTGAG TTGTTGCTC AACTAGAGA AAAACAGTGT TCCGCTAAGT 240
GATGCTCTTT TAAATAAATT GATTGGTCGT TACAGTCAAG CAATTGAAGC GCTTCCCCCA 300
GATAAATATG GCCAAATATG AGTTTTGTCT AGAATTCAG TGAGATTGCT TGAATTAAGA 360
GCTATTCAAG AGCCAGATGA TGCACGTGAC TACTTTCAAA TGGCCAGAGC AAAGTCAAG 420
AAATTGCTTT TTGTTCTAT ATCTTTTGCA CAATTGTAAC TGTCACAAGG TAATGTCAA 480
AAAAGTAAAC AACTTCTTCA AAAAGCTGTA GAACGTGGAG CAGTACCATT AGAAATGCTG 540
GAAATTGCCC TGCGGAATTT AAACCTCCAA AAAAGCAGC TGCTTTTCAA GGAGGAAAG 600
AAGAATTAT CAGCATCTAC GGTATTAACT GCCCAAGAA CATTTTCCGG TTCACCTGGG 660
CATTTACAGA ATAGGAACAA CAGTTGTGAT TCCAGAGGAG AGACTACTAA AGCCAGGTTT 720
TTATATGAGG AGAATCATGC ACCACAAGAT GCAGAAATAG GTTACCGGAA TTCATTGAGA 780
CAAACTAACA AAACATAACA GTCATGCCCA TTTGGAAGAG TCCCAAGTAA CCTTCTAAT 840
AGCCAGATT GTGATGTGAA GACAGATGAT TCAGTTGTAC CTTGTTTAT GAAAAGACAA 900
ACCTCTAGAT CAGATAGCCG AGATTGGTT GTGCCTGGAT CTAACCAAG TGGAAATGAT 960
TCCTGTGAAT TAAGAAATTT AAGTCTGTT CAAATAGTC ATTTCAAGGA ACCTCTGTGT 1020
TCAGATGAAA AGAGTTCTGA ACTTATTATT ACTGATTCAA TAACCTGAA GAATAAAACG 1080
GAATCAAGTC TTCTAGCTAA ATTAGAAGAA ACTAAGAGAT ATCAAGAAC AGAGGTTCCA 1140
GAGAGTAACC AAAACAGTG GCAATCTAAG AGAAAGTCAG AGTGATTAA CCAGATCCT 1200
GCTGCATCTG CAATCACTG CAGATTCCG GAGTTAGCCC GAAAAGTTAA TACAGAGCAG 1260
AAACATACCA CTTTGTAGCA ACCTGTCTTT TCAGTTTCAA AACAGTCACC ACCAATATCA 1320
ACATCTAAT GGTGTGACCC AAAATCTATT TGTAAAGAC CAAGCAGCAA TACCTTGGAT 1380

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5	GATTACATGA	GCTGTTTATG	AACCTCCAGTT	GTAAAGAATG	ACTTTCACAC	TGCTTGTTCAG	1440
	TTGTCAACAC	CTTATGGCCA	ACCTGCCTGT	TCCAGCAGC	AACAGCATCA	AATACCTGCC	1500
	ACTCCACTTC	AAAATTTACA	GGTTTTCAG	TCTTCTTCAG	CAAAATGAATG	CATTTCGGTT	1560
	AAAGGAAGAA	TTTATTCAT	TTTAAAGCAG	ATAGGAAGTG	GAGGTTCAAG	CAAGGTATTT	1620
	CAGGTGTTAA	ATGAAAGAA	ACAGATATAT	GCTATAAAAT	ATGTGAACCT	AGAAGAAGCA	1680
	GATAACCAAA	CTCTTGATAG	TTACCGGAAC	GAAATAGCTT	ATTTGAATAA	ACTACAACAA	1740
	CACAGTGATA	AGATCATCOG	ACTTTATGAT	TATGAAATCA	CGGACCACTA	CATCTACATG	1800
	GTAATGGAGT	GTGGAAATAT	TGATCTTAAT	AGTTGGCTTA	AAAAGAAAAA	ATCCATTGAT	1860
10	CCATGGGAAC	GCAAGAGTTA	CTGGAATAAT	ATGTTAGAGG	CAGTTTCACG	AATCCATCAA	1920
	CATGGCATTG	TTACAGTGA	TCTTAAACCA	GCTAACTTTC	TGATAGTTGA	TGGAATGCTA	1980
	AAGCTAATTG	ATTTTGGGAT	TGCAAAACCA	ATGCAACCAG	ATACAACAAG	TGTTGTTAAA	2040
	GATTCTCAGG	TTGGCACAGT	TAATTATATG	CCACCAGAAG	CAATCAAAGA	TATGTCCTCC	2100
	TCCAGAGAGA	ATGGGAATATC	TAAGTCAAAG	ATAAGCCCCA	AAAGTGATGT	TTGGTCCTTA	2160
	GGATGTATT	TGTACTATAT	GACTTACGGG	AAAACACCAT	TTCAGCAGAT	AATTAATCAG	2220
15	ATTTCTAAAT	TACATGCCAT	AATTGATCCT	AATCATGAAA	TTGAATTTCC	CGATATTCCA	2280
	GAGAAAGATC	TTCAAGATGT	GTAAAGTGT	TGTTTAAAAA	GGGACCCAAA	ACAGAGGATA	2340
	TCCATTCTCG	AGCTCCTGGC	TCATCCCTAT	GTTCAAATTC	AAACTCATCC	AGTTAACCAA	2400
	ATGGCCCAAG	GCAACCTGTA	AGAAATGAAA	TATGTTCTGG	GCCAACCTGT	TGGTCTGAAT	2460
20	TCTCCTAACT	CCATTTTGAA	AGCTGCTAAA	ACTTTATATG	AACACTATAG	TGGTGGTGAA	2520
	AGTCATAATT	CTTCATCCTC	CAAGACTTTT	GAIAAAAAAA	GGGGAAAAAA	ATGA	

Seq ID NO: 647 Protein sequence
Protein Accession #: NP_003309.1

25	1	11	21	31	41	51	
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	NPEDWLSLLL	KLEKNSVPLS	DALLNKLIGR	YSQAIEALPP	DKYQONESPFA	RIQVRFAPLAK	120
	ATQEPDDARD	YFQMARANCK	KFAFVHISFA	QFELSQQNVK	KSKQLLQKAV	ERGAVPLEML	180
30	ETALRNRLNQ	KKQLLSSEEEK	KNLSASTVL	AQESFSSGLG	HLQNRNNSCD	SRGQTTKARF	240
	LYGENMPPQD	AEIGYRNSLR	QTNKTKQSCP	FGRVPVNLN	SPDCVKTD	SVPVCFMKRQ	300
	TSRSECDRLV	VPGSKPSGND	SCELRNLKSV	QNSHPKEPLV	SDEKSELII	TDSITLKNKT	360
	ESSLLAKLEE	TKYQEPPEVP	ESNQKQWQSK	RKSECINQNP	AASSNHWQIP	ELARKVNTBQ	420
	KHTTFEPVFP	SVSQSPPIIS	TSKWFDPKSI	CKTPSNTLTD	DYMSCRPT	VKNDFPPACQ	480
35	LSTPYGQAPC	FQQQOHQILA	TPLQNLQVLA	SSSANECISV	KGRIVSILKQ	IGSGGSSKVF	540
	QVLNEKKQY	AIKIVNLEEA	DNQTLDSYRN	EIAYLNKLQ	HSDKIRLYD	YEITDQYIM	600
	VMECGNIDLN	SWLKIKKSID	PWERKSYWKN	MLEAVHTIHO	HGIVHSDLKP	ANFLIVDGM	660
	KLIDFGIANQ	MQPDTSVVK	DSQVGTVMYM	PPEAIKDMSS	SRENKSKSK	ISPKSDVWSL	720
	GCILYMYTK	KTPPQIINQ	ISKLHAIIDP	NHEIEFPDIP	EKDLQDVLKC	CLKRDPKQRI	780
40	SIPPELLAHY	VQIQTHPVNQ	MAKGTTEEMK	VVLGQLVLGN	SPNSILKAAK	TLYEHYSGGE	840
	SHNSSSSKTF	EKKRGKK					

Seq ID NO: 648 DNA sequence
Nucleic Acid Accession #: NM_015507
Coding sequence: 241..1902

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50	CGCCCCCTGC	GCGGTGCTGT	GCCTCCCCCT	CCAGACTGCA	GGGACAGCAC	CCGGTAACTG	120
	CGAGTGGAGC	GGAGGACCCG	AGCGGCTGAG	GAGAGAGGAG	GCGGCGGCTT	AGCTGCTACG	180
	GGGTCCGGCC	GGCGCCCTCC	CGAGGGGGGC	TCCAGAGGAG	GAAGGAGGAC	CCGTGCGAGA	240
	ATGCTCTGCG	CCTGGAGCTG	TGCGCTCCCG	CTGCTGCTCT	CCTGGGTGGC	AGGTGGTTTC	300
55	GGGAACGCGG	CCAGTGCAGG	GCATCACGGG	TTGTTAGCAT	CGGCACGTCA	GCCTGGGGTC	360
	TGTCACTATG	GAATCAAACT	GGCTGCTGCT	TACGCTGGA	GAAGAAGACG	CAAGGGAGTC	420
	TGTGAAGCTA	CATCGCAACC	TGGATGTAAG	TTTGGTGAGT	CGGTGGGACC	AAACAAATGC	480
	AGATGCTTTC	CAGGATACAC	CGGGAAAAAC	TGCAGTCAAG	ATGTGAATGA	GTGTGGAATG	540
	AAACCCCGGC	CATGCCAACA	CAGATGTGTG	AATACACACG	GAAGCTACAA	GTGCTTTTGC	600
60	CTCAGTGGCC	ACATGCTCAT	GCCAGATGCT	ACGTGTGTGA	ACTCTAGGAC	ATGTGCCATG	660
	ATAAACTGTC	AGTACAGCTG	TGAAGACACA	GAAGAAGGGC	CACAGTGCTC	GTGTCCATCC	720
	TCAGGACTGC	GCCTGGGCCC	AAATGGGAAG	GACTGTCTAG	ATATTGATGA	ATGTGCCCTC	780
	GGTAAAGTCA	TCTGTCCCTA	CAATCGAAGA	TGTGTGAACA	CATTGGAAG	CTACTACTGC	840
	AAATGTCAAC	TTGGTTTCGA	ACTGCAATAT	ATCAGTGGAC	GATATGACTG	TATAGATATA	900
65	AATGAATGTA	CTATGGATAG	CCATACGTGC	AGCCACCATG	CCAATTGCTT	CAATACCCAA	960
	GGGTCTCTCA	AGTGTAATAG	CAAGCAGGGA	TATAAAGGCA	ATGGACTTCC	GTGTTCTGCT	1020
	ATCCCTGAAA	ATTCTGTGAA	GGAAAGTCTC	AGAGCACCTG	GTACCATCAA	AGACAGAATC	1080
	AAGAAAGTGC	TTGCTCACAA	AAACAGCATG	AAAAAGAAGG	CAAAAATTA	AAATGTTACC	1140
	CCAGAACCCA	CACGAGCTCC	TACCCCTAAG	GTGAACCTGC	AGCCCTTCAA	CTATGAAGAG	1200
70	ATAGTTTCCA	GAGGCGGGAA	CTCTCATGGA	GGTAAAAAAG	GGAATGAAGA	GAAGATGAAA	1260
	GAGGGGCTTG	AGGATGAGAA	AAGAGAAGAG	AAAGCCCTGA	AGAATGACAT	AGAGGAGCGA	1320
	AGCCTGCGAG	GAGATGTGTT	TTTCCCTAAG	GTGAATGAAG	CAGGTGAATT	CGGCTGATT	1380
	CTGGTCCAAA	GGAAAGCGCT	AACCTCCAAA	CTGGAACATA	AAGATTAA	TATCTCGGTT	1440
	GACTGCAGCT	TCAATCATGG	GATCTGTGAC	TGGAAACAGG	ATAGAGAAGA	TGATTTTGAC	1500
75	TGGAATCCTG	CTGATCGAGA	TAATGCTATT	GGCTTCTATA	TGGCAGTTCC	GGCCTTGGCA	1560
	GGTCAACAAG	AAGACATTGG	CCGATTGAAA	CTTCTCTTAC	CTGACCTGCA	ACCCCAAAGC	1620
	AACCTCTGTT	TGCTTTTGA	TTACCGGCTG	GCCGGAGACA	AAGTCGGGAA	ACTTCGAGTG	1680
	TTTGTGAAAA	ACAGTAACAA	TGCCCTGGCA	TGGGAGAAGA	CCACGAGTGA	GGATGAAAAG	1740
	TGGAAGACAG	GGAAATTTCA	GTGTATATCA	GGAACTGATG	CTACCAAAG	CATCATTTT	1800
	GAAGCAGAAC	GTGGCAAGGG	CAAAACCGGC	GAAATCGCAG	TGGATGGCGT	CTTGCTTGTT	1860
80	TTCAGCTTAT	GTCCAGATAG	CCTTTTATCT	GTGGATGACT	GAATGTTACT	ATCTTTATAT	1920
	TTGACTTTGT	TGCTCAGTTC	CCTGGTTTTT	TTGATATTGC	ATCATAGGAC	CTCTGGCATT	1980
	TAGAATTTAC	TAGCTGAAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTGT	AAGATGCCTT	2040
	TCTTGATATA	GATATGCCAA	TATTTGCTTT	AAATATCATA	TCACTGTATC	TTCTCAGTCA	2100
	TTTCTGAATC	TTTCCACATT	ATATTATAAA	ATATGGAAT	GTCAGTTTAT	CTCCCTCCT	2160
85	CAGTATATCT	AGTTGTATGA	AGTAAGTTGA	TGAGCTTCTC	TCTACAACAT	TCTAGAAAA	2220
	TAGAAAAAAA	AGCACAGAGA	AATGTTTAA	TGTTTGACTC	TTATGATACT	TCTTGAAAC	2280
	TATGACATCA	AAGATAGACT	TTTGCCTAAG	TGGCTTAGCT	GGGTCTTTCA	TAGCCAAACT	2340

TGTATATTTA AATCTTTGT AATAATAATA TCCAAATCAT CAAAAAATAA AAAAAAAA

Seq ID NO: 649 Protein sequence
Protein Accession #: NP_056322

	1	11	21	31	41	51	
5	MPLPWSLALP	LLLSWVAGGF	GNAASARHHG	LLASARQPGV	CHYGTKLACC	YGWRRNSKGV	60
10	CEATCEPGCK	FGECVGPNNK	RCPPGYTGKT	CSQDVNECGM	KPRPCQHRVC	NTGHSYKCFK	120
	LSGHMLMPDA	TCVNSRTCAM	INCQYSCEDT	EEGPQCLCPS	SGLRLAPNGR	DCLDIDECAS	180
	GKVICPNRR	CVNFTGSIYC	KCHIGFELQY	ISGRYDCIDI	NECTMDSHTC	SHHANCFTNQ	240
	GSFKCKCKQG	YKGNGLRCSA	IPENSVKEVL	RAPGTIKDRI	KKLLAHKNSM	KKKAKIKNVT	300
15	PEPTRTPPK	VNLQPFNYEE	IVSRGGNSHG	GKKGNEEKMK	EGLEDEKREE	KALKNDIEER	360
	SLRGDVFFPK	VNEAGFGLI	LQQRKALTSK	LEHKDLNISV	DCSFNNGICD	WKQDREDDFD	420
	WNPADRDNAI	GFYMAVPALA	GHKKDIGRLK	LLLPDLQPS	NFCLLFDFYRL	AGDKVGLLRV	480
	FVKNSNNALA	WEKTTSEDEK	WKTGKIQLYQ	GTDATKSIIF	EAERKGKGTG	EIAVDGVLLV	540
	SGLCPDSLLS	VDD					

Seq ID NO: 650 DNA sequence
Nucleic Acid Accession #: NM_003506.1
Coding sequence: 259..2379

	1	11	21	31	41	51	
25	GCAGCTCCAG	TCCCGGACGC	AACCCCGGAG	CCGTCTCAGG	TCCCTGGGGG	GAACGGTGGG	60
	TTAGACGGGG	ACGGGAAGGG	ACAGCGGCCT	TCGACCGCCC	CCCGAGTAAT	TGACCCAGGA	120
	CTCATTTTCA	GGAAAGCCTG	AAAATGAGTA	AAATAGTGAA	ATGAGGAATT	TGAACATTTT	180
30	ATCTTTGGAT	GGGGATCTTC	TGAGGATGCA	AAGAGTGATT	CATCCAAGCC	ATGTGGTAAA	240
	ATCAGGAATT	TGAAGAAAAA	GGAGATGTTT	ACATTTTGTG	TGACGTGTAT	TTTTCTACCC	300
	CTCCTAAGAG	GGCAGAGTCT	CTTCACCTGT	GAACCAATTA	CTGTTCCAG	ATGTATGAAA	360
	ATGGCTTACA	ACATGACGTT	TTTCCCTAAT	CTGATGGGTC	ATTATGACCA	GAGTATTGCC	420
	GCGGTGGAAA	TGGAGCATTT	TCCTCTCTCT	GCAAATCTGG	AATGTTCAAC	AAACATTGAA	480
35	ACTTTCCTCT	GCAAAGCATT	TGTACCAACC	TGCATAGAAC	AAATTCATGT	GGTTCACCT	540
	TGTCGTAAAC	TTTGTGAGAA	AGTATATTCT	GATTGCAAAA	AATTAATTGA	CACTTTGGG	600
	ATCCGATGGC	CTGAGAGCTT	TGAATGTGAC	AGATTACAAT	ACTGTGATGA	GACTGTTCCT	660
	GTAACTTTGT	ATCCACACAC	AGAATTCTCT	GGTCTCTAGA	AGAAAACAGA	ACAAGTCCAA	720
	AGAGACATTG	GATTTTGGTG	TCCAAGGCAT	CTTAAGACTT	CTGGGGGACA	AGGATATAAG	780
40	TTTCTGGGAA	TGACCCAGTG	TGCGCCTCCA	TGCCCAACA	TGTATTTTAA	AAGTGATGAG	840
	CTAGAGTTTG	CAAAAAGTTT	TATTGGAAAC	GTTCATATAT	TTTGTCTTTG	TGCAACTCTG	900
	TTCACTTTCC	TTACTTTTTC	AATTGATGTT	AGAAGATTCA	GATACCCAGA	GAGACCAATT	960
	ATATATTACT	CTGTCTGTGA	CAGCATGTGA	TCTCTTATGT	ACTTCATTGG	ATTTTGTGCTG	1020
	GGCGATAGTC	CAGCTTCGAA	TAAAGCAGAT	GAGAAGCTAG	AACCTGGTGA	CACCTGTTGC	1080
45	CTAGGCTCTC	AAAATAAGGC	TTGCACCGTT	TTGTTCATGC	TTTTGTATTT	TTTCACAATG	1140
	GCTGGCAGTG	TGTGGTGGGT	GATTCTTACC	ATTACTTGGT	TCTTAGCTGC	AGGAAGAAAA	1200
	TGGAGTTTGG	TAGGATCTGA	GCAAAAAGCA	GTGTGGTTTC	ATGCTGTTGC	ATGGGGAACA	1260
	CCAGGTTTCC	TGACTGTGAT	GCTTCTTGCT	CTGAACAAGG	TTGAAGGAGA	CAACATTAGT	1320
	GGAGTTTGCT	TTGTTGGCCT	TTATGACCTG	GATGCTTCTC	GCTACTTTGT	ACTCTTGCCA	1380
50	CTGTGCCCTT	GTGTGTTTGT	TGGGCTCTCT	CTTCTTTTAG	CTGGCATTAT	TTCTTTAAAT	1440
	CATGTTTCAG	AAGTCATACA	ACATGATGGC	CGGAACCAAG	AAAAACTAAA	GAAATTTATG	1500
	ATTGCAATTG	TGAGCTTCAG	CGGCTTGTAT	CTTGTGCCAT	TAGTGACACT	TCTCGGATGT	1560
	TACGCTTAGT	AGCAAGTGAA	CAGGATTACC	TGGGAGATAA	CTTGGGTCTC	TGATCATTGT	1620
	CGTCAGTACC	ATATCCCATG	TCCTTATCAG	GCAAAAAGCA	AAGCTCGACC	AGAATTGGCT	1680
55	TTATTTATGA	TAAATACCTT	GATGACATTA	ATTGTTGGCA	TCTCTGCTGT	CTTCTGGGTT	1740
	GGAAGCAAAA	AGACATGCAC	AGAAATGGCT	GGGTTTTTTA	AACGAAATCG	CAAGAGAGAT	1800
	CCAATCAGTG	AAAGTCGAAG	AGTACTACAG	GAATCATGTG	AGTTTTTCTT	AAAGCACAT	1860
	TCTAAAGTTA	AACACAAAAA	GAAGCACTAT	AAACCAAGTT	CACACAAGCT	GAAGGTCAAT	1920
	TCCAATCCGA	TGGGAACCCG	CACAGGAGCT	ACAGCAAATC	ATGGCACTTC	TGCAGTAGCA	1980
60	ATTACTAGCC	ATGATTACCT	AGGACAAGAA	ACTTTGACAG	AAATCCAAC	CTCACCAGAA	2040
	ACATCAATGA	GAGAGGTGAA	AGCGGACCGA	GCTAGCACCC	CCAGGTTAAG	AGAACAGGAC	2100
	TGTGGTGAAC	CTGGCTCGCC	AGCAGCATCC	ATCTCCAGAC	TCTCTGGGGA	ACAGGTCGAC	2160
	GGGAAGGGCC	AGGCAGGCAG	TGTATCTGAA	AGTGCGCGGA	GTGAAGGAAG	GATTAGTCCA	2220
	AAGAGTGATA	TTACTGACAT	TGGCCTGGCA	CAGAGCAACA	ATTGTCAGGT	CCCCAGTTCT	2280
65	TCAGAACCAA	GCAGCCTCAA	AGGTTCCACA	TCTCTGCTTG	TTCAACCCAGT	TTCAAGGAGT	2340
	AGAAAAGAGC	AGGGAGGTGG	TTGTCTTCA	GATACTTGAA	GAACATTTTC	TCTCGTTACT	2400
	CAGAAGCAAA	TTTGTGTTAC	ACTGGAAGTG	ACCTATGCAC	TGTTTTGTAA	GAATCACTGT	2460
	TACGTTCTTC	TTTTGCACTT	AAAGTTGCAT	TGCTTACTGT	TATCTAGGAA	AAATAGAGT	2520
	TCAAGAATAA	TATGACTCAT	TTTCAACAAA	GGTTAATGAC	AACAATATAC	CTGAAAACAG	2580
70	AAATGTGCAG	GTTAATAATA	TTTTTTTAA	AGTGTGGGAG	GACAGAGTTA	GAGGAATCTT	2640
	CCTTTTCTAT	TTATGAAGAT	TCTACTCTTG	GTAAGAGTAT	TTTAAGATGT	ACTATGCTAT	2700
	TTTACCTTTT	TGATATAAAA	TCAAGATATT	TCTTTGCTGA	AGTATTTAAA	TCTTATCTTT	2760
	GTATCTTTTT	ATACATATTT	GAAAATAAGC	TTATATGTAT	TTGAACTTT	TTGAAATCCT	2820
	ATTCAGATAT	TTTTATCATG	CTATTGTGAT	ATTTTAGCAC	TTTGGTAGCT	TTTCACTGTA	2880
75	ATTTCTAAGA	AAATTGTAAA	ATAGTCTTCT	TTTATACTGT	AAAAAAGAT	ATACCAAAAA	2940
	GTCTTATAAT	AGGAATTTAA	CTTTAAAAAC	CCACTTATTG	ATACCTTACC	ATCTAAAAAG	3000
	TGTGATTTTT	ATAGTCTCGT	TTTAGGAATT	TCACAGATCT	AAATTTATGTA	ACTGAATAAA	3060
	GGTGCTTACT	CAAGAAGTGT	CCACTATTGA	TTGTATTATG	CTGCTCACTG	ATCCTTCTGC	3120
	ATATTAAAA	TAAAGGTTC	TAAAGGTTTA	GTAGACAAAA	TGTTAGTCTT	TTGTATATTA	3180
	GGCCAGGTGC	AATTGACTTC	CCTTTTTTAA	TGTTTATGTA	CCACCCATTG	ATTGTATTAT	3240
80	AACCACTTAC	AGTTGCTTAT	ATTTTTTGT	TTAACTTTTG	TTTCTTAAAC	TTTAGAATAT	3300
	TACATTTTGT	ATTATACAGT	ACCTTTCTCA	GACATTTTGT	AG		

Seq ID NO: 651 Protein sequence
Protein Accession #: NP_003497.1

	1	11	21	31	41	51

WO 02/086443

PCT/US02/12476

MEMPTFLLTC IFLLPLLRGHS LFTCEPITVP RCMKMYNMT FFPNLMGHVD QSIAAIVEMEH 60
 FLPLANLECS PNIETFLCKA FVPTCIEQIH VVPPCRKLCE KVVSDCKKLI DTFGIRWPPEE 120
 LBCDRLQYCD ETPVPTFDPH TEFLGPQKKT EQVQRDIGFW CPHRLKTSGG QGYKFLGIDQ 180
 CAPPCPNMYF KSDELEPAKS FIGTVSIFCL CATLFTPLTF LIDVRRFRYP ERPIIYYSVC 240
 YSIVSLMYFI GFLLGDSSTAC NKADEKLELG DTVVLGSSQNK ACTVLFMLLY FFTMAGTVMW 300
 VILITITWFLA AGRKWSCEAI EQKAVWPHAV AWGTPGFLTV MLLALNKVEG DNISGVCFVG 360
 LYDLASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVQRVI QHDSRNQEKI KKFMRIRIGVF 420
 SGLYLVLPLVT LLGCVYVEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELALFMIKY 480
 LMTLIVGISA VFWVGSKKT TEWAGFFKRN RKRDPISSESR RVLQESCEFP LKHSKVKHKH 540
 KGHYKPSHHK LKVISKSMGT STGATANHGT SAVAITSHDY LGQETLLEIQ TSPETSMREV 600
 KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660
 TGLAQSNMLQ VPSSESPSSL KGSTSLLVHP VSGVRKEQGG GCHSDT

Seq ID NO: 652 DNA sequence
 Nucleic Acid Accession #: NM_014791.1
 Coding sequence: 171..2126

1 11 21 31 41 51
 TTGGCGGGCG GAAGCGGCCA CAACCGGGCG ATCGAAAAGA TTCTTAGGAA CGCGTACCA 60
 GCGCGGTCTC TCAGGACAGC AGGCCCTGT CCTTCTGTGG GCGCGGCTC AGCCGTGCCC 120
 TCCGCCCCCTC AGGTTCTTTT TCTAATTCCA AATAAACTTG CAAGAGGACT ATGAAAGATT 180
 ATGATGAAC TCTCAATAT TATGAATTAC ATGAAACTAT TGGGACAGGT GGCCTTTGCA 240
 AGGTCAAAC TGCTTCCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA 300
 AAAACACACT AGGGAGTGAT TTGCCCCGGA TCAAAACGGA GATTGAGGCC TTGAAGAAC 360
 TGAGACATCA GCATCTATGT CAACTCTACC ATGTGCTAGA GACAGCCAAC AAAATATTCA 420
 TGGTCTCTGA GTACTGCCCT GGAGGAGAGC TGTTTGACTA TATAATTCC CAGGATCGCC 480
 TGTCAAGAAG GGAGACCCGG GTTGTCTTCC GTCAGATAGT ATCTGCTGTT GCTTATGTGC 540
 ACAGCCAGGG CTATGCTCAC AGGACCTCA AGCCAGAAAA TTTGCTGTTT GATGAATATC 600
 ATAAATTAAG GCTGATTGAC TTGGTCTCT GTGCAAAACC CAAGGGTAAC AAGGATTACC 660
 ATCTACAGAC ATGCTGTGGG AGTCTGGCTT ATGCAGCACC TGAGTTAATA CAAGGCAAT 720
 CATATCTTGG ATCAGAGGCA GATGTTTGA GCATGGGCAT ACTGTTATAT GTTCTTATGT 780
 GTGGATTCTT ACCATTGAT GATGATAAG TAATGGCTTT ATACAAGAAG ATTATGAGAG 840
 GAAATATAGA TGTTCCTAAG TGGCTCTCT CCAGTAGCAT TCTGCTTCTT CAACAAATGC 900
 TGCAGGTGGA CCCAAGAAAA CGGATTCTTA TGAAAAATCT ATTGAACCAT CCCTGGATCA 960
 TGCAAGATTA CAACTATGCT GTTGAAGTGG AAAGCAAGAA TCCTTTTATT CACCTCGATG 1020
 ATGATTGCGT AACAGAACTT TCTGTACATC ACAGAAACAA CAGGCAACAA ATGGAGGATT 1080
 TAATTTCACT GTGGCAGTAT GATCACCTCA CGGCTACCTA TCTTCTGCTT CTAGCCAAGA 1140
 AGGCTCGGGG AAAACCAAGT CGTTTAAAGC TTTCTTCTT CTCTGTGGA CAAGCCAGTG 1200
 CTACCCCATC CACAGACATC AAGTCAATA ATTGGAGTCT GGAAGATGTG ACCGCAAGTG 1260
 ATAAAAATTA TGTGGCGGGA TTAATAGACT ATGATTGGTG TGAAGATGAT TTATCAACAG 1320
 GTGCTGTCTAC TCCCGAACA TCACAGTTTA CCAAGTACTG GACAGATCA AATGGGGTGG 1380
 AATCTAAATC ATTAATCTCA GCCTTATGCA GAACACCTGC AAATAAATTA AAGAACAAG 1440
 AAAATGTATA TACTCTTAAG TCTGCTGTAA AGAATGAAGA GTACTTTATG TTTCTGAGC 1500
 CAAAGACTCC AGTTAATAAG AACACGATA AGAGAGAAAT ACTCACTACG CCAATCGTT 1560
 ACATACACAC CTAACAAGAG GCCTGAAGA AACTCCAATT AAAATACAG 1620
 TAAATTCAC AGGAACAGAC AAGTTAATGA CAGGTGTCTAT TAGCCCTGAG AGGCGGTGCC 1680
 GCTCAGTGA ATTGCACTCT AACCAAGCAC ATATGGAGGA GACTCCAAAA AGAAAGGGAG 1740
 CCAAAGTGT TGGGAGCCTT GAAAGGGGGT TGGATAAGGT TATCACTGTG CTCACCAGGA 1800
 GCAAAGGAA GGGTCTTGCC AGAGACGGGC CCAGAAAGACT AAAGCTTAC TATAATGTGA 1860
 CTACACCTAG ATTAGTGAAT CAGATCAAC TGTGAATGA AATAATGTCT ATTCTTCAA 1920
 AGAAGCATGT TGACTTTGTA CAAAGGGTAT ATCACTGAA GTGTCAACA CAGTCAGATT 1980
 TTGGGAAAT GACATGCAA TTTGAATTAG AAGTGTGCCA GCTTCAAAA CCGATGTGG 2040
 TGGGTATCAG GAGGCAGCGG CTTAAGGGCG ATGCCTGGGT TTACAAAAGA TTAGTGAAG 2100
 ACATCTATC TACTGTCAAG GTATAATTGA TGGATTCTTC CATCTGCCG GATGAGTGTG 2160
 GGTGTGATAC AGCCTACATA AAGACTGTTA TGATCGCTTT GATTTTAAAG TTCATTGGA 2220
 CTACCAACTT GTTCTTAAAG AGCTATCTTA AGACCAATAT CTCTTTGTT TTAACAAAA 2280
 GATATTATT TGTGTATGAA TCTAATCAA GCCCATCTGT CATTATGTTA CTGTCTTTT 2340
 TAATCATGTG GTTTTGTATA TTAATAATTG TTGACTTTCT TAGATTCACT TCCATATGTG 2400
 AATGTAAGCT CTTAACATAG TCTCTTGTGA ATGTGTAATT TCTTCTGAA ATAAACCAT 2460
 TTGTGAATAT

Seq ID NO: 653 Protein sequence
 Protein Accession #: NP_055606.1

1 11 21 31 41 51
 MKDYDELLKY YELHETIGTG GFAKVKLACH ILTGEMVAIK IMDKNTLGSD LPRIKTEIEA 60
 LKNLRHQHIC QLYHVLETAN KIFMVLEYCP GGELEFDYIIS QDRLSEETR VVFRQIVSAV 120
 AYVHSQGYAH RDLKPENLLE DEYHKLKID FGLCAKPKGN KDYHLQTCG SLAYAAPELI 180
 QGKSYLGSEA DVNSMGILLY VLMCGFLPPD DDNVMALYKK IMRGKYDVPK WLSPPSILL 240
 QQMLQVDFPK RISMKNLLNH PWIMQDYNYP VEWQSKNFFI HLDDCVTEL SVHHRNNRQT 300
 MEDLISLWQY DHLTATYLLL LAKKARGKEV RLRLSSFSFG QASATPFTDI KSNMWSLEDV 360
 TASDKNVVAG LIDYDWCEDD LSTGAATPRT SQFTKYWTES NGVESKSLTP ALCRTPANKL 420
 KKNKENVYTPK SAVKNEEYFM FPEPKTFVNK NQHKREILT PNRYTTPSKA RNQCLKETPI 480
 KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAUVFSG ERGLDKVITV 540
 LTRSKRKGS RDGPRRLKLH YNVTTRLVN PDQLNEIMS ILPKGHVDFV QRGYTLKQCT 600
 QSDFGKVTMQ FELEVCLQK PDVVGIRRRR LKGDWVYKR LVEDILSSCK V

Seq ID NO: 654 DNA sequence
 Nucleic Acid Accession #: NM_000582
 Coding sequence: 88..990

1 11 21 31 41 51
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 AACGCCGACC AAGGAAACT CACTACCATG AGAATTGCAG TGATTGCTT TTGCTCCTA 120

	GGCATCACT	GTGCCATACC	AGTTAAACAG	GCTGATTCTG	GAAGTTCTGA	GGAAAAGCAG	180
	CTTTACAACA	AATACCCAGA	TGCTGTGGCC	ACATGGCTAA	ACCCTGACCC	ATCTCAGAAG	240
	CAGAACTCTC	TAGCCCCACA	GACCCCTCCA	AGTAAGTCCA	ACGAAAGCCA	TGACCACATG	300
5	GATGATATGG	ATGATGAAGA	TGATGATGAC	CATGTGGACA	GCCAGGACTC	CATTGACTCG	360
	AACGACTCTG	ATGATGTAGA	TGACACTGAT	GATTCTCACC	AGTCTGATGA	GTCTCACCAT	420
	TCTGATGAAT	CTGATGAAC	GGTCACTGAT	TTTCCCACGG	ACCTGCCAGC	AACCGAAGTT	480
	TTCACCTCCG	TTGTCCCCAC	AGTAGACACA	TATGATGGCC	GAGGTGATAG	TGTGGTTTAT	540
	GGACTGAGGT	CAAAATCTAA	GAAGTTTCGC	AGACCTGACA	TCCAGTACCC	TGATGCTACA	600
10	GACGAGGACA	TCACCTCACA	CATGGAAAGC	GAGGAGTTGA	ATGGTGCATA	CAAGGCCATC	660
	CCCGTTGCC	AGGACCTGAA	CGCGCCTTCT	GATTGGGACA	GCCGTGGGAA	GGACAGTTAT	720
	GAAACGAGTC	AGCTGGATGA	CCAGAGTGCT	GAAACCCACA	GCCACAAGCA	GTCCAGATTA	780
	TATAAGCGGA	AAGCCAATGA	TGAGAGCAAT	GAGCATTCCG	ATGTGATTGA	TAGTCAGGAA	840
	CTTTCCAAAG	TCAGCCGTGA	ATTCCACAGC	CATGAATTC	ACAGCCATGA	AGATATGCTG	900
15	GTTGTAGACC	CCAAAAGTAA	GGAAGAAGAT	AAACACCTGA	AATTTGCTAT	TTCTCATGAA	960
	TTAGATAGTG	CATCTTCTGA	GGTCAATTAA	AAGGAGAAAA	AATACAATTT	CTCACTTTGC	1020
	ATTTAGTCAA	AAGAAAAAAT	CTTTTATAGC	AAAATGAAAG	AGAACATGAA	ATGCTTCTTT	1080
	CTCAGTTTAT	TGGTTGAATG	TGTATCTATT	TGAGTCTGGA	AATAACTAAT	GTGTTTGATA	1140
	ATTAGTTTAG	TTTGTGGCTT	CATGGAAACT	CCCTGTAAAC	TAAAAGCTTC	AGGGTTATGT	1200
20	CTATGTTTAT	TTTATAGAAG	AAATGCAAA	TATCACTGTA	TTTTAATATT	TGTTATTCTC	1260
	TCATGAATAT	AAATTTATGT	AGAAGCAAAC	AAAATACTTT	TACCCACTTA	AAAAGAGAAT	1320
	ATAACATTTT	ATGCTCATAT	ATCTTTTGT	TTTTTAAGTT	AGTGTATATT	TGTTGTGATG	1380
	TATCTTTTGT	TGGTGTGAAT	AAATCTTTTA	TCTTGAATGT	AATAAGAAAT	TGGTGGTGTC	1440
	AATTGCTTAT	TTGTTTTCCT	ACGGTTGTCC	AGCAATTAAT	AAAACATAAC	CTTTTCTACT	1500
25	GCCTAAAAAA	AAAAAAAATA	AAAA				

Seq ID NO: 655 Protein sequence
Protein Accession #: NP_000573

30	1	11	21	31	41	51	
	MRIAVICFCL	LGITCAIPVK	QADSGSSEK	QLYNKYPDV	ATWLNPDPSQ	KQNLLAPQTL	60
	PSKSNESHDH	MDDMDDDDDD	DHVDSDSDID	SNDSDDVDDT	DDSHQSDSH	HSDESDELVT	120
	DFPTDLFATE	VFTPVVPTVD	TYDGRGDSVV	YGLRSKSKKF	RRPDIQYVDA	TDEDITSHME	180
35	SEELNGAYKA	IPVAQDLNAP	SDWDSRGKDS	YETSQLDDQS	AETHSHKQSR	LYKRRANDES	240
	NHSDVIDSQ	ELSKVSRFPH	SHEFHSHEDM	LVVDFPKSKEE	DKHLKFRISH	ELDSASSEVN	

Seq ID NO: 656 DNA sequence
Nucleic Acid Accession #: NM_003108.1
Coding sequence: 76..1401

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	GGGGTGGGAG	GGGGAGGGGG	ACCTCCGCAC	GAGACCCAGC	GGCCCGGGTT	GGAGCGTCCA	60
45	GCCCTGCAAC	GGATCATGGT	GCAGCAGGCG	GAGAGCTTGG	AAGCGGAGAG	CAACCTGCCC	120
	CGGGAGGGCG	TGGACACGGA	GGAGGGCGAA	TTCAATGGCTT	GCAGCCCGGT	GGCCCTGGAC	180
	GAGAGCGACC	CAGACTGGTG	CAAGACGGCG	TCCGGCCACA	TCAAGCGGCC	GATGAACGCG	240
	TTCAATGGTAT	GGTCCAAGAT	CGAACGCAAG	AAGATCATGG	AGCAGTCTCC	GGACATGCAC	300
50	AACGCGGAGA	TCTCCAAGAG	GCTGGGCAAG	CGCTGGAAGA	TGCTGAAGGA	CAGCGAGAAG	360
	ATCCCGTTCA	TCCGGGAGGC	GGAGCGGCTG	CGGCTCAAGC	ACATGGCCGA	CTACCCCGAC	420
	TACAAGTACC	GGCCCCGGAA	AAAGCCCAAA	ATGGACCCCT	CGGCCAAGCC	CAGCGCCAGC	480
	CAGAGCCAG	AGAAGAGCGC	GGCCGGCGGC	GGCGCGGGGA	GGCGGGCGGG	AGCGCGGGCC	540
	GGTGCCAAAG	CTCCAAAGGG	CTCCAGCAAG	AAATGCGGCA	AGCTCAAGGC	CCCCCGGGCC	600
55	GCGGGCGCCA	AGGCGGGCGC	GGCAAGGCG	GCCCAAGTCC	GGGACTACGG	GGGCGGGGGC	660
	GACGACTACG	TGCTGGGCAG	CCTGCGCGTG	AGCGGCTCGG	GCGGCGGCGG	CGCGGGCAAG	720
	ACGGTCAAGT	GCCTGTTTCT	GGATGAGGAC	GACGACGACG	ACGACGACGA	CGACGAGCTG	780
	CAGCTGCAGA	TCAAAACAGGA	GCCGACGAG	GAGGACGAGG	AACCAACGCA	CCAGCAGCTC	840
	CTGACAGCGC	CGGGCGACGA	GCCGTCGAG	CTGCTGAGAC	GCTACAAAGT	CGCCAAAGTG	900
60	CCCGCCAGCC	CTAGCTGTAG	CAGCTCGGCG	GAGTCCCCCG	AGGGAGCGAG	CCTCTACGAC	960
	GAGGTGCGGG	CCGCGCGGAC	CTCGGCGGCC	GGGGCGGCA	GCCGCTCTTA	CTACAGCTTC	1020
	AAGAATATCA	CCAAGCAGCA	CCGCGCGCGG	CTCGCGCAGC	CCGCGCTGTC	GCCCGCGTCC	1080
	TGCGGCTCGG	TGTCCACCTC	CTCGTCCAGC	AGCAGCGGCA	GCAGCAGCGG	CAGCAGCGGC	1140
	GAGGACGCGG	ACGACCTGAT	GTTCCGACCT	AGCTTGAATT	TCTCTCAAAG	CGCGCACAGC	1200
65	GCCAGCGAGC	AGCAGCTGGG	GGCGCGGCGG	GCGGCGGGGA	ACCTGTCCCT	GTGCTGTGTT	1260
	GATAAGGATT	TGGATTCGTT	CAGCGAGGCG	AGCCTGGGCT	CCCACTTCGA	GTTCCCGGAC	1320
	TACTGCACGC	CGGAGCTGAG	CGAGATGATC	GCGGGGAGCT	GGCTGGAGGC	GAACCTTCTC	1380
	GACCTGGTGT	TCACATATTG	AAAGGCGCCC	GCTGCTCGCT	CTTTCTCTCG	GAGGGTGATG	1440
	AGCTGGGTTT	CTGGGAGGA	AGTTGTAGTG	GTGATGATGA	TGATGATGAT	AATGATGATG	1500
70	ATGATGGTGG	TGTTGATGGT	GCGGTGGTA	GGGTGGAGGG	GAGAGAAGAA	GATGCTGATG	1560
	ATATTGTATA	GATGTCGTGA	CGCAAGAAA	TTGGAAAACA	TGATGAAAAT	TTGGTGGAG	1620
	TTAAAGTGAA	ATGATGATTT	TTTAAACATT	TTTCTGTGTC	TTTTTTTGTG	CCCCCTCCCT	1680
	TCCTTTATCG	TGCTCAAGG	TAGTTGCATA	CCTAGTCTGG	AGTTGTGATT	ATTTTCCCAA	1740
	AAAATGTGTT	TTTGTAAATTA	CTATTTCTTT	TTCTGAAAT	TCGTGATTGC	AACAAGGCA	1800
75	GAGGGGGCGG	CGCGCGGAG	GGGAGGTAGG	ACCGCTCCG	GAAGGCGCTG	TTTGAAGCTT	1860
	GTCGGTCTTT	GAACTCTGGA	AGACGCTGCG	AGAGGACCTT	TTTGGCAGCA	CAACTGTTAC	1920
	TCTAGGGAGT	TGGTGGAGAT	ATTTTTTTTT	CTTAAGAGAA	CTTAAAGAAC	TGGTGATTTT	1980
	TTTTTAACAA	AAAAAGGG					

Seq ID NO: 657 Protein sequence
Protein Accession #: NP_003099.1

80	1	11	21	31	41	51	
	MVQQAESLEA	ESNLPREALD	TEEGEFMACS	FVALDESDPD	WCKTASGHIK	RPMNAFMVWS	60
85	KIERRKIMQ	SPDMHNAEIS	KRLGKRWKML	KDSEKIPFIR	EAERLRRLKH	ADYPDYKYRP	120
	RKKPKMNDPSA	KPSASQSEPK	SAAGGGGGSA	GGGAGGAKTS	KGSSKCKGKL	KAPAAAGAKA	180
	GAGKAQSGD	YGGAGDDYVL	GSLRVSGSGG	GGAGKTVKCV	FLDEDDDDDD	DDDELQLQIK	240

QEPDEDEEP PHQQLLPFG QPSPQLRRY NVAKVPASPT LSSSAESPEG ASLYDEVBRAG 300
 ATSGAGGGSR LYSYFKNITK QHPPLAQPA LSPASSRSVS TSSSSSSGSS SGSSGEDADD 360
 LMFDSLNLFS QSAHSASEQQ LGGAAAAGNL SLSLVDKOLD SPSEGLSGSH FEPFDYCTPE 420
 LSEMIAGDWL EANFSDLVFT Y

Seq ID NO: 658 DNA sequence
 Nucleic Acid Accession #: NM_001719
 Coding sequence: 123..1418

10 1 11 21 31 41 51
 | | | | | |
 GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
 CTGCCACCTG GGGCGGTGCG GGGCCGGAGC CGGAGAGCCG GGTAGCGCGT AGAGCCGGCG 120
 CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC 180
 15 CCCTGTTCTT GCTGCGTCCG GCCTTGCCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240
 GCTTCATCCA CCGCGCGCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
 CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
 CCATGTTTCT GCTGGAGCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
 GCGAGGGCTT CTCTACACCC TACAAGGCGG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
 20 GCCTGCAAGA TAGCATTTC CTACCGAGC CCGACATGGT CATGAGCTTC GTCAACCTCG 540
 TGGAAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
 TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT 660
 ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
 AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCTCCGG 780
 25 AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACAGCAA CCACTGGGTG GTCAATCCGC 840
 GGCACAACCT GGGCTGTGCG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900
 AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT 960
 TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AAACAGCGCA 1020
 GCGAGAACC CGCTCAAGAC CCAGAAGACC AGGAAGCCCT CGGATGGGCC AACGTGGCGA 1080
 30 AGAAGCAGCA CAGGACAGC AGGACGGCCT GTAAGAAGCA CGAGCTGTAT GTCACTTCC 1140
 GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG 1200
 AGGGGGAGTG TGCCTTCCTT CTGAATCCTT ACATGAACGC CACCAACCAC GCCATCGTGC 1260
 AGACGCTGGT CCACCTTCATC AACCCGGAAG CGGTGCCCAA GCCCTGCTGT GCGCCACGCG 1320
 AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTATCT CTGAAGAAAT 1380
 35 ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCTT 1440
 TTGGGGCCAA GTTTTCTGCG ATCTCCTATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
 CTGCCTTTTG TGAGACCTTC CCTCCCTAT CCGCAACTTT AAAGGTGTGA GAGTATTAGG 1560
 AAACATGAGC AGCATATGGC TTTTGTATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
 TCTTACAAGC TGTGCAGGCA AAACCTAGCA GGAAGAAAAA ACACGCATA AAGAAAAATG 1680
 40 GCGGGGCGAG GTACATTGGT GGAAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
 TTATGAGGCG CTACCAAGCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
 GGGCACAATT GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
 CAATAAAACG AATGAATG

Seq ID NO: 659 Protein sequence
 Protein Accession #: NP_001710

1 11 21 31 41 51
 | | | | | |
 50 MHVRSRAAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRRLSQB RREMQRILS 60
 ILGLPHRRPP HLGQKHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
 LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHREFRFDL SKIPEGEAVT AAEFRIYKDY 180
 IRERFDNETF RISVYQVLQE HLGRESDLPL LDSRTLWASE EGWLVDITA TSNHWVNVPR 240
 55 HNLGLQLSVE TLDQGSINPK LAGLIGRHGP QNKQPPMVAP FKATEVHFRSIRSTGSKQRS 300
 QNRSTPKNQ EALRMANVAE NSSSDQRQAC KKHELYVSFR DLGWQDWIIA PEGYAAYYCE 360
 GECAFLNSY MNATNHAIVQ TLVHFINPET VFKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
 RNMVVRACGC H

Seq ID NO: 660 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 211..1895

1 11 21 31 41 51
 | | | | | |
 65 GGATCTGAGG GGGCCCCAGT CACTTCCTCC ACGTTCTCGT GCTGGGCGGG AGGAGCGGAT 60
 GGGGCTTGGG AGGCAGCCTG CTCTCCAGTC CCTATCCACC CACAGGTTTT TTGGGTGCGA 120
 GAGGAATTAT CTGATAAAAT TCCTGGGTGA ATATTTTAA AAACGGAGAG TTTTAAATAA 180
 TGATTTTTTT CCCTCGAAAA TGACCTTTTT ATGCTTCGAA GCAGTTTGTC AACCAGCATA 240
 70 GTGCTTTTTC TTTTCTCTTC TTTTCTACG ATAAATGAAA GCATTTCTTC AAGAAAAAGG 300
 CACAGGTTCC TTGAACAGCT GGATTCTGAT GGCACCATTA CTATAGAGGA GCAGATTGTC 360
 CTTGTGCTGA AAGCGAAAGT ACAATGTGAA CTCACATCA CAGCTCAACT CCAGGAGGGA 420
 GAAGGTAATT GTTTCCCTGA ATGGGATGGA CTCATTGTGT GGCCAGAGG AACAGTGGG 480
 AAAATATCGG CTGTTCCATG CCCTCCTTAT ATTTATGACT TCAACCATAA AGGAGTTGCT 540
 75 TTCCGACACT GTAACCCCAA TGGACATGG GATTTTATGC ACAGCTTAA TAAACATGG 600
 GCCAATTATT CAGACTGCCT TCGCTTCTG CAGCCAGATA TCAGCATAGG AAGCAAGAA 660
 TTCTTTGAAC GCCTCTATGT AATGTATACC GTTGGCTACT CCATCTCTTT TGGTTCCTTG 720
 GCTGTGGCTA TTCTCATCAT TGGTTACTTC AGACGATTGC ATTGCACATG GAACTATATC 780
 CACATGCATC TATTGTGTCT TTTTCATGCT AGAGCTACAA GCATCTTTGT CAAAGACAGA 840
 80 GTAGTCCATG CTCACATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA 900
 CAAAATTCGA TTGAGGCAAC TTTCTGGAC AAATCACAAT ATATCGGGTG CAAGATTGCT 960
 GTTGTGATGT TTATTTACTT CTTGGCTACA AATTATTATT GGATCCTGGT GGAAGGTCTC 1020
 TACCTGCATG ATCTCATCTT TGTGGCTTTC TTTTCGGACA CCAATACCT GTGGGGCTTC 1080
 ATCTTGATAG GCTGGGGGTT TCAGCAGCA TTTGTTCAG CATGGGCTGT GGCACAGCA 1140
 85 ACTCTGGCTG ATGCGAGGTG CTGGGAACCT AGTGTCTGAG ACATCAAGTG GATTTATCAA 1200
 GCACCGATCT TAGCAGCTAT TGGGCTGAAT TTTATCTGT TTCTGAATAC GGTTAGAGTT 1260
 CTAGCTACCA AAATCTGGGA GACCAATGCA GTTGGGCATG ACACAAGGAA GCAATACAGG 1320
 AAATGGCCA AATCGACACT GGTCTGGTCT CTAGTCTTTG GAGTGCATTA CATCGTGTTC 1380

GTATGCCCTGC CTCACCTCCTT CACTGGGCTC GGGTGGGAGA TCCGCATGCA CTGTGAGCTC 1440
 TTCTTCAACT CCTTTCAGGG TTTCTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG 1500
 GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CCGTGAATC TCTCCGTGGA CTGGAAGAG 1560
 ACACCGCCAT GTGGCAGCCG CAGATGCGCG TCAGTGCTCA CCACCGTGAC GCACAGCACC 1620
 AGCAGCCAGT CACAGGTGGC GCCCAGCACA CGCATGGTGC TTATCTCTGG CAAAGCTGCC 1680
 AAGATCGCCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGGAGTAAC 1740
 TCAGAGCAGG ACTGCCCTGCC ACACCTCTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG 1800
 CAGGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCCTA TGAATCTAA CCCAGACACT 1860
 GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA

Seq ID NO: 661 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MLRSSLSSTSI VLFLPSSFST INESSISRKR HRFLEQLDSD GTITIEEQIV LVLKAKVQCE 60
 LNTAQLQEQ EQNCFPEWDG LICWPRGTVG KISAVFCPPY IYDFNHKGVA FRHCNPNGTW 120
 DFMHSLNKTW ANYSDCLRFL QPDISIGKQE FFERLYVMYT VGYSISFGSL AVAILLIQYF 180
 RRLHCTRNYYI HMHLFVSPML RATSIFVKDR VVHAHIGVKE LESLIMQDDP QNSIEATSVD 240
 KSOYIGCKIA VVMFIYFLAT NYYWILVEGL YLHNLIFVAF FSDTKYLWGF ILIGWFPFAA 300
 FVAWAVARA TLADARCWEL SAGDIKWIYQ ABILAAIGLN FILFLNTRV LATKIWETNA 360
 VGHDRKQYR KLAKSTLVLV LVFGVHYIVF VCLPHSFTGL GWEIRMHCEL PFNSFQGFV 420
 SLIYCYNGE VQAEVKMWS RWNLSVDWKR TPFCGSRRCG SVLTTVTHTS SSQSQAAS 480
 RMVLISGKAA KIASRQPDH ITPGYVWSN SEQDCLPHSF HEETKEDSGR QGDDILMEKP 540
 SRPMESNPDT EGCGQETEDV L

Seq ID NO: 662 DNA sequence
 Nucleic Acid Accession #: NM_005048
 Coding sequence: 143..1795

1 11 21 31 41 51
 GGCCGGTGGC CCGGGCCCGA CCACCCAGC TGCGCGTCTG TACTGGCCAC AAGTTTGCTC 60
 TGGGCCAGCC AAGTTGGCAA CTTGGAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT 120
 TCTTCTTACA GCGGTTCCGG GCATGGCCGG GCTGGGGGCG TCGCTCCACG TCTGGGGTTG 180
 GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCAGCTG GATTCTGATG GCACCATPAC 240
 TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300
 AGCTCAACTC CAGGAGGGAG AAGGTAATG TTTCCCTGAA TGGGATGGAC TCATTGTGTTG 360
 GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCATGCG CCTCCTTATA TTTATGACTT 420
 CAACCATAAA GGAAGTTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480
 CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTCTGCG AGCCAGATAT 540
 CAGCATAGGA AAGCAAGAA TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600
 CATCTCTTTT GGTCTCTTGG CTGTGGCTAT TCTCATCAT GGTACTTCA GACGATTGCA 660
 TTGCACTAGG AACTATATCC ACATGCACTT ATTTGTGTCT TTATGCTGA GAGCTACAAG 720
 CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780
 AATAATGAGC AGTACGCCAC AAAAATCCAT TGAGGCAACT TCTGTGGACA AATCACAATA 840
 TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATTG 900
 GATCCTGCTG GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTCTT TTTCCGACAC 960
 CAAATACCTG TGGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTTGCAGC 1020
 ATGGGCTGTC GCACGAGCAA CTCTGGCTGA TGCGAGGTGC TGGGAACCTA GTGCTGGAGA 1080
 CATCAAGTGG ATTTCTCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140
 TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA 1200
 CACAAGGAAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCCTGGTCC TAGTCTTTGG 1260
 AGTGCATTAC ATCGTGTTCG TATGCCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT 1320
 CCGCATGCAG TGTGAGCTCT TCTTCAACTC CTTTCAGGGT TTCTTTGTGT CTATCATCTA 1380
 CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT 1440
 CTCCGTGGAG TGGAAAAGGA CACCGCCATG TGGCAGCCCG AGATGCGGCT CAGTGCTCAC 1500
 CACCGTGACG CACAGCACA CAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560
 TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACTTTACC 1620
 TGGCTATGTC TGGAGTAACT CAGAGCAGGA CTGCCTGCCA CACTCTTTCC ACGAGGAGAC 1680
 CAGGAAGAT AGTGGGAGGC AGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT 1740
 GGAATCTAAC CCAGACACTG AAGGATGCCA AGGAGAACT GAGGATGTTT TCTGAATGGA 1800
 CATTTGTGGC TGACTTTTCAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG 1860
 ATACTCCTAT GCTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTACTT TAATAATAGT 1920
 TTTTAGGCTC CATGAATTGG CTCTGTAAA TACTAACGAC ATGAAAATGC AAGTGTCAAT 1980
 GGAGTAGATT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATTT 2040
 GCTCTGTGAT TGTTCATTTT TTTCTGCTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG 2100
 GCTGTAGCTT TCTCTCATAT ATATCACCTT AAATATAATG AAGATCTTTT AGTGTGTATC 2160
 ATTTTCTCTT TAGAACTAG TATTCTCTTA TTTCTTACTT TAATGTACTT CTATCACTGC 2220
 ATTTATTTTG CCTGTGCATA GGAGCAATTA GATCTAAAA AAATATATGG GAAGATAAAA 2280
 GATCTAAGAA CAAGTACTTG CTGGAAAAAT AGTTGGCTGG ACATTGATAA AATAATGCAT 2340
 TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAAATT CTCAAAAAAG AATATTTCAC 2400
 ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC 2460
 TTCTTTGTAA ACCATGTCTAT GTGGAAAGAT TTCTCAGTT AGTGAGCTTG TGTCTGCAAA 2520
 TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTTCTTG 2580
 TTTGAGCTGT TACTACATTG TACATGGCAT GTGGATCAAA TTAATAAATT GTTTTAAAAA 2640

Seq ID NO: 663 Protein sequence
 Protein Accession #: NP_005039

1 11 21 31 41 51
 MAGLQASLHV WGLMLGSLC LARAQLDSGD TITIEEQIVL VLKAKVQCEL NITAEQLQEG 60
 GNCPEWDGL ICWPRGTGK ISAVFCPPYI YDFNHKGVA FRHCNPNGTW FMSLNLKNTWA 120
 NYSDCLRFLQ PDISIGKQEF FERLYVMYT VGYSISFGSL VAILLIQYPR RLHCTRNYYI 180
 MHLFVSPMLR ATSFVVDKRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240

WO 02/086443

PCT/US02/12476

5 VMPIYFLATN YYWILVEGLY LHNLIIVVAF SDTKYLWGF IIGWGFPAAF VAAWAVARAT 300
LADARCWELS AGDIKWIYQA PILAAIGLNF ILFLNIVRVL ATKIWETNAV GHDTRKQYRK 360
LAKSTLVLVL VFGVHYIVFV CLPHSFTGLG WEIRMHCELF FNSFGGFVS IYCYCNGEV 420
QAEVKMWSR WNLSDWKRT PPCGSRRCS VLTTVTHSTS SQSQVAASR MVLISGKAAK 480
IASRQPDSEI TLPGYVWSN EQDCLPHSFH EETKEDSGRQ GDDILMEKPS RPEMESNPDE 540
GCQGETEDVL

Seq ID NO: 664 DNA sequence
Nucleic Acid Accession #: NM_012152
Coding sequence: 43..1104

1 11 21 31 41 51
15 CTCTTTTAAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTGCA TGAAGTGACA 120
GGAACAAAGC TTGTGATTTG TTTGTGTGTT GGGACGTTTT TCTGCCTGTT TATTTTTTTT 180
TCTAATTTCT TGGTCATGCG GGCAGTGATC AAAACAGAAA AATTTCATT CCCTTCTTAC 240
TACCTGTGCG CTAATTTAGC TGCTGCCGAT TTCTTCGCTG GAATTCGCTA TGTATTCTCG 300
ATGTTTAAAC CAGGCCAGT TTCAAAACT TGACTGTCA ACCGCTGGTT TCTCCGTGAG 360
20 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG 420
AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480
CTGCTCATTT TGCTTGTCTG GGCATCTGCC ATTTTATGCG GGGCGTCCC CACACTGGGC 540
TGAATTTGCC TCTGCAACAT CTCTGCCTGC TCTTCCCTGG CCCCATTATA CAGCAGGAGT 600
25 TACCTTGTGT TCTGGACAGT GTCCAACTTC ATGGCCTTCC TCATCATGGT TGTGGTGATC 660
CTGCGGATCT ACGTGTAGCT CAAGAGGAAA ACCAACCTCT TGTCTCCGCA TACAAGTGGG 720
TCCATCAGCG CCGGAGGAGC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780
GCGTTTGTGG TATGCTGGAC CCGGGGCTCG GTGGTCTGCT TCCTCGACGG CTGAACTGCG 840
AGGCAGTGTG CGCTGCAGCA TGTGAAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC 900
30 GTGCGAACC CCATCTCTCA CTCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960
ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGCGTC CCTCTCGCAT CCCCTCCACA 1020
GTCTCAGCA GAGTGTACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080
GTCTGCAATA AAAGCACTTC CTAACTCTG GATGCTCTC GGGCCACCCA GGTGATGACT 1140
GTCTTAGG

35 Seq ID NO: 665 Protein sequence
Protein Accession #: NP_036284

1 11 21 31 41 51
40 MNECHYDKHM DFFYNRSNTD TVDDWTGKTL VIVLCVGTFF CLFIFFSNSL VIAAVIKNRK 60
PHEPFYYLLA NLAAADFAPG IAYVFLMFT GPVSKTLTVN RWPLRQGLLD SSLTASLTNL 120
LVIAVERHMS IMRMVHNSL TKKRVTLILL LVMAIAIFMG AVPTLGNCL CNISACSSLA 180
PIYSRSYLVF WTVSNLMAFL IMVVVYLRIV VVVKRKTNLV SPHTSGSISR RRTFPMKLMKT 240
45 VMTVLGAFVW CWTPLGVLLD LDGLNCRQCG VQHKRWKPLF LALLNSVNP IISYKDEDM 300
YGTMKMIMCC FSQNPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

Seq ID NO: 666 DNA sequence
Nucleic Acid Accession #: NM_002821
Coding sequence: 150..3362

1 11 21 31 41 51
50 AACTCCCGCC TCGGGACGCC TCGGGTCCGG GCTCCGGCTG CGGCTGCTGC TCGGGGCCCC 60
GCGCTCCGGT GCGTCCGGCT CCTGTGCCCC CGCGGAGCA GTCTGCGGCC CGCGTGCGCC 120
55 CCTCAGCTCC TTTTCTGAG CCGCGCGCGA TGGGAGCTGC CGCGGGATCC CCGGCCAGAC 180
CCGCGCGGTT GCGTCTGCTC AGCGTCCCTG TGCTGCCGCT GCTGGCGGTT ACCCAGACAG 240
CCATTGTCTT CATCAGCAG CCGTCTCTCC AGGATGCACT GCAGGGGCGC CGGGCGCTGC 300
TTGCTGTGTA GGTGTAGGCT CCGGGCCCGG TACATGTGTA CTGGCTGCTC GATGGGGCCC 360
60 CTGTCCAGGA CACGAGCGCG CGTTTCGCCC AGGCGAGCAG CCTGAGCTTT GCAGCTGTGG 420
ACCGGCTGCA GAGCTCTGGC ACCTTCCAGT GTGTGGCTCG GGATGATGTC ACTGGAGAAG 480
AAGCCCGCAG TGCCCAACGCC TCCTTCAACA TCAAAATGGT TGAGGCAGGT CCTGTGGTCC 540
TGAAGCATCC AGCCTCGGAA GCTGAGATCC AGCCACAGAC CCAGGTCACT CTTCGTGTCC 600
ACATTGATGG GCACCTCGG CCACTTACC AATGGTTCCG AGATGGGACC CCCCTTTCTG 660
65 ATGGTCAGAG CAACACACA GTGAGCAGCA AGGAGCGGAA CCTGAGCTCT CGGCCAGCTG 720
GTCTCTGAGCA TAGTGGGCTG TATCTCTGCT GCGCCACAG TGCTTTTGGC CAGGCTTGCA 780
GCAGCCAGAA CTTCACCTTG AGCATTTGCT ATGAAAGCTT TGCCAGGGTG GTGCTGGCAC 840
CCGAGGACGT GGTAGTAGCG AGGTATGAGG AGGCCATGTT CCATTGCCAG TTCTCAGCCC 900
AGCCACCCCC GAGCTGTCAG TGGCTCTTTG AGGATGAGAC TCCCATCACT AACCGCAGTC 960
70 GCGCCCCACA CCTCCGAGA GCCACAGTGT TTGCCAACGG GTCTCTGCTG CTGACCCAGG 1020
TCGCGCCAGC CAATGCAGGG ATCTACCGCT GCATTGGCCA GGGGCGAGGG GCGCCACCCA 1080
TCATCTGGA AGCCACACTT CACTAGCAG AGATTGAAGA CATGCCGCTA TTTGAGCCAC 1140
GGGTGTTTAC AGCTGGCAGC GAGGAGCGTG TGACCTGCCT TCCCCCAAG GGTCTGCCAG 1200
AGCCAGCGT GTGGTGGGAG CACGCGGGAG TCCGGCTGCC CACCCATGGC AGGGTCTACC 1260
75 AGAAGGGCCA CGAGCTGGTG TTGGCAATA TTGCTGAAAG TGATGCTGGT GTCTACACCT 1320
GCCACGCGC CAACCTGGCT GGTGAGGGA GACAGGATGT CAACATCACT GTGGCCACTG 1380
TCCCTCTCTG GCTGAAGAAG CCCCAGACA GCCAGCTGGA GGAGGGCAAA CCGGCTACT 1440
TGGATTGCGT GACCCAGGCC ACACCAAAAC CTACAGTTGT CTGTGACAGA AACCATGTC 1500
TCATCTGGA GAGCTCAGG TCGAGGTCT TCAAGAAATG GACCTTGCGC ATCAACAGCG 1560
80 TGAGGTGTA TGATGGGACA TGGTACCGTT GTATGAGCAG CACCCAGGCC GGCAGCATCG 1620
AGGCGCAAGC CCGTGTCCAA GTGCTGGAAG AGCTCAAGTT CACACCAACA CCCCAGCCAC 1680
AGCAGTGCAT GGAGTTTGAC AAGGAGGCCA CGGTGCCCTG TTCAGCCACA GCGGAGAGA 1740
AGCCCACTAT TAAGTGGGAA CGGCGAGATG GGAGCAGCCT CCCAGAGTGG GTGACAGACA 1800
ACGCTGGGAG CCGTCAATTT CCGCGGGTGA CTCGAGATGA CGCTGGCAAC TACACTTGCA 1860
85 TTGCTCCAA CGGGCCGAG GGCAGATTC GTGCCCATGT CCAGCTCACT GTGGCAGTTT 1920
TTATCACCTT CAAAGTGGAA CCAGAGCGTA CGACTGTGTA CCAGGGCCAC ACAGCCCTAC 1980
TGCAGTGCGA GCGCCAGGGG GACCCCAAGC CGCTGATTCA GTGGAAGGCG AAGGACCGCA 2040
TCCTGGACCC CACCAAGCTG GGACCCAGGA TGACATCTT CCAGAAATGG TCCTGGTGA 2100

	TCCATGACGT	GGCCCCGTGAG	GACTCAGGCC	GCTACACCTG	CATTGCAGGC	AACAGCTGCA	2160
	ACATCAAGCA	CACGGAGGCC	CCCTCTATG	TCGTGGACAA	GCCTGTGCCG	GAGGAGTCGG	2220
	AGGGCCCTGG	CAGCCCTCCC	CCCTACAAGA	TGATCCAGAC	CATTGGGTTG	TCGGTGGGTG	2280
5	CGCTGTGGC	CTACATCATT	GCCGTGCTGG	GCCTCATGTT	CTACTGCAAG	AAGCGCTGCA	2340
	AAGCCAAAGC	GCTGCAGAAG	CAGCCCCGAG	GCGAGGAGCC	AGAGATGGAA	TGCCTCAACG	2400
	GAGGGCCCTT	GCAGAACGCG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
	GCTTGGGCTC	CGGCCCGCG	GCCACCAACA	AACGCCACAG	CACAAGTGAT	AAGATGCACT	2520
	TCCACGCTC	TAGCTGTCAG	CCCATCACCA	CGCTGGGGA	GAGTGAGTTT	GGGGAGGTGT	2580
10	TCCTGGCAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCCTGGTA	CTTGTGAAGA	2640
	GCCTGCAGAC	GAAGGATGAG	CAGCAGCAGC	TGGACTTCCG	GAGGGAGTTG	GAGATGTTTG	2700
	GGAAAGCTGAA	CCACGCCAAC	GTGGTGGCGC	TCCTGGGGCT	GTGCCGGGAG	GCTGAGCCCC	2760
	ACTACATGGT	GCTGGAATAT	GTGGATCTGG	GAGACCTCAA	GCAGTTCCCTG	AGGATTTCCA	2820
	AGAGCAAGGA	TGAAAAATTG	AAGTCACAGC	CCCTCAGCAC	CAAGCAGAAG	GTGGCCCTAT	2880
15	GCACCCAGGT	AGCCCTGGGC	ATGGAGCACC	TGTCCAACAA	CCGCTTTGTG	CATAAGGACT	2940
	TGGCTGCGCG	TAACTGCGTG	GTCACTGCCC	AGAGACAAGT	GAAGGTGTCT	GCCCTGGGCC	3000
	TCAGCAAGGA	TGTTGACAAC	AGTGAAGTACT	ACCACCTTCG	CCAGGCTCGG	GTGCGCTGCG	3060
	GCTGGATGTC	CCCCGAGGCC	ATCCTGGAGG	GTGACTTCTC	TACCAAGTCT	GATGTCTGGG	3120
	CCTTCGGTGT	GCTGATGTGG	GAAGTGTTTA	CACATGGAGA	GATGCCCAT	GGTGGGCAGG	3180
20	CAGATGATGA	AGTACTGGCA	GATTTGCAGG	CTGGGAAGGC	TAGACTTCCT	CAGCCCGAGG	3240
	GCTGCCCTTC	CAAACTCTAT	CGGCTGATGC	AGCCTCTGCT	GGCCCTCAGC	CCCAGGACC	3300
	GGCCCTCCTT	CAGTGAAGAT	GCCAGCGCCC	TGGGAGACAG	CACCGTGAC	AGCAAGCCGT	3360
	GAGGAGGAG	CCGCTCAGG	ATGGCCTGGG	CAGGGGAGGA	CATCTCTAGA	GGGAAGCTCA	3420
	GCCATGATG	GCAAGATTC	CTGTCTCTCT	GGGCCCTGAG	GTGCCCTAGT	GCAACAGGCA	3480
25	TTGCTGAGGT	CTGAGCAGGG	CCTGGCCTTT	CCTCCTCTTC	CTCACCTCA	TCCTTTGGGA	3540
	GGCTGACTTG	GACCCAAACT	GGGCGACTAG	GGCTTTGAGC	TGGGCAGTTT	CCCCTGCCAC	3600
	CTCTCTCCTT	ATCAGGGACA	GTGTGGGTGC	CACAGGTAAC	CCCAATTCT	GCCCTTCAAC	3660
	TTCTCCCTTT	CAGCGGTGCC	AACTCTGCCA	CTCATCTGCC	AACTTTGCTC	GGGGAGGGCT	3720
	AGGCTTGGGA	TGAGCTGGT	TTGTGGGGAG	TTCCTTAATA	TTCTCAAGTT	CTGGGCACAC	3780
30	AGGGTTAATG	AGTCTCTTGC	CCACTGGTCC	ACTTGGGGGT	CTAGACCAGG	ATTATAGAGG	3840
	ACACAGCAAG	TGAGTCTCTC	CCACTCTGGG	CTTGTGCACA	CTGACCAGG	CCCACGCTTT	3900
	CCCCACCCTT	CTCTCTTTTC	CTCATCTTAA	GTGCTTGSCA	GATGAAGGAG	TTTTCAGGAG	3960
	CTTTTGACAC	TATATAAACC	GGCCTTTTTG	TATGCACCAC	GGGCGGCTTT	TATATGTAAT	4020
	TGACGCTGG	GGTGGGTGGG	CATGGGAGGT	AGGGGTGGGC	CCTGAGATG	AGGAGGGTGT	4080
35	GCCATCCTTA	CCCCACACTT	TTATTGTTGT	CGTTTTTTGT	TTGTTTTGTT	TTTTTGTTTT	4140
	TGTTTTTGT	TTTACACTCG	CTGCTCTCAA	TAAATAAGCC	TTTTTTA		

Seq ID NO: 667 Protein sequence

Protein Accession #: NP_002812

40	1	11	21	31	41	51	
	MGAARGSPAR	PRRLPLLSVL	LLPLLGTTQT	AIVPIKQPS	QDALQRRAL	LRCEVEAPGP	60
	VHVYVLLDGA	PVDQTERFPA	QSSLSFAAV	DRLQDSGTFQ	CVARDDVTGE	EARSANASFN	120
45	IKWIEAGPVV	LKHPASAEI	QPTQVTLRC	HIDGHPRTY	QWFRDGTPLS	DGQSNHTVSS	180
	KERNLTLRPA	CPEHSGLYSC	CAHSAFGQAC	SSQNFLLSIA	DESFAFVULA	PQDVVVARYE	240
	EAMPHCQFSA	QPPPSLQWLF	EDETPITNRS	RPPHLRRATV	FANGSLLLTQ	VRPRNAGIYR	300
	CIGQQQRGPP	IILEATLHLA	ETEDMPLFEP	RVFTAGSEER	VTCLPFGKLP	EPFVWWEHAG	360
	VRLPPTHGRVY	QKGEHLVLAN	IAESDAGVYT	CHAANLAGOR	RQDVNITVAT	VPFWLKKPQD	420
50	SQLBEGKPGY	LDCLTQATPK	PTVVWYRNQM	LISEDSPREF	FKNGTLRINS	VEVYDGTWYR	480
	CMSSTFAGSI	EAGARVQVLE	KLKFTPPPPQ	QCCMEFDKEA	TVPCSATGRE	KPTIKWERAD	540
	GSSLPFWVTD	NAGTLHFARV	TRDDAGNYTC	IASNGPQQQI	RAHVQLTVAV	FITFRVEPER	600
	TTVYQGHATL	LQCEAQGDPK	PLIQWKGKDR	ILDPTKLGRP	MHIFQNGSLV	IHDVAPEDSG	660
	RYTCLAGNSC	NKHTTEAPLY	VVDKPVPEES	EGPGSPPPYK	MIQTIGLSVG	AAVAYIIAIV	720
55	GLMPYCKKRC	KAKRLQKQPE	GEEPEMECLN	GGPLQNGQPS	AEIQEEVALT	SLGSGPAAATN	780
	KRHSTSDKMH	PPRSSTLQPI	TLGKSEFGEV	FLAKAQGLEE	GVAETLVLVK	SLQTKDEQQQ	840
	LDPRRELEMF	GKLNHANVVR	LLGLCREAEP	HYMVLEYVDL	GDLKQFLRIS	RSKDEKLSQ	900
	PLSTKQKVAL	CTQVALGMEH	LSNNRPFVHK	LAARNCLVSA	QRQVKVSALG	LSKDVYNSEY	960
	YHFRQAWVPL	RWMSPEAILE	GDFSTKSDVW	AFGLVMWEVF	THGEMPHGGQ	ADDEVLDLQ	1020
60	AGKARLPQPE	GCPSKLYRLM	QRCWALSPKD	RPSFSEIASA	LGDSTVDSKP		

Seq ID NO: 668 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1389

65	1	11	21	31	41	51	
	ATGGGCTACC	AGAGGCAGGA	GCCTGTCTATC	CCGCCGACAGA	GAGATTAGA	TGACAGAGAA	60
	ACCTTGTCTT	CTGAACATGA	GTATAAAGAG	AAAACCTGTC	AGTCTGCTGC	TCTTTTAAAT	120
70	GTTGTCAACT	CGATTATAGG	ATCTGGTATA	ATAGGATTGC	CTTATTCAAT	GAAGCAAGCT	180
	GGGTTTCCTT	TGGGAATATT	GCTTTTATTC	TGGGTTTCAT	ATGTTACGGA	CTTTCCCTT	240
	GTTTATTGTA	TAAAGGAGG	GGCCCTCTCT	GGAACAGATA	CCTACCAGTC	TTTGGTCAAT	300
	AAAACCTTCG	GCTTTCAGG	GTATCTGCTC	CTCTCTGTTC	TTCAGTTTTC	GTATCCTTTT	360
	ATAGCAATGA	TAAGTTACAA	TATAATAGCT	GGAGATACTT	TGAGCAAAGT	TTTTCAAAGA	420
	ATCCAGGAG	TTGATCTGTA	AAACGTGTTT	ATTGGTGGCC	ACTTCATTAT	TGGACTTTCC	480
75	ACAGTTACTT	TTACTCTGCC	TTTATCCTTG	TACCGAAATA	TAGCAAAGCT	TGGAAAGGTC	540
	TCCCTCATCT	CTACAGGTTT	AACAACCTCTG	ATTCCTGGAA	TTGTAATGGC	AAGGGCAATT	600
	TCACCTGGGT	CACACATACC	AAAAACAGAA	GACGCTGGG	TATTTGCAAA	GCCCAATGCC	660
	ATTCAAGCGG	TCGGGGTTAT	GTCTTTTGCA	TTTATTGGCC	ACCATAACTC	CTTCTTAGTT	720
	TACAGTTCTC	TAGAAGAACC	CACAGTAGCT	AAGTGGTCCC	GCCTTATCCA	TATGTCCATC	780
80	GTGATTTCTG	TATTTATCTG	TATATCTCTT	GCTACATGTG	GATACCTTAC	ATTTACTGGC	840
	TTCAACCAAG	GGGACTTATT	TGAAAATTAC	TGCAGAAATG	ATGACCTGGT	AACATTTGGA	900
	AGATTTTGTG	ATGCTGTCTC	TGTCAATTTG	ACATACCCTA	TGGAATGCTT	TGTGACAAGA	960
	GAGGTAATTG	CCAATGTGTT	TTTTGGTGGG	AATCTTTTCT	CGGTTTTCCT	CATTGTTGTA	1020
	ACAGTGAATG	TCATCACTGT	AGCCAGCTTT	GTGTCATTGC	TGATTGATTG	CCTCGGGATA	1080
85	GTTCTAGAAC	TCAATGAGGT	GCTCTGTGCA	ACTCCCTTCA	TTTTTATCAT	TCCATCAGCC	1140
	TGTATCTGTA	AACGTCTGTA	AGAACCAAGG	ACACACTCCG	ATAAGATTAT	GTCTTGTGTC	1200
	ATGCTTCCA	TTGGTGTCTG	GGTGATGGTT	TTTGGATTGC	TCATGGCTAT	TACAAATACT	1260

WO 02/086443

PCT/US02/12476

CAAGACTGCA CCCATGGGCA GGAAATGTTT TACTGCTTTC CTGACAATTT CTCTCTCACA 1320
AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTTAAA TATTAGTATC 1380
TTTCAATGA

5 Seq ID NO: 669 Protein sequence
Protein Accession #: Eos sequence

1	11	21	31	41	51	
MGYQRQEPVI	PPQRDLDDRE	TLVSEHEYKE	KTCQSAALFN	VVNSIIGSGI	IGLPYSMKQA	60
GFPLGILLFF	WVSYYTDFSL	VLLIKGGALS	GTDTYQSLVN	KTFGPPGYLL	LSVLQFLYPF	120
IAMISYNIIA	GDTLKVFQFR	IPGVDPENVF	IGRHFIIGLS	TVFTFLPLSL	YRNIACLKGV	180
SLISTGLTTL	ILGIVMARAI	SLGPHIEKTE	DAMVFAKENA	IQAVGVMSFA	FICHENSFLV	240
YSSLEPTVA	KWSRLIHMSI	VISVFCIPFF	ATCGYLTFPTG	FTQGDLFENY	CRNDLVLTFG	300
RFCYGVTVIL	TYPMECFVTR	EVIANVFFGG	NLSSVPHIVV	TMVITVATL	VSLLIDCLGI	360
VLELNGVLCA	TFPLFIIPSA	CYLKSEEPER	THSKIMSCV	MLPIGAVVMV	FGFVMAITNT	420
QDCTHGQEMF	YCFPDNFSLT	NTSESHVQQT	TQLSTLNISI	FQ		

20 Seq ID NO: 670 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1284

1	11	21	31	41	51	
ATGGGCTACC	AGAGGCAGGA	GCCTGTCATC	CCGCCGCGAGA	GAGGATTGCC	TTATTCAATG	60
AAGCAAGCTG	GGTTTCCTTT	GGGAATATTG	CTTTTATTCT	GGGTTTCATA	TGTTACAGAC	120
TTTTCCTCTG	TTTATTGATG	AAAAGGAGGG	GCCCTCTCTG	GAACAGATAC	CTACCACTCT	180
TTGGTCAATA	AACTTTCCGG	CTTCCAGGG	TATCTGCTCC	TCTCTGTTCT	TCAGTTTTTG	240
TATCCTTTTA	TAGCAATGAT	AAGTTACAAT	ATAATAGCTG	GAGATACTTT	GAGCAAAAGT	300
TTTCAAAGAA	TCCCAGGAGT	TGATCCTGAA	AACGTGTTTA	TTGGTGGCCA	CTTCATTATT	360
GGACTTTCCA	CAGTTACCTT	TACTCTGCCT	TTATCCTTGT	ACCGAAATAT	AGCAAAGCTT	420
GGAAAGGCTT	CCCTCATCTC	TACAGGTTTA	ACAACTCTGA	TTCTTGGAA	TGTAATGGCA	480
AGGGCAATTT	CACCTGGGTC	ACACATACCA	AAAACAGAAG	ACGCTTGGGT	ATTTGCAAG	540
CCCAATGCCA	TTCAGCGSGT	CGGGGTTATG	TCTTTTGCAT	TTATTTGCCA	CCATAACTCC	600
TTCTTAGTTT	ACAGTTCTCT	AGAAGAAGCC	ACAGTAGCTA	AGTGGTCCCG	CCTTATCCAT	660
ATGTCCATCG	TGATTCTCTG	ATTATCTGT	ATATTCTTTG	CTACATGTGG	ATACTTGACA	720
TTTACTGGCT	TCACCCAGGG	GGACTTATTT	GAATAATTACT	GCAGAAATGA	TGACCTGGTA	780
ACATTGGGAA	GATTTTGTTA	TGGTGTCACT	GTCATTTTGA	CATACCCCTAT	GGAAATGCTTT	840
GTGACAAGAG	AGGTAATTGC	CAATGTGTTT	TTTGGTGGGA	ATCTTTCATC	GGTTTTCCAC	900
ATTGTTGTAA	CAGTGATGGT	CATCACTGTA	GCCACGCTTG	TGTCATTGCT	GATTGATTGC	960
CTCGGGATAG	TTCTAGAACT	CAATGGTGTG	CTCTGTGCAA	CTCCCTCAT	TTTTATCATT	1020
CCATCAGCCT	GTATCTGTA	ACTGTCTGAA	GAACCAAGGA	CACACTCCGA	TAAGATTATG	1080
TCTTGTGTCA	TGCTTCCCAT	TGGTGCTGTG	GTGATGGTTT	TTGGATTGCT	CATGGCTATT	1140
ACAAATACCT	AAGACTGCAC	CCATGGGCAG	GAAATGTTCT	ACTGCTTCC	TGACAATTTC	1200
TCTCTCACA	ATACCTCAGA	GTCTCATGTT	CAGCAGACAA	CACAACCTTC	TACTTTAAAT	1260
ATTAGTATCT	TTCAACTCGA	GTAA				

50 Seq ID NO: 671 Protein sequence
Protein Accession #: Eos sequence

1	11	21	31	41	51	
MGYQRQEPVI	PPQRGLPYSM	KQAGFPLGIL	LLFWVSYYTD	PSLVLLIKGG	ALSGTDTYQS	60
LVNKTFGPPG	YLLSLVLQPL	YPIAMISYN	IIAGDTLSKV	FORIPGVDP	NVFIGRHFII	120
GLSTVFTPLP	LSLVRNIARL	GKVSLLISTGL	TTLLILGIVMA	RAISLGPHE	KTEDAWVFAK	180
PNAIQAVGVM	SFAFICHNS	FLVYSSLEEP	TVAKWSRLIH	MSIVISVFIC	IFFATCGYLT	240
FTGFTQGGDL	ENYCRNDLVL	TGFRFCYGV	VILTYPMECF	VTREIVANVF	PGGNLSSVFF	300
IVTVVMVITV	ATLVSLIDLC	LGIVLELNGV	LCATPLFIPI	PSACYLKLSE	EPRTHSKIM	360
SCVMLPIGAV	VMVPGFVMAI	TNTQDCTHGQ	EMFYCFPDNF	SLTNTSESHV	QQTTLSTLN	420
ISIFQLE						

65 Seq ID NO: 672 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1203

1	11	21	31	41	51	
ATGGGCTACC	AGAGGCAGGA	GCCTGTCATC	CCGCCGCGAGT	TTTCCCTTGT	TTTATTGATA	60
AAAGGAGGGG	CCCTCTCTGG	AACAGATACC	TACCACTCTT	TGGTCAATAA	AACCTTCGGC	120
TTTCCAGGGT	ATCTGCTCCT	CTCTGTTCTT	CAGTTTTTGT	ATCCTTTTAT	AGCAATGATA	180
AGTTACAATA	TAATAGCTGG	AGATACTTTG	AGCAAAGTTT	TTCAAAGAAT	CCCAGGAGTT	240
GATCCTGAAA	ACGTGTTTAT	TGGTCGCCAC	TTCAATTATG	GACTTTCCAC	AGTTACCTTT	300
ACTCTGCCTT	TATCCTTGTA	CCGAAATATA	GCAAAGCTTG	GAAAGGTCTC	CCTCATCTCT	360
ACAGGTTTAA	CAACTCTGAT	TCTTGGAAAT	GTAATGGCAA	GGGCAATTTT	ACTGGGTCCA	420
CACATACCAA	AAACAGAAGA	CGCTTGGGTA	TTTGCAAAGC	CCAATGCCAT	TCAAGCGGTC	480
GGGGTTATGT	CTTTTGCAAT	TATTTGCCAC	CATAACTCCT	TCTTAGTTTA	CAGTTCTCTA	540
GAAGAACCCA	CAGTAGCTAA	GTGGTCCCGC	CTTATCCATA	TGTCCATCGT	GATTCTGTGA	600
TTTATCTGTA	TATCTTTTGC	TACATGTGGA	TACTTGACAT	TTACTGGCTT	CACCCAAGGG	660
GACTTATTTG	AAAATTACTG	CAGAAATGAT	GACCTGGTAA	CATTTGGAAG	ATTTTGTATT	720
GGTGTCATCG	TCTTTTGTAC	ATACCCTATG	GAATGCTTTG	TGACAAGAGA	GGTAATTGCC	780
AATGTGTTTT	TGGTGGGAA	TCTTTCATCG	GTTTTCACAC	TTGTGTGAAC	AGTGATGGTC	840
ATCATGTAG	CCAGCTTGT	GTCAATGCTG	ATTGATTGCC	TCGGGATAGT	TCTAGAACTC	900
AATGGTGTGC	TCTGTGCAAC	TCCCTCATTT	TTTATCATTC	CATCAGCCTG	TTATCTGAAA	960
CTGTCTGAAG	AACCAAGGAC	ACACTCCGAT	AAGATTATGT	CTTGTGTCAT	GCTTCCCAT	1020
GOTGCTGTGG	TGATGGTTTT	TGGATTCGTC	ATGGCTATTA	CRAAATCTCA	AGACTGCACC	1080
CATGGGCAGG	AAATGTTCTA	CTGCTTTCCT	GACAATTTCT	CTCTCACAAA	TACCTCAGAG	1140
TCTCATGTTT	AGCAGACAAC	ACAACCTTCT	ACTTTAAATA	TTAGTATCTT	TCAACTCGAG	1200

TAA

Seq ID NO: 673 Protein sequence
Protein Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
MGYQRQEPVI PPQFSVLVLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QPLYPFIAMI 60
SYNIIAGDTL SKVFQRIPIV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGRVSLIS 120
TGLTLLILGI VMARAIISLP HIPKTEDAWV FAKPNAIQAV GVMSFAFICH HNSFLVYSSL 180
EEPTVAKWSR LIHMSIVISV PICIPFATCG YLFTPTGPTQG DLFPENYCRND DLVTFGRPCY 240
GVTVLITYPM ECFVTREIVN NVFPGGNLSS VFHIVVTVMV ITVATLVSLI IDCLGIVLEL 300
NGVLCATPLI FIIPSACYLK LSEEPRTSHD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT 360
HGQEMFYCFP DNFSLTNTSE SHVQQTTLQS TLNISIFQLE
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Seq ID NO: 674 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1140

```
1      11      21      31      41      51
|      |      |      |      |      |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGG TCAATAAAAC TTTCGGCTTT 60
CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120
TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTC AAAGAATCCC AGGAGTTGAT 180
CCTGAAAACG TGTATTATGG TCGCCACTTC ATTATTGGAC TTCCACAGT TACCTTTACT 240
CTGCCCTTAT CTTTGTACCG AAATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA 300
GGTTTAACAA CTCGTATTCT TGGAAATGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC 360
ATACCAAAAA CAGAAGACGC TTGGGTATTG GCAAAGCCCA ATGCCATTCA AGCGGTCGGG 420
GTTATGTCTT TTGCATTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480
GAACCCACAG TACTTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATT 540
ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600
TTATTGTAA AATTACTGAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660
GTCACGTGCA TTTTGACATA CCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
GTGTTTTTTG GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC 780
ACTGTAGACA CGCTGTGTGC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840
GGGTGTGCTT CTGCAACTCC CCTCATTTT ATCATTTCCAT CAGCCGTGTA TCTGAAACTG 900
TCTGAAGAAC CAGGACACCA CTCGATAAG ATTATGCTT GTGTCATGCT TCCCATTGGT 960
GCTGTGGTGA TGGTTTTTGG ATTGCTCATG GCTATTACAA ATACTCAAGA CTCACCCAT 1020
GGGCAGGAAA TGTCTACTG CTTTCTGAC AATTCTCTC TCACAAATAC CTCAGAGTCT 1080
CATGTTTCAGC AGACAACACA ACTTTCTACT TTAATATTA GTATCTTTCA ACTCGAGTAA
```

Seq ID NO: 675 Protein sequence
Protein Accession #: Eos sequence

```
1      11      21      31      41      51
|      |      |      |      |      |
MGYQRQEPVI PPQVNKTGFG PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPIVD 60
PENVFGRHF IIGLSTVTFI LPLSLYRNIA KLGRVSLIST GLTTLILGIV MARAISLGP 120
IPKTEDAWVF AKPNAIQAVG VMSFAFICHH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF 180
ICIPFATCGY LFTPTGPTQG LFENYCRNDD LVTFGFRFCY VTVILTYPME CFTVTREIVN 240
VFFGGNLSVV FHVIVVTVMV TVATLVSLLI DCLGIVLELN GVLCATPLIF IIPSACYLKL 300
SEEPRTSHDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NPSLTNTSES 360
HVQQTTLQST LNISIFQLE
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Seq ID NO: 676 DNA sequence
Nucleic Acid Accession #: NM_006853.1
Coding sequence: 26..874

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1      11      21      31      41      51
|      |      |      |      |      |
AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTTGAGG TGGCTGCGGG ACTGGAAGTC 60
ATCGGGCAGA GGTCTCACAG CAGCCAAGGA ACCTGGGGCC CGCTCCTCCC CCTCCAGGC 120
CATGAGGATT CTGCAAGTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGAGAGAC 180
CAGGATCATC AAGGGGTTG AGTGCAAGCC TCACTCCAGC CCTGGCAGG CAGCCCTGTT 240
CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCCAGATGGC TCCTGACAGC 300
AGCCCACTGC CTCAGGCCCC GCTACATAGT TCACCTGGGG CAGCACAAAC TCCAGAAGGA 360
GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCTCTC CCCCACCCCG GCTTCAACAA 420
CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT 480
CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCTCA CGCTGTGTCA CTGCTGGCAC 540
CAGCTGCCTC ATTTCCGGCT GGGGCGACAC GTCCAGCCCC CAGTTAGGCC TGCTTCACAC 600
CTTGCGATGC GCCAATATCA CCATCATTGA GCACCAAGG TGTGAGAAGC CCTACCCCGG 660
CAACATCACA GACACCATGG TGTGTGCCAG CGTGCAAGAA GGGGGCAAGG ACTCCTGCCA 720
GGGTGACTCC GAGGGGCCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCTGGGG 780
CCAGGATCCG TGTGCGATCA CCGGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAAAATATG 840
GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC 900
ACCTCCATT TCCACTTGGT GTTTGGTCC TGTTCATCT GTTAATAAGA AACCTAAGC 960
CAAGACCTC TAGCAACATT CTTTGGGCTT CCTGGACTAC AGGAGATGCT GTCATTAAAT 1020
AATCAACCTG TACGTTGAAA TCAGTGAGAC CTGGATTCAA ATTCTGCCTT GAAATATTGT 1080
GACTCTGGGA ATGACAACAC CTGGTTTGT CTCTGTTGTA TCCCCAGCCC CAAAGACAGC 1140
TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG
```

Seq ID NO: 677 Protein sequence
Protein Accession #: NP_006844.1

```
1      11      21      31      41      51
|      |      |      |      |      |
MRILQLILLA LATGLVGGET RIIKGFECKP HSQPWQAALF EKTRLLCGAT LIAPRWLLTA 60
```

AHCLKPRYIV HLGQHNLOKE EGCEQTRTAT ESPPHPGFNN SLPNKDHRND IMLVKMASPV 120
SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIE HQKCNAYPG 180
NITDTMVCAS VQEGGKDSQ GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVTYKVKYV 240
DWIETMKNN

Seq ID NO: 678 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..933

1 11 21 31 41 51
| | | | | |
ATGTGCACGA ATGGACGGTG CATCCCGGGC GCCTGGCAGT GTGACGGGCT GCCTGACTGC 60
TTGACAAGA GTGATGAGAA GGAGTGCCCC AAGGCTAAGT CGAAATGTGG CCCGACCTTC 120
TTCCCTCTGT CCAGCGGCAT CCATTGCATC ATTGGTCGCT TCCGGTGCAA TGGGTTTGAG 180
GACTGTCCCG ATGGCAGCGA TGAAGAGAAC TGCACAGCAA ACCCTCTGCT TTGCTCCACC 240
GCCCCGTACC ACTGCAAGAA CGGCCTCTGT ATTGACAAGA GCTTCATCTG CGATGGACAG 300
AATAACTGTC AAGACAACAG TGATGAGGAA AGCTGTGAAA GTTCTCAAGA ACCGGGCACT 360
GGGCAGGTGT TTGTGACTTC AGAGAACCAG CTGTGTGATT ACCCCAGCAT CACCTATGCC 420
ATCATCGGCA GCTCCGTCAT TTTGTGCTGT GTGGTGGCCC TGCTGGCACT GGTCTTGAC 480
CACCAGCGGA AGCGGAACAA CCTCATGACG CTGCCCCGTC ACCGGCTGCA GCACCCTGTG 540
CTGTGTCTCC GCCTGGTGGT CCTGGACCAC CCCCACTACT GCAACGTCAC CTACAACGTC 600
AATAATGGCA TCCAGTATGT GGCCAGCCAG CGGAGCAGA ATGCGTCGGA AGTAGGCTCC 660
CCACCTCTCT ACTCCGAGGC CTTGCTGGAG CAGAGGCGCTG CGTGGTATGA CCTTCTCTCA 720
CCGCCTACT CTCTGACAC GGAATCTCTG AACCAGCCG ACCTGCCCCC CTACCGCTCC 780
CGGTCGGGA GTGCTGACG TGCCAGCTCC CAGGCAGCCA GCAGCTCTCT GAGGCTGGAA 840
GACACGACCC ACAGCCCGGG GCAGCTGGC CCCAGGAGG GCACTGCTGA GCCCAGGGAC 900
TCTGAGCCCA GCCAGGGCAC TGAAGAAGTA TAA

Seq ID NO: 679 Protein sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
| | | | | |
MCSNGRCIPG AWQCDGLPDC FDKSDEKECP KAKSKCGPTF FPCASGIHCI IGRFRNGFE 60
DCPDGSDDEEN CTANPLLCST ARYHCKNGLC IDKSFICDQ NNCQDNSDEE SCESSQEPGS 120
GQVFVTSBENQ LVVYPSITYA IIGSSVIFVL VVALLALVLH HQKRNNLMT LPVHRLQHPV 180
LLSRLVLVDH PHHCNVYINV NNGIQYVASQ AEQNASEVGS PPSYSEALD QRPANYDLFP 240
PPYSSDTESL NQADLPPYRS RSGSANSASS QAASSLLSVE DTSHPGQPG PQEGTAEPED 300
SEPSQGTTEE

Seq ID NO: 680 DNA sequence
Nucleic Acid Accession #: S78203.1
Coding sequence: 1..2190

1 11 21 31 41 51
| | | | | |
ATGAATCCTT TCCAGAAAAA TGAGTCCAAG GAAACTCTTT TTTACCTGT CTCATTGAA 60
GAGGTACCAC CTCGACCACC TAGCCCTCCA AAGAAGCCAT CTCGACAAT CTGTGGCTCC 120
AACTATCCAC TGAGCATTGC CTTCATGTGT GTGAATGAAT TCTGCGAGCG CTTTTCCTAT 180
TATGGAATGA AAGCTGTGCT GATCCTGTAT TTCTGTATT TCCTGCACTG GAATGAAGAT 240
ACCTCCACAT CTATATACCA TGCCCTTCAGC AGCCTCTGTT ATTTTACTCC CATCCTGGGA 300
GCAGCCATTG CTGACTCGTG GTTGGGAAAA TTCAAGACAA TCATCTATCT CTCTTGGTG 360
TATGTGCTTG GCCATGTGAT CAAGTCCTTG GGTGCCTTAC CAATACTGGG AGGACAAGTG 420
GTACACACAG TCCTATCATT GATCGGCCTG AGTCTAATAG CTTTGGGAGC AGGAGGCATC 480
AAAACCTGTG TGGCAGCTTT TGGTGGAGAC CAGTTTGAAG AAAACATGCG AGAGGAACCG 540
ACTAGATACT TCTCAGTCTT CTACCTGTCC ATCAATGCGG GGAGCTTGAT TTCTACATT 600
ATCACACCCA TGCTGAGAGG AGATGTGCAA TGTTTGGAG AAGACTGCTA TGCAATTGGCT 660
TTTGGAGTTC CAGGACTGCT CATGGTAATT GCACTTGTG TGTTTGAAT GGGGAAGCAA 720
ATATACAATA AACCAACCCC TGAAGGAAAC ATAGTGGCTC AAGTTTCAA ATGTATCTGG 780
TTTGCTATT CCAATCGTTT CAAGAACCCT TCTGGAGACA TTCCAAGCG ACAGCACTGG 840
CTAGACTGGG CAGCTGAGAA ATATCCAAG CAGCTCATT TGGATGTAAA GGCAGTGACC 900
AGGTAATCAT CTCTTATAT CCCATTGCC ATGTTCTGGG CTCTTTTGA TCAGCAGGGT 960
TCAGATGGA CTTTGCAAGC CATCAGGATG AATAGGAATT TGGGGTTTT TGTGCTTCAG 1020
CCGACACAGA TGCAGGTTCT AAATCCCTTT CTGGTTCTTA TCTTCATCCC GTTGTTCGAC 1080
TTTGTCAATT ATCGTCTGGT CTCCAAGTGT GGAATTAAT TCTCATCACT TAGGAAAATG 1140
GCTGTTGGTA TGATCTAGC GTGCCTGGCA TTGTCAGTTG CGGCAGCTGT AGAGATAAAA 1200
ATAAATGAAA TGGCCCCAGC CCAGTCAGGT CCCCAGGAGG TTTTCTACA AGTCTTGAAT 1260
CTGGCAGATG ATGAGGTGAA GGTGACAGTG GTGGGAAATG AAAACAATTC TCTGTTGATA 1320
GAGTCCATCA AATCCTTTCA GAAACACCCA CACTATTCCA AACTGCACCT GAAACAAAAA 1380
AGCCAGGATT TTCATTCCA CCTGAAATAT CACAATTGT CTCTCTACAC TGAGCATTCT 1440
GTGCAGGAGA AGAAGTGGTA CAGTCTGTGC ATTGCTGAAG ATGGGAACAG TATCTCCAGC 1500
ATGATGGTAA AGGATACAGA AAGCAAAACA ACCAATGGGA TGACAACCGT GAGGTTTGGT 1560
AACACTTTGC ATAAAGATGT CAACATCTCC CTGAGTACAG ATACCTCTCT CAATGTTGGT 1620
GAAGACTATG GTGTGCTGTC TTATAGAACT GTGCAAGAG GAGAATACCC TGCACTGCAC 1680
TGTAAGACAG AAGATAAGAA CTTTCTCTG AATTGGGTC TTCTAGACTT TGGTGCAGCA 1740
TATCTGTTTG TTATTACTAA TAACACCAAT CAGGGCTCTC AGGCCTGGAA GATTGAAGAC 1800
ATTCCAGCCA ACAAATGTC CATTGCGTGG CAGCTACCAC AATATGCCCT GGTACAGCT 1860
GGGGAGGTCA TGTTCTCTGT CACAGGTCTT GAGTTTTCTT ATTCTCAGGC TCCCTCTAGC 1920
ATGAAATCTG TGCTCCAGGC AGCTTGGCTA TTGACAATTG CAGTTGGGAA TATCATCGTG 1980
CTGTGTGGG CACAGTTTCAG TGGCCTGGTA CAGTGGGCGG AATTCAATTT GTTTCTCTGC 2040
CTCCTGCTGG TGATCTGCCT GATCTTCTCC ATCATGGGCT ACTACTATGT TCCTGTAAG 2100
ACAGAGGATA TGGGGGGTCC AGCAGATAAG CACATTCTCT ACATCCAGGG GAACATGATC 2160
AAACTAGAGA CCAAGAGAC AAAACTCTGA

Seq ID NO: 681 Protein sequence
Protein Accession #: AAB34388.1

1 11 21 31 41 51
 MNPPQKNESK ETLFSPVSI EPPPPPPSP KPSPTICGS NYPLSIAPIV VNEFCERFSY 60
 YGKAVILLY FLYFLHWNED TSTSIYHAFS SLCYFTPILO AAIADSWLQK FKTIYLSLV 120
 YVLGHVILKSL GALPILGGQV VHTVLSLIGL SLIALGTGGI KPCVAAFQGD QPEEKHABER 180
 TRYFSVFLYS INAGSLISTF ITPMLRGDVO CFGEDCYALA FGVPGLLMVI ALVVPFAMGSK 240
 IYNKPPPEGN IVAQVFKCIW PAISNRPFKNR SGDIPKRQHW LDWAAEKYFK QLMIDVKALT 300
 RVLFLYIPLP MFWALLDQGG SRWTLQAI RM NRNLGPFVLO PDQMQLNPF LVLIFIPLFD 360
 FVIYRLVSKC GINFSSLRKM AVGMILACLA FAVAAAVEIK INEMAPAQSG PQEVFLQVLN 420
 LADDEVKTVV VGNENNSLLI ESIKSFQKTP HYSKLHLKTK SQDPHFLKY HNLSTLYTEHS 480
 VQEKNWYSLV IREDGNSISS MMVKDTESKT TNGMTTVRFV NTLHKOVNIS LSTDTSLNVG 540
 EDYGVSAIRT VQRGEYPAVH CRTEDKNFSL NLGLLDFGAA YLFVITNNTN QGLQAWKIED 600
 IPANKMSIAW QLPQYALVTA GEVMSFVTGL EFSYSQAPSS MKSVLQAAWL LTIAVGNIIIV 660
 LVVAQPSGLV QWAEFILFSC LLLVICLIFS IMGYVYPVK TEDMRGPADK HIPHIQGNMI 720
 KLETKKTKL

Seq ID NO: 682 DNA sequence
 Nucleic Acid Accession #: NM_016077.1
 Coding sequence: 128..667

1 11 21 31 41 51
 TCGCTTTGTG ATTCTTGATC CGGAACCTTG TCACCCAGGA ACCCCGGAAG AGGTAGCTCA 60
 CGCGATAGAA ACCTGTTCGC TTGCCAGAA GAAGGGAAGG CGCGAGTGAG GAAAGGAGGT 120
 ACTGTAGATG CCTTCCAAAT CCTTGGTTAT GGAATATTG GCTCATCCCA GTACACTCGG 180
 CTTGGCTGTT GGAGTTGCTT GTGGCATGTG CCTGGGCTGG AGCCTTCGAG TATGCTTTGG 240
 GATGCTCCCC AAAAGCAAGA CGAGCAAGAC ACACACAGAT ACTGAAAGTG AAGCAAGCAT 300
 CTTGGGAGAC AGCGGGGAGT ACAAGATGAT TCTTGTGGTT CGAAATGACT TAAAGATGGG 360
 AAAAGGGAAA GTGGCTGCC AGTGCTCTCA TGTGCTGTT TCAGCCTACA AGCAGATTCA 420
 AAGAAGAAAT CCTGAAATGC TCAACAATG GGAATACTGT GGCCAGCCCA AGGTGGTGGT 480
 CAAAGCTCCT GGATGAAGAA CCTGATTGCT ATTATTGGCC CATGCAAAAA TGCTGGGACT 540
 GACTGTAAGT TTAATTCAAG ATGCTGGACG TACTCAGATT GCACCAAGCT CTCAACTGT 600
 CCTAGGGATT GGGCCAGGAC CAGCAGACCT AATTGACAAA GTCACTGGTC ACCTAAACT 660
 TTACTAGGTG GACTTTGATA TGACACACAC CCTCCATCA CAAGTGTTTG AAGCCTGTCA 720
 GATTCTAACA ACAAAGCTG AATTTCTTCA CCCAACTTAA ATGTTCTTGA GATGAAAAATA 780
 AAACCTATTC CCATGTTCTA AAAAAA

Seq ID NO: 683 Protein sequence
 Protein Accession #: NP_057161.1

1 11 21 31 41 51
 MPKSLVMEY LAHPSTLGLA VGVACGMCLG WSLRVCFGML PKSKTSKTHT DTESEASILG 60
 DSGEYKMLLV VRNDLKMKGK KVAAQCASHA VSAYKQIQRR NPEMLKQWEY CGQPKVVVKA 120
 PDETTLIALL AHAKMLGLTV SLIQDAGRTO IAPGSQTVLG IGPFPADLID KVTGHLKLY

Seq ID NO: 684 DNA sequence
 Nucleic Acid Accession #: NM_004864.1
 Coding sequence: 26..952

1 11 21 31 41 51
 CGGAACGAGG GCAACCTGCA CAGCCATGCC CGGGCAAGAA CTCAGGACGG TGAATGGCTC 60
 TCAGATGCTC CTGGTGTTCG TGGTGCTCTC GTGGCTGCCG CATGGGGGCG CCCTGTCTCT 120
 GGCCGAGGCG AGCCGCGCAA GTTTCGCGG ACCCTCAGAG TTGCACTCCG AAGACTCCAG 180
 ATTCGAGAG TTGCGGAAAC GCTACGAGGA CCTGCTAACC AGGCTGCGGG CCAACAGAG 240
 CTGGGAAGAT TCGAACACCG ACCTCGTCCC GGCCCGTCCA GTCCGGATAC TCACGCCAGA 300
 AGTGCGGCTG GATCGCGCG CGCACCTGCA CTGCGGTATC TCTCGGGCCG CCCTTCCGGA 360
 GGGGCTCCCC GAGGCTCTCC GCCTTCACCG GGCTCTGTTC CGGCTGTCCC CGACGGCGTC 420
 AAGGTCGTGG GACGTGACAC GACCGCTGCG GCGTCAGCTC AGCCTTGCAA GACCCCAAGC 480
 GCCCGCGCTG CACCTGCGAC TGTGCGCGCC GCCGTGCGAG TCGGACCAAC TGCTGGCAGA 540
 ATCTTCGTCC GCACGCGCCC AGCTGGAGTT GCACTTGCGG CCGCAAGCCG CCAGGGGGCG 600
 CCGCAGAGCG CGTGCAGCGA ACGGGGACGA CTGTCCGCTC GGGCCCGGGC GTTGTGCGCG 660
 TCTGCACACG GTCGCGCGGT CGCTGGAAGA CCTGGGCTGG GCCGATTGGG TGCTGTGCGC 720
 ACGGGAGGTG CAAGTGACCA TGTGCATCGG CGCGTGCCCG AGCCAGTTCC GGGCGGCAAA 780
 CATGCACGCG CAGATCAAGA CGAGCCTGCA CCGCCTGAAG CCGGACACCG AGCCAGCGCC 840
 CTGCTGCGTG CCCGCCAGCT ACAATCCCAT GGTGCTCATT CAAAAGACCG ACACGGGGGT 900
 GTCGCTCCAG ACCTATGATG ACTTGTAGC CAAAGACTGC CACTGCATAT GAGCAGTCTC 960
 GGTCTCTCCA CTGTGCACCT GCGCGGGGGA GGCGACCTCA GTTGTCTGCT CCTGTGGAAT 1020
 GGGCTCAAGG TTCTGTAGAC ACCCGATTCC TGCCCAAACA GCTGTATTTA TATAAGTCTG 1080
 TTATTATTA TTAATTTAT TGGGTGACCT TCTTGGGGAC TCGGGGGCTG GTCTGATGGA 1140
 ACTGTGTATT TATTTAAAC TCTGTGATA AAAATAAAGC TGCTGAACT GTTAAAAAAA 1200
 AAAA

Seq ID NO: 685 Protein sequence
 Protein Accession #: NP_004855.1

1 11 21 31 41 51
 MPQQLRLTVN QSQMLLVLLV LSWLPHGGAL SLAEASRAS FPGSELHSED SRFRELKRY 60
 EDLLTRLRAN QSWEDSNTDL VPAPAVRIIT PEVRLGSGGH LHLRISRAAL PEGLEASRL 120
 HRALFRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPPSQSDQLL AESSSARPQL 180
 ELHLRPQAAR GRRRARARNG DDCLGPGRG CRLHTVRASL EDLGDWADWL SPREVQVTMC 240
 IGACPSQFRA ANMHAQIKTS LHRLKPDTEP APCCVPASYN PMVLIQKTDI GVSQTYDDL 300
 LAKDCHCI

Seq ID NO: 686 DNA sequence

Nucleic Acid Accession #: NM_002423.2
Coding sequence: 48..851

```
5      1      11      21      31      41      51
      |      |      |      |      |      |
      ACCAAATCAA CCATAGGTCC AAGAACAATT GTCTCTGGAC GGCAGCTATG CGACTCACCG 60
      TGCCTGTGTC TGTGTGCTGT CTGCCTGGCA GCCTGGCCCT GCCGCTGCCT CAGGAGGCGG 120
      GAGGCATGAG TGAGCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTATCTCT 180
      ATGACTCAGA AACAAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAAAAAAT 240
10     TCCTTGGCCT ACCTATAACT GGAATGTTAA ACTCCGCGT CATAGAAATA ATGCAGAAGC 300
      CCAGATGTGG AGTGCCAGAT GTTGCAGAAAT ACTCACTATT TCCAAATAGC CCAAAATGGA 360
      CTTCCAAAGT GGTCACTTAC AGGATCGTAT CATATACTCG AGACTTACCG CATATTACAG 420
      TGGATCGATT AGTGTCAAAG GCTTTAAACA TGTGGGGCAA AGAGATCCCC CTGCATTTCA 480
      GGAAAGTTGT ATGGGGAACT GCTGACATCA TGATTGGCTT TGCGCGAGGA GCTCATGGGG 540
15     ACTCTTACCC ATTTGATGGG CCAGGAAACA CGCTGGCTCA TGCCTTTGCG CCGGGACAG 600
      GTCTCGAGAG AGATGCTCAC TTCGATGAGG ATGAACGCTG GACGGATGGT AGCAGTCTAG 660
      GGATTAACCT CCTGTATGCT GCAACTCATG AACTTGGCCA TTCTTTGGGT ATGGGACATT 720
      CCTCTGATCC TAATGCAATG ATGTATCCAA CCTATGGAAA TGGAGATCCC CAAAATTTTA 780
      AACTTTCCCA GGATGATATT AAAGGCATTC AGAAACTATA TGGAAAGAGA AGTAATTCAA 840
20     GAAAGAAATA GAAACTTCAG GCAGAACATC CATTATTCCA TTCATTGGAT TGTATATCAT 900
      TGTTCACAA TCAGAAATGA TAAGCACTGT TCCTCACTC CATTAGCAA TTATGTCACC 960
      CTTTTTATT GCAGTTGGTT TTTGAATGTC TTTCACTCCT TTTATTGGTT AAACCTCCTT 1020
      ATGGTGTGAC TGTGTCTTAT TCCATCTATG AGCTTTGTCA GTGCGCGTAG ATGTCAATAA 1080
      ATGTTACATA CACAAATAAA TAAATGTTT ATTCCATGST AAATTTA
```

Seq ID NO: 687 Protein sequence
Protein Accession #: NP_002414.1

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30     1      11      21      31      41      51
      |      |      |      |      |      |
      MRLTVLCAVC LLPGSLALPL PQEAGGMSLE QWEQAQDYLK RPYLYDSETK NANSLEAKLK 60
      EMQKFFGLPI TGMLNSRVIE IMQKPRCGVP DVAEYSLFPN SPKWTISKVVT YRIVSYTRDL 120
      PHITVDRLVS KALHNMWGKEI PLHFRKVVWG TADIMIGFAR GAHGDSYFPD GPGNTLAHAF 180
35     APGTGLGGDA HFDEDERWTD GSSLGINFLY AATHELGHSL GMGHSSDPNA VMYPTYGNDD 240
      PQNFKLSQDD IKGIQKLYGK RSNSRKK
```

Seq ID NO: 688 DNA sequence
Nucleic Acid Accession #: NM_005221.3
Coding sequence: 1..870

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40     1      11      21      31      41      51
      |      |      |      |      |      |
      ATGACAGGAG TGGTTTGACAG AAGGGTCCCC AGCATCCGAT CCGGCGACTT CCAAGCTCCG 60
      TTCCAGACGT CCGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACTTT GCCCGAGTCT 120
      TCAGCTACCG ATTCTGACTA CTACAGCCCT ACGGGGGGAG CCCCGCACGG CTAAGTCTCT 180
      CCTACCTCGG CTCTCTATGG CAAAGCTCTC AACCCCTACC AGTATCAGTA TCACGGCGTG 240
      AACGGCTCCG CCGGGAGCTA CCAGCCCAA GCTTATGCCG ACTATAGTA CGTAGCTCC 300
      TACCAACAGT ACGGCGGGCG CTACAACCGC GTCCCAAGCG CCACCAACCA GCCAGAGAAA 360
      GAAGTGACCG AGCCCGAGGT GAGAATGGTG AATGGCAAAC CAAAGAAAGT TCGTAAACCC 420
45     AGGACTATTT ATTCCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG 480
      TACCTCGCCT TGCCGGAACG CGCCGAGCTG GCCGCTCGC TGGGATTGAC ACAAAACACAG 540
      GTGAAAATCT GGTTCAGAA CAAAAGATCC AAGATCAAGA AGATCATGAA AACCGGGAG 600
      ATGCCCCCGG AGCACAGTCC CAGCTCCAGC GACCCAAATG CGTGTAACTC GCCCGAGTCT 660
      CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCACCC TCATGCCAC 720
55     CCTCCGACCT CCAACCAATC CCCAGCGTCC AGCTACCTGG AGAACTCTGC ATCCTGGTAC 780
      ACAAGTGCAG CCAGCTCAAT CAATCCCAC CTGCCGCCGC CGGCTCCTT ACAGCACCCG 840
      CTGGCGCTGG CCTCCGGGAC ACTCTATTAG
```

Seq ID NO: 689 Protein sequence
Protein Accession #: NP_005212.1

```
60     1      11      21      31      41      51
      |      |      |      |      |      |
      MTGVFDRRVF SIRSGDFQAP FQTSAAHHP SQESPTLPES SATDSDYSP TGGAPHGYCS 60
      PTSASYGKAL NPYQYQYHGV NGSAGSYPK AYADYSYASS YHQYGGAYNR VPSATNQPEK 120
      EVTEPEVRMV NGKPKVKRKP RTIYSSFOLA ALQRRFQKTQ YLALPERAEL AASLGLTOTO 180
      VKIWFQNKRS KIKKIMKNGE MPPEHSPSSS DPMACNSPQS PAVWEPQSSS RSLSHPHAH 240
      PPTSQSPAS SYLENSASWY TSAASSINSH LPPPGSLQHP LALASGTLTY
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It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting a lung cancer-associated transcript in a cell
2 from a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
4 as shown in Tables 1A-16.
- 1 2. The method of claim 1, wherein the polynucleotide selectively
2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16.
- 1 3. The method of claim 1, wherein the biological sample is a tissue
2 sample.
- 1 4. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 5. The method of claim 4, wherein the nucleic acids are mRNA.
- 1 6. The method of claim 4, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 7. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1A-16.
- 1 8. The method of claim 1, wherein the polynucleotide is labeled.
- 1 9. The method of claim 8, wherein the label is a fluorescent label.
- 1 10. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 11. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat lung cancer.
- 1 12. The method of claim 1, wherein the patient is suspected of having lung
2 cancer.
- 1 13. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated transcript in the
6 biological sample by contacting the biological sample with a polynucleotide that selectively
7 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16,
8 thereby monitoring the efficacy of the therapy.

1 14. The method of claim 13, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated transcript to a level of the lung cancer-associated
3 transcript in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 15. The method of claim 13, wherein the patient is a human.

1 16. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated antibody in the biological
6 sample by contacting the biological sample with a polypeptide encoded by a polynucleotide
7 that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in
8 Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated
9 antibody, thereby monitoring the efficacy of the therapy.

1 17. The method of claim 16, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated antibody to a level of the lung cancer-associated
3 antibody in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 18. The method of claim 16, wherein the patient is a human.

1 19. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated polypeptide in the
6 biological sample by contacting the biological sample with an antibody, wherein the antibody
7 specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to
8 a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby
9 monitoring the efficacy of the therapy.

1 20. The method of claim 19, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated
3 polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 21. The method of claim 19, wherein the patient is a human.

1 22. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1A-16.

1 23. The nucleic acid molecule of claim 22, which is labeled.

1 24. The nucleic acid of claim 23, wherein the label is a fluorescent label

1 25. An expression vector comprising the nucleic acid of claim 22.

1 26. A host cell comprising the expression vector of claim 25.

1 27. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1A-16.

1 28. An antibody that specifically binds a polypeptide of claim 27.

1 29. The antibody of claim 28, further conjugated to an effector component.

1 30. The antibody of claim 29, wherein the effector component is a
2 fluorescent label.

1 31. The antibody of claim 29, wherein the effector component is a
2 radioisotope or a cytotoxic chemical.

1 32. The antibody of claim 29, which is an antibody fragment.

- 1 33. The antibody of claim 29, which is a humanized antibody
- 1 34. A method of detecting a lung cancer cell in a biological sample from a
2 patient, the method comprising contacting the biological sample with an antibody of claim
3 28.
- 1 35. The method of claim 34, wherein the antibody is further conjugated to
2 an effector component.
- 1 36. The method of claim 35, wherein the effector component is a
2 fluorescent label.
- 1 37. A method of detecting antibodies specific to lung cancer in a patient,
2 the method comprising contacting a biological sample from the patient with a polypeptide
3 encoded by a nucleic acid comprises a sequence from Tables 1A-16.
- 1 38. A method for identifying a compound that modulates a lung cancer-
2 associated polypeptide, the method comprising the steps of:
3 (i) contacting the compound with a lung cancer-associated polypeptide, the
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least
5 80% identical to a sequence as shown in Tables 1A-16; and
6 (ii) determining the functional effect of the compound upon the polypeptide.
- 1 39. The method of claim 38, wherein the functional effect is a physical
2 effect.
- 1 40. The method of claim 38, wherein the functional effect is a chemical
2 effect.
- 1 41. The method of claim 38, wherein the polypeptide is expressed in a
2 eukaryotic host cell or cell membrane.
- 1 42. The method of claim 38, wherein the functional effect is determined by
2 measuring ligand binding to the polypeptide.
- 1 43. The method of claim 38, wherein the polypeptide is recombinant.

1 44. A method of inhibiting proliferation of a lung cancer-associated cell to
2 treat lung cancer in a patient, the method comprising the step of administering to the subject a
3 therapeutically effective amount of a compound identified using the method of claim 38.

1 45. The method of claim 44, wherein the compound is an antibody.

1 46. The method of claim 45, wherein the patient is a human.

1 47. A drug screening assay comprising the steps of
2 (i) administering a test compound to a mammal having lung cancer or a cell
3 isolated therefrom;
4 (ii) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a
6 treated cell or mammal with the level of gene expression of the polynucleotide in a control
7 cell or mammal, wherein a test compound that modulates the level of expression of the
8 polynucleotide is a candidate for the treatment of lung cancer.

1 48. The assay of claim 47, wherein the control is a mammal with lung
2 cancer or a cell therefrom that has not been treated with the test compound.

1 49. The assay of claim 47, wherein the control is a normal cell or mammal.

1 50. A method for treating a mammal having lung cancer comprising
2 administering a compound identified by the assay of claim 47.

1 51. A pharmaceutical composition for treating a mammal having lung
2 cancer, the composition comprising a compound identified by the assay of claim 47 and a
3 physiologically acceptable excipient.

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— of inventorship (Rule 4.17(iv)) for US only

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

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(57) Abstract:



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PATENT COOPERATION TREATY

PCT

DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a), Rule 13ter.1(c) and 39)

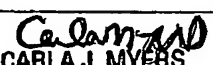
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Applicant EOS BIOTECHNOLOGY, INC		

This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
 - a. ☐ scientific theories.
 - b. ☐ mathematical theories
 - c. ☐ plant varieties.
 - d. ☐ animal varieties.
 - e. ☐ essential biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
 - f. ☐ schemes, rules or methods of doing business.
 - g. ☐ schemes, rules or methods of performing purely mental acts.
 - h. ☐ schemes, rules or methods of playing games.
 - i. ☐ methods for treatment of the human body by surgery or therapy.
 - j. ☐ methods for treatment of the animal body by surgery or therapy.
 - k. ☐ diagnostic methods practised on the human or animal body.
 - l. ☐ mere presentations of information.
 - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.
2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:

☐ the description
☐ the claims
☐ the drawings
3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions prevents a meaningful search from being carried out:

☐ the written form has not been furnished or does not comply with the standard.
☒ the computer readable form has not been furnished or does not comply with the standard.
4. Further comments:

Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US Commissioner for Patents P.O. Box 1450 Alexandria, Virginia 22313-1450 Facsimile No. (703)305-3230	Authorized officer <div style="text-align: center;">  CARLA J. MYERS PRIMARY EXAMINER </div> Telephone No. 703-308-0196
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PATENT COOPERATION TREATY

From the INTERNATIONAL SEARCHING AUTHORITY

To:
TOWNSEND AND TOWNSEND AND CREW LLP
TWO EMBARCADERO CENTER
EIGHTH FLOOR
SAN FRANCISCO, CA 94111-3834

PCT

NOTIFICATION OF TRANSMITTAL OF
THE INTERNATIONAL SEARCH REPORT
OR THE DECLARATION

(PCT Rule 44.1)

Applicant's or agent's file reference 18501-15-3PC	Date of Mailing (day/month/year) 15 AUG 2003
International application No. PCT/US02/12476	International filing date (day/month/year) 18 April 2002 (18.04.2002)
Applicant EOS BIOTECHNOLOGY, INC	

1. ☐ The applicant is hereby notified that the international search report has been established and is transmitted herewith.

Filing of amendments and statement under Article 19:

The applicant is entitled, if he so wishes, to amend the claims of the international application (see Rule 46):

When? The time limit for filing such amendments is normally two months from the date of transmittal of the international search report.

Where? Directly to the International Bureau of WIPO, 34, chemin des Colombettes
1211 Geneva 20, Switzerland, Facsimile No.: (41-22) 740.14.35

For more detailed instructions, see the notes on the accompanying sheet.

2. ☒ The applicant is hereby notified that no international search report will be established and that the declaration under Article 17(2)(a) to that effect is transmitted herewith.

3. ☐ With regard to the protest against payment of (an) additional fee(s) under Rule 40.2, the applicant is notified that:

☐ the protest together with the decision thereon has been transmitted to the International Bureau together with the applicant's request to forward the texts of both the protest and the decision thereon to the designated Offices.

☐ no decision has been made yet on the protest; the applicant will be notified as soon as a decision is made.

4. Reminders

Shortly after 18 months from the priority date, the international application will be published by the International Bureau. If the applicant wishes to avoid or postpone publication, a notice of withdrawal of the international application, or of the priority claim, must reach the International Bureau as provided in Rules 90 bis.1 and 90 bis.3, respectively, before the completion of the technical preparations for international publication.

Within 19 months from the priority date, but only in respect of some designated Offices, a demand for international preliminary examination must be filed if the applicant wishes to postpone the entry into the national phase until 30 months from the priority date (in some Offices even later); otherwise the applicant must, within 20 months from the priority date, perform the prescribed acts for entry into the national phase before those designated Offices.

In respect of other designated Offices, the time limit of 30 months (or later) will apply even if no demand is filed within 19 months.

See the Annex to Form PCT/IB/301 and, for details about the applicable time limits, Office by Office, see the *PCT Applicant's Guide*, Volume II, National Chapters and the WIPO Internet site.

Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US Commissioner for Patents P.O. Box 1450 Alexandria, Virginia 22313-1450 Facsimile No. (703)305-3230	Authorized officer <i>Valerie Bell-Harris</i> Carla Myers Telephone No. 703-308-0196
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Form PCT/ISA/220 (April 2002)

(See notes on accompanying sheet)